

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 20, 2005, 19:09:59 ; Search time 10473 Seconds
(without alignments)
13400.455 Million cell updates/sec

Title: US-10-614-524-1
Perfect score: 3687
Sequence: 1 ttgacttcaaataggaaaaa.....tactccttatggagggaatag 3687

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: gb_est1.*
2: gb_est2.*
3: gb_hc.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gss1.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	1.7	880	8	AZ669474
2	59	1.6	908	8	AZ548467
3	57.4	1.6	843	8	AZ551618
4	55.8	1.5	748	9	BX137558
5	55.2	1.5	931	8	BH160272
6	52.8	1.4	1101	9	CNS0039G
7	52.4	1.4	877	8	AZ531291
8	52	1.4	849	8	AZ546009
9	51.8	1.4	886	5	BX422107
10	51.8	1.4	1101	9	CNS00EVL
11	51.2	1.4	900	8	AZ549980
12	51	1.4	1101	9	CNS00EMH
13	51	1.4	1337	9	AG280055
14	50.6	1.4	912	8	AZ551092
15	50.2	1.4	467	4	BM163521
16	49.8	1.4	1253	9	AG289789
17	48.8	1.3	1064	4	BM416119
18	48.6	1.3	890	8	AZ530768
19	48.4	1.3	543	4	BI397189
20	48.4	1.3	905	8	AZ550256
21	48.4	1.3	1101	9	CNS0106X
22	47.6	1.3	828	8	AZ669217
23	47.6	1.3	906	8	AZ529180
24	47.6	1.3	939	8	AZ540454

25	47.6	1.3	1101	9	CNS0100X
26	47.4	1.3	654	4	BM164708
27	47.4	1.3	997	9	CNS005TE
28	47	1.3	811	4	BJ403374
29	47	1.3	976	8	BH149983
30	46.8	1.3	531	4	BJ363051
31	46.8	1.3	568	4	BJ363776
32	46.8	1.3	582	4	BJ366397
33	46.8	1.3	782	9	AG444032
34	46.8	1.3	1101	9	CNS0026Z
35	46.8	1.3	1307	9	AG347197
36	46.6	1.3	537	5	BU498625
37	46.6	1.3	548	4	BI670654
38	46.6	1.3	556	4	BI814240
39	46.6	1.3	585	5	BU496406
40	46.6	1.3	921	8	BH149893
41	46.4	1.3	680	4	BJ384484
42	46.4	1.3	683	4	BJ386441
43	46.4	1.3	826	4	BJ383101
44	46.4	1.3	875	8	AZ671853
45	46.2	1.3	609	4	BJ444006

ALIGNMENTS

RESULT 1
AZ669474
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AZ669474
ENTY188TR Entamoeba histolytica Sheared DNA
genomic, genomic survey sequence.
GSS.
GSS.
Entamoeba histolytica
Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 880)
Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HM1:IMSS sheared DNA library
Unpublished (2000)
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjlftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
DNA library
Seq primer: M13-Reverse
Class: shotgun
High quality sequence start: 22
High quality sequence stop: 853.
Location/Qualifiers
1..880
/organism="Entamoeba histolytica"
/mol_type="genomic DNA"
/strain="HM1:IMSS"
/db_xref="taxon:5759"
/notes="Vector: pHO81; Site 1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, I.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome

[illegible]

and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

```

FEATURES             source
  Location/Qualifiers
    1..1101
      /organism="Drosophila melanogaster"
      /mol_type="genomic DNA"
      /db_xref="taxon:7227"
      /clone="BACR08K10"
      /clone_lib="RpCI-98"
      /note="end : TET3"

ORIGIN
Query Match      1.4%; Score 52.8; DB 9; Length 1101;
Best Local Similarity 15.7%; Pred. No. 0.052;
Matches 99; Conservative 264; Mismatches 269; Indels 0; Gaps 0;

QY 1601 GAACCTAACGTTAATGCTAGTACTAGTATGGTCTTAATTTTAATAATACATCATC 1660
DB 1095 GDDTWRDTRKDDWTKWTTWKDRADRRWAGDADRWADGAGTWTATWMMWWWW 1036
QY 1661 AGCGGTATCGGTGAGAGTTCGTTATCTCTCAACAACTGCTCCTGAGGTAAC 1720
DB 1035 ATWDTWDDKWWWATAKTATFTATWRTAWRADWAGDRGKDRDAATDADGAGRDG 976
QY 1721 TCGGAGGAGTACTACTTTTTCATCAAGGATTCCTAGTACTAGTGCAGAAATGAGTCTT 1780
DB 975 GRKRDKKRKGDDDKGKKKKAACAAKAWATKWDWDDWDDWKGWKGAKRDKADDDG 916
QY 1781 TGACATCTCAATCATTTAGATTGTCAGAAATTTCTGTAGTATTTAGTGCATCGGCAGTC 1840
DB 915 AGDKDDGKGDADDDTDDGDKDDDKDWDKAKGTWGDATWMAAATDWWMMGWADAD 856
QY 1841 AAACCTGCTGAATAAGTATAAGTAATAATGACAGTACAGCAACGTTTCACTTTGATAAAA 1900
DB 855 WWTWDAADDDWADDDRDWADWAWKDDDAWANGARTADRRDWDGKGGARKRDRKRD 796
QY 1901 TTGAATTCATTCACATCTGCAACCTTCGAAGCAGAAATACGATTTAGAAAGGCGCAAG 1960
DB 795 DKRDAADRDADAATTTTWTDTTDDWKWKTDTWTRWAADRTWDRDDDDDRDRAGTAG 736
QY 1961 AGCGGTGAATGCTCTCTTTACTAATACGAATCAAGAAATGAAACAGATGTGACAG 2020
DB 735 RKWRRTWKRRKRRDTRWDADADDTARDRRRRGDDGADAGKGTGKRRRRDRATWD 676
QY 2021 ATTATCATATTGATCAAGTATCAATTTAGTGGGTCTTTATCGGATGATTCGCTTAG 2080
DB 675 RTDAWMAAATAWTTTDTDDDKDRRRRKGAARRRRRTTARAADWMMWKAADWAKWMDWK 616
QY 2081 ATGAAAGAGAGAAATTAATGAGAAAGTGAATATGCAAAACGACTCAGTGTGAAAGAA 2140
DB 615 TRADRWDAADTWTWDARKADRWAKARAWRRDRARARADRRWTGKTTTATWTTW 556
QY 2141 ACTTATCCCAAGATCCAAATTCACATCCATCAATAAGCAACGAGCTTCATATCTACTA 2200
DB 555 AARAAWMAWAWATTTATTTTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWT 496
QY 2201 ATGAGCAATCGAATTCACATCTATCCATCA 2232
DB 495 AAWAAAAAATAATTTTTTTTTTTTWTWATAA 464

```

```

RESULT 7
LOCUS AZ531291/c
DEFINITION ENTB034TR Entamoeba histolytica Sheared DNA Entamoeba histolytica genomic, genomic survey sequence.
ACCESSION AZ531291
VERSION AZ531291.1 GI:11085838
KEYWORDS GSS.
SOURCE Entamoeba histolytica
ORGANISM Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.

```

```

REFERENCE
AUTHORS Loftus, B., Van Aken, S. and Fraser, C.
TITLE Determination of clone end sequences from Entamoeba histolytica
JOURNAL HM1:IMSS sheared DNA library
COMMENT Unpublished (2000)
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjlftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared DNA library
Seq primer: M13-Reverse
Class: shotgun
High quality sequence start: 22
High quality sequence stop: 829.
Location/Qualifiers
  1..877
    /organism="Entamoeba histolytica"
    /mol_type="genomic DNA"
    /strain="HM1:IMSS"
    /db_xref="taxon:5759"
    /clone_lib="Entamoeba histolytica Sheared DNA"
    /notes="Vector: pHO51; Site 1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999)."
```

ORIGIN

```

Query Match      1.4%; Score 52.4; DB 8; Length 877;
Best Local Similarity 48.0%; Pred. No. 0.062;
Matches 189; Conservative 0; Mismatches 196; Indels 9; Gaps 1;

QY 3257 AAGAGGATGATGAGAGGGTTGTGTAACGATCCATCAATGAAATACGAGCAATACAGACGAAC 3316
DB 451 AAGAAGAAGATGAAGAAGATGATGAAGAAGATGATGAAGAAGATGATGAAGAAGAAG 392
QY 3317 TAAATTTTAAAACTGTGAAGAAGAGAGTGTATCCACGGATACAGGAACTGTTAATG 3376
DB 391 ATGATGATGAAGATGATGAAGACGATGAAGACGAAATATGAATTAGAAGATGATGATG 332
QY 3377 ATTATCTGCACACCAAGGTACAGCATGTATTCCTCGGTATGCTGGATATGAGATG 3436
DB 331 AAGAAGAAGATGATGATGAAGAAGAAGATGATGATGAAGAAGATGATGAAGAAG 272
QY 3437 CATATGAAGTTGATCTACAGCATCTGTTAATTTACAAACCGACTTATGAAGAAGAAACGT 3496
DB 271 AAGATGAAGATGATGATGAAGAAGATGAAGA-----TGATGAAGAAGAAG 221
QY 3497 ATACAGATGACGAAGAGATAATCATTTGTGAATATGACAGAGGGTATGTGAATATCCAC 3556
DB 220 ATGATGATGAAGAAGAAGATGAAGAAGAAGATGATGAAGAAGATGATGAAGAAGAAG 161
QY 3557 CACTACCGCTGGTTATATGACAAAGAAATAGAACTTCCAGAAACCGATAAGTAT 3616
DB 160 AAGATGATGATGAAGACGACGAATATGAATTAGAAGATGATGAAGAAGATGATGAAGAAG 101
QY 3617 GGATTCGATTTGGAGAAACCGAAGGGAAGTTTAT 3650
DB 100 ATGATGAAGAAGATGATGAAGAAGAAGAT 67

```

D	b		494	TGATGAAGATGAAGAAGATGATGATGATGAAGAAGACGAAGAAGATGATGATGATGA	435
Q	y		3108	ATTAGCATGCTGGAATGTAAAGGGCGATGTAGATGTACAACAGAGCCATCACCGTTTCTGT	3167
D	b		434	ATTGTAATTAGAAGATGAAGAAGATGAAGAAGATGAAGAAGATGATGATGATGATGA	375
Q	y		3168	CCTTGTTATCCCAGANTGGGAAGCAGAAGTGTCAAGCAGTTTCGGCTCTGTCGGGGCG	3227
D	b		374	AGATGATGAAGATGATCAAGATGATGAAGATGATGAAGATGATGAAGATGATGAAGATGA	315
Q	y		3228	TGCCTATATCTCTCGTGCACAGCGTACAAGAAGGGCATGGAGAGGGTGTGTGAACGAT	3287
D	b		314	TGATGATGATGAAGAAGATGAAGAAGATGATGATGATGATGATGATGATGATGATGATGA	255
Q	y		3288	CCATGAAATTCGAAACAATACACAGCAACTATAAATTTAAAACTGTCAAGAAGAGGAAGT	3347
D	b		254	AGAAGATGAAGATGATGATGAAGACGAAGAAGATGATGATGATGATGATGATGATGATGA	195
Q	y		3348	GTAATCAACGGATPACAGGAACGTGTAATGATTATATCTGCACACCAGGTACACGATATG	3407
D	b		194	AGATGAAGATGAAGATGAAGATGAAGAAGATGAAGATGATGAAGAAGACGAAGAAGA	135
Q	y		3408	TAATTCCTGTAATCGTGTATGAGATGCATATGAAGTTGATGATGATGATGATGATGATGAT	3467
D	b		134	AGATGATGATGAAGATGAAGAAGATGATGATGATGATGATGATGATGATGATGATGATGA	75
Q	y		3468	TTACAAACCGACTTATGAAGAAGA	3491
D	b		74	TGACGAAGATGTTGATGAAGATGA	51

RESULT 9
BX422107
LOCUS
DEFINITION BX422107 Homo sapiens T CELLS (JURKAT CELL LINE) Homo sapiens cDNA clone CS0DH007YD10 3-PRIME, mRNA sequence.
ACCESSION BX422107
VERSION BX422107.2 GI:46930727
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 886)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Pollayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 13, 2003 this sequence version replaced gi:30651307.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.

This sequence belongs to sequence cluster 3628.r
For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?CS=CS0DH007YD10&WP1&c=3628.r>.
Location/Qualifiers
1. .886
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DH007YD10"
 /tissue type="T CELLS (JURKAT CELL LINE)"
 /cell_line="JURKAT CELL LINE"
 /clone lib="Homo sapiens T CELLS (JURKAT CELL LINE)"
 /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector."

FEATURES
source

Tel: 301 838 0208
 Fax: 301 838 3543
 Email: bilofus@igrr.org
 Clones are derived from the Entamoeba histolytica HM1:IMSS sheared DNA library
 Seq primer: M13-Forward
 Class: shotgun
 High quality sequence start: 20
 High quality sequence stop: 890.
 Location/Qualifiers
 source
 1. 900
 /organism="Entamoeba histolytica"
 /mol_type="genomic DNA"
 /strain="HM1:IMSS"
 /db_xref="taxon:5759"
 /clone_lib="Entamoeba histolytica Sheared DNA"
 /notes="Vector: pBOS1; Site 1: Bst I; Constructed at The Institute for Genomic Research (IGRR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999)."

FEATURES

source

ORIGIN

Query Match 1.4%; Score 51.2; DB 8; Length 900;
 Best Local Similarity 48.0%; Pred. No. 0.13;
 Matches 146; Conservative 0; Mismatches 158; Indels 0; Gaps 0;

QY 3290 ATGAATCGAGAACAAATACAGCAACTAAATTTAAAACTGTGGAAGAGAGAAAGTGT 3349
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 323 ATGAAGATGATGAAGATGATGAAGATGATGAAGATGATGAAGATGATGAAGATGAAG 382
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 3350 ATCCACCGATACAGGACGTGTAATGATATATCTGCACACCGAGGTACGACGATGTGA 3409
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 383 ATGATGAAGATGATGAAGATGATGAAGATGATGAAGATGATGAAGATGATGAAGATG 442
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 3410 ATTCCCCTAATGCTGGATATGAGATGCATATGAAGTTGATCTACAGCATCTGTTAATT 3469
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 443 AAGAAGATGAAGATGAAGATGATGAAGATGATGAAGATGATGAAGATGATGAAGATG 502
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 3470 ACAACCGATTATGAAGAGAAACGTTATACAGATGTACGAAGAGATAATCATTTGTAAT 3529
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 503 ATGAAGATGATGAAGATGATGAAGATGATGAAGATGATGAAGATGATGAAGATGATGAAG 562
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 3530 ATGACAGGGTATGTAATTTCCACCCTACCGCTGGTTATATGACAAAAGATTAG 3589
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 563 ATGATGAAGATGATGAAGATGATGAAGATGATGAAGATGATGAAGATGATGAAGATG 622
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 3590 AATA 3593
 |||||
 Db 623 AAGA 626
 |||||

RESULT 12

CNS00EMH/c

LOCUS

DEFINITION

Drosophila melanogaster genome survey sequence T7 end of BAC:

BACR29M06 of RP11-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

AL069378.1

GI:4949521

GSS.

KEYWORDS

SOURCE

ORGANISM

Drosophila melanogaster (fruit fly)

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1101)

Genoscope.

Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila

melanogaster genome using these BACs. For further information

please see <http://www.fruitfly.org> The BDGP Drosophila

melanogaster BAC library was prepared by Kazutoyo Osoegawa and

Aaron Mamoser in Pieter de Jong's laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,

NY. The library is named RP11-98 and was constructed by partial

EcoRI digestion of Drosophila DNA provided by the BDGP from the

isogenic strain Y2; cn bw sp, the same strain used for the BDGP's

P1 and EST libraries. A more detailed description of the library

and how to order individual BAC clones, the entire library, or

filters for hybridization from the BACPAC Resource Center can be

found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

Location/Qualifiers

1. 1101

/organism="Drosophila melanogaster"

/mol_type="genomic DNA"

/db_xref="taxon:7227"

/clone="BACR29M06"

/clone_lib="RP11-98"

/notes="end : T7"

ORIGIN

Query Match 1.4%; Score 51; DB 9; Length 1101;
 Best Local Similarity 32.0%; Pred. No. 0.15;
 Matches 102; Conservative 69; Mismatches 148; Indels 0; Gaps 0;

QY 2681 GCGTGTGGGTGATTAACAGATTAAAGACGAGGAGGTCTATGCAAGACTAGGAAATCTGG 2740
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 932 GCGTGTGAGKAGGATKTKDWTAKAWDTRWTAWAAWATAATATATGATDAATAWTGTGG 873
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 2741 AATTATTAGAGAAACCATTAATTAGGAGAGACCTGCTCTGTTGGAAGAGCAGAGA 2800
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 872 AKTGATGAGDARDRARARAAKTKTGATGATWKAKAKAKAWKKKATGTGKAGATRTD 813
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 2801 AAAAAATGAGAGACAAACGTGAAAAAATACTCAATTGGAACAAACGAGTATATACAGAG 2860
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 812 AGAKAGAGTREGWAGTATATKATRAARADAGATATAAGGDRATRKARRAKATETAGRA 753
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 2861 CAAAAGAGCTGTGGATGCTTTATTTTGTAGATTCTCAATATATAGATTACAAGCGGATA 2920
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 752 KRWAAKAWKAWGAGTGWKAWAKATGTGWTATTTKAKWRKARKRWGTAKATDTGAAAAA 693
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 2921 CAAACATTCGATGATTCATCGGAGATAACTTTGTTTATCGAATTCGAGAGCTTATC 2980
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 692 AARTAAAGAGATRTTRRKRWKAWAWATATAAGTCGWTAGAAAAAAGAAAGTGTGTG 633
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 2981 TGTCAGAATTATCTGTTAT 2999
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 632 TDGGGKKRDKRTDGGWGT 614
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 13

AG280055/c

LOCUS

DEFINITION

Mus musculus molossinus DNA, clone:MSMg01-051D13.T7, genomic survey

sequence.

AG280055

GI:47852932

GSS.

KEYWORDS

SOURCE

ORGANISM

Mus musculus molossinus

Mus musculus molossinus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

REFERENCE
AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE BAC end Sequences of Library MSMg01
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 1337)
Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@gsc.riken.jp URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111 Fax:81-45-503-9170)
COMMENT Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : T7
LIBRARY
Vector : pBACE3.6
R.Site 1 : EcoRI.
R.Site 2 : EcoRI.
FEATURES             source
source               Location/Qualifiers
1..1337
    /organism="Mus musculus molossinus"
    /mol_type="genomic DNA"
    /sub_species="molossinus"
    /db_xref="taxon:57486"
    /clone="MSMg01-051D13.T7"
    /sex="male"
    /tissue type="mixture of kidney and spleen"
    /clone_lib="MSMg01 Mouse Male BAC Library"
ORIGIN
Query Match      1.4%; Score 51; DB 9; Length 1337;
Best Local Similarity 49.4%; Pred. No. 0.16;
Matches 133; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

QY   3252 GTCAAAAGAGGGATATCGAGAGGTGTGTGAACGATCGTGAATCGAGAACAATACAGA 3311
Db   1109 GAAAAAAGAAAGAACAGGAGGAATAAAGAAAAGAAAGAAATTAAGAAAAGAGGAA 1050
QY   3312 CGAACTAAAAATTAAAAAACGTGTGAAGAGAGGAGTAGTGATCCACGCATACAGCAACGTG 3371
Db   1049 AAGAAGAAAAGAAAGAAAAGAAAAGAAAGAAAGAAAGAGAGAGATGGAAGAAAAGACAGA 990
QY   3372 TAATGATTACTGTCACACCAAGGTACAGCAGATGTGTAATTCCCGTTAATCTGCGATATGA 3431
Db   989 ACAAGGAGAAAAGAAAAGNAGAAAANAATAAGAAAAGGGAATAAAGATAAAAAAGA 930
QY   3432 GGATGCNATGAAGTTGATCTACAGCATCTGTTTAATTACAAACCGACTTATGAAGAAGA 3491
Db   929 GAAAAGAAAATATAGAAAAGAAAAGAAAAGAAATTAATATAAGAAAAGAAAAGAAAAAAA 870
QY   3492 AACGTATACAGATGTCAGAGAGATAA 3518
Db   869 AATATATAAAAAAAGAGGAAAAAGAA 843

RESULT 14
AZ551092
LOCUS ENTJ22TF Entamoeba histolytica Sheared DNA linear GSS 14-NOV-2000
DEFINITION genomic, genomic survey sequence.
ACCESSION AZ551092
VERSION AZ551092.1 GI:11176393
KEYWORDS GSS.
SOURCE Entamoeba histolytica
ORGANISM Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.

```

```
Db 663 GATGAAGAAGAGATGATGATGAAGAAGAAGATGATGATGAAGATGATGAA 722
QY 3487 GAAGAAACGTTATCAGATGACGAAGATATCAATTCATGTAATGACAGAGGTTATG 3546
Db 723 GAAGAAGATGAAGATGATGATGAAGAAGAAGATGAAGATGATGATGAAGAAGAAGATGAT 782
QY 3547 AATTATCCACCTACACGCTGGTTATGACAAAAGAATAGAAATATCTCCAGAAACC 3606
Db 783 GATGAAGAAGATGAAGAAGAAGATGATGAAGAAGATGATGAAGAAGAAGAT 842
QY 3607 GATAAGGTA 3615
Db 843 GATGATGAA 851
```

```
RESULT 15
BM163521
LOCUS EST566044 PyBS Plasmodium yoelii cDNA clone PYCLG23 5' end,
DEFINITION mRNA sequence.
ACCESSION BM163521
VERSION BM163521.1 GI:17309202
KEYWORDS EST.
SOURCE Plasmodium yoelii yoelii
ORGANISM Plasmodium yoelii yoelii
REFERENCE 1 (bases 1 to 467)
AUTHORS Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
Fraser, J.M., Daly, T.M., Long, C.A., Bergman, L.W., Vaidya, A.B.,
Plasmodium yoelii EST project at TIGR
Unpublished (2001)
Contact: Jane Carlton
Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-530-9319
Fax: 301-838-0208
Email: carlton@tigr.org
For clone info, please contact the Malaria Research and Reference
Reagent Resource Center, ARCC
http://www.malaria.mr4.org/mr4pages/index.html
Seq primer: ADF.
```

```
FEATURES
Source
1..467
/organism="Plasmodium yoelii yoelii"
/mol_type="mRNA"
/strain="17XL"
/sub_species="yoelii"
/db_xref="taxon:73239"
/clone="PYCLG23"
/dev_stage="Asexual blood stages"
/lab_host="E. coli XL-1 Blue"
/clone_lib="PyBS"
/note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was
collected from BALB/cBYJ mice infected with Py17XL
parasites, and leukocytes removed by passage over
microcrystalline cellulose columns. Total RNA was
isolated using the guanidium isothiocyanate method, and
mRNA isolated using oligo(dT)-cellulose chromatography.
First strand cDNA synthesis was completed using a 50-base
primer and reverse transcriptase in the presence of
5-methyl dCTP. After second strand synthesis, uneven
termini were treated with Pfu DNA polymerase and EcoRI
adaptors ligated to the blunt ends. The sample was cleaved
with XhoI and separated on a Sephacryl S-500 column.
Size-fractionated cDNA was precipitated and ligated to
HybridZAP arms directionally using EcoRI-XhoI cleaved arms.
After packaging, the phagemid vector (pAD-GAL4) was
excised from the HybridZAP vector and plasmid DNA
isolated."
```

ORIGIN

```
Query Match 1.4%; Score 50.2; DB 4; Length 467;
Best Local Similarity 48.7%; Pred. No. 0.2;
Matches 136; Conservative 0; Mismatches 143; Indels 0; Gaps 0;
QY 3290 ATGAAATCGAACAATACAGACGACTAAATTTTAAACCTGTGAAGAAGAGGAGTCT 3349
Db 189 ATGAAATAGAAATGAAATATGAAATAGAAATGAAATATGAAATGCGGATGAAA 248
QY 3350 ATCCAAACGGATACAGGAACGTGTAATGATTATCTGACACCAAGGTACAGCAGTATGTA 3409
Db 249 TAGAAATGAAATATGAAAGGCGATGAATAGAAATATGAAATAGAAAG 308
QY 3410 ATTCCCGTAAATGCTGATGATGAGGATGCATATGAAGTTGATCTACAGCATCTGTTAAT 3469
Db 309 ATGAAATATGAAATAGAAATGAAATATGAAATAGAAATGAAATATGAAATAG 368
QY 3470 ACNAACCGACTTATGAAGAAGAAACGTATACAGATGTACGAAGAGATAATCATTTGTGAAT 3529
Db 369 AAGATAAAATATGAAATAGAAATGAAATATGAAATATGAAATAGAAATGAAATAGACG 428
QY 3530 ATGACACAGAGGATGTGAATTTATCCACCACCTACCAGCTG 3568
Db 429 ATGAAAGAAGATGAAAGAGATGAAGATGAAGATG 467
```

Search completed: April 21, 2005, 03:27:07
Job time : 10478 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 21, 2005, 03:27:14 ; Search time 54 Seconds
(without alignments)
2188.040 Million cell updates/sec

Title: US-10-614-524-2
Perfect score: 6479
Sequence: 1 LTSNRKNEIINALSIPAV.....IGTEGKFVDSVELLMEE 1228

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5745	88.7	1228	S00873	parasporal crystal
2	3791	58.5	1176	A48970	parasporal crystal
3	3484.5	53.8	1189	S00944	parasporal crystal
4	3433.5	53.0	1165	S11446	parasporal crystal
5	3433	53.0	1166	S32645	parasporal crystal
6	3426.5	52.9	1181	A41052	parasporal crystal
7	3421	52.8	1171	A40572	parasporal crystal
8	3413.5	52.7	1174	S32649	parasporal crystal
9	3413.5	52.7	1176	J70241	parasporal crystal
10	3412.5	52.7	1174	A42459	parasporal crystal
11	3411	52.6	1160	S32647	parasporal crystal
12	3405.5	52.6	1176	JC2219	parasporal crystal
13	3400.5	52.5	1176	S02215	parasporal crystal
14	3399.5	52.5	1176	A22617	parasporal crystal
15	3399.5	52.5	1178	USBSKH	parasporal crystal
16	3399	52.5	1171	A37829	parasporal crystal
17	3387	52.3	1177	A49785	parasporal crystal
18	3323.5	51.3	1172	S32689	parasporal crystal
19	3283	50.7	1155	JD0002	parasporal crystal
20	3269	50.5	1155	A26513	parasporal crystal
21	3268	50.4	1155	S02134	parasporal crystal
22	3257.5	50.3	1156	A29125	parasporal crystal
23	3251	50.2	1155	I39838	parasporal crystal
24	3161.5	48.8	1156	A29838	parasporal crystal
25	2434	37.6	934	A22798	parasporal crystal
26	2294.5	35.4	1138	A48944	parasporal crystal
27	2200.5	34.0	1157	I549247	parasporal crystal
28	2170.5	33.5	719	I2140590	cryV465 protein -
29	2116	32.7	719	I39815	insecticidal prote

30	2107	32.5	719	2	S25383	parasporal crystal
31	2101	32.4	719	2	I39814	insecticidal prote
32	2002	30.9	1160	2	I40589	parasporal crystal
33	1947.5	30.1	1154	2	S39536	parasporal crystal
34	1930	29.8	823	2	S04181	parasporal crystal
35	1621	25.0	1156	2	S19306	parasporal crystal
36	1616.5	24.9	1136	1	USBS81	parasporal crystal
37	1511.5	23.3	1180	2	I39870	parasporal crystal
38	1498.5	23.1	1180	2	A26858	parasporal crystal
39	1227	18.9	380	2	B42459	hypothetical prote
40	1164	18.0	655	2	JC7140	protoxin - Bacillu
41	1064	16.4	652	2	A27323	parasporal crystal
42	1062.5	16.4	659	2	S10228	parasporal crystal
43	1053.5	16.3	652	2	I39811	parasporal crystal
44	999.5	15.4	649	1	JH0261	parasporal crystal
45	987.5	15.2	618	2	S11445	parasporal crystal

ALIGNMENTS

RESULT 1

S00873
N:Alternate names: Parasporal crystal protein cryA4
C:Species: Bacillus thuringiensis subsp. thuringiensis
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C:Accession: S00873
R:Brizzard, B.L.; Whiteley, H.R.
Nucleic Acids Res. 16, 2723-2724, 1988
A:Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus t
A:Reference number: S00873; MUID:88203216; PMID:3362680
A:Accession: S00873
A:Molecule type: DNA
A:Residues: 1-1228 <BRI>
A:Cross-references: UNIPROT:P05517; EMBL:X06711; NID:g40264; PIDN:CAA29898.1; PID:g58094;
C:Genetics:
A:Gene: cryA4
A:Start codon: TTG
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 88.7%; Score 5745; DB 2; Length 1228;

Best Local Similarity 89.1%; Pred. No. 0;

Matches 1098; Conservative 35; Mismatches 90; Indels 10; Gaps 3;

QY	1	LTSNRKNEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVOTGI	60
DB	1	MTSNRKNEIIN-----AVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVOTGI	55
QY	61	NIAGRILGLGVFPFAGQIASFYSLVGEIWPGRDOWEIFLEHVEQLINQOITENARNTA	120
DB	56	NIAGRILGLGVFPFAGQIASFYSLVGEIWPGRDOWEIFLEHVEQLINQOITENARNTA	115
QY	121	LARLQGLGDSFRAYQOSLEWLENRDDARTSRVLYTOYIALELDFLNAPLFAIRNOEVP	180
DB	116	LARLQGLGDSFRAYQOSLEWLENRDDARTSRVLYTOYIALELDFLNAPLFAIRNOEVP	175
QY	181	LLMVYQAANLHLLLRDASLFGSEGLTSQETQRYVEROVEQTRDSDYCVEMWNTGLN	240
DB	176	LLMVYQAANLHLLLRDASLFGSEGLTSQETQRYVEROVEQTRDSDYCVEMWNTGLN	235
QY	241	SLRGTNAASVRYNQFRDLTLGLVDLVALFPSYDTRTPINTSAQLTREYITDAIGATG	300
DB	236	SLRGTNAASVRYNQFRDLTLGLVDLVALFPSYDTRTPINTSAQLTREYITDAIGATG	295
QY	301	VNMASMNWYNNAPSAIAETAVIRSPHLLDFLEQLTFTSTSSWSATRMTYWRGHTIQ	360
DB	296	VNMASMNWYNNAPSAIAETAVIRSPHLLDFLEQLTFTSTSSWSATRMTYWRGHTIQ	355
QY	361	SRPIGGGLNTSTHGSTNTSINPVRLSPFSDRVYVWTSYAGVLLWGIYLEPHGVPTVREN	420
DB	356	SRPIGGGLNTSTHGATNTSINPVTLRFASRDVYVWTSYAGVLLWGIYLEPHGVPTVRFN	415

QY 421 FRNPONTFERGTANYSPQYBSPGLQKDSLETLPETTERPNVSYSHRSLHIGLISQSR 480
 Db 416 FTNPQNSDRGTANYSPQYBSPGLQKDSLETLPETTERPNVSYSHRSLHIGLISQSR 475
 QY 481 VHPVYVSWTHRSADRTNTISDSITQIPLVKSFNLNSGTSVSGPGTGGDIIRTNVNGS 540
 Db 476 VNPVYVSWTHRSADRTNTIGPNRITQIPMKASLPGTIVVRGPGTGGDILLRNTTGG 535
 QY 541 VLSGLNPNNTSQRVRYRYAASQTMVLRTVTVGGSTTFDQGPSTMSANESLTSQSR 600
 Db 536 FGIIRTVNGLTQRYRIGRYASTVDFDFVSRGGTIVNFRFLRTMNSGDELKYGNFV 595
 QY 601 FAFEPVIGSAGSG--TAGISISNAGQTFHFKIEPIPTATFEAYDYDLERAQEAVAL 659
 Db 596 RRAFTPTFTTQDIIRTSIQGLSGNGEYIYDIEIIPVATFEAYDYDLERAQEAVAL 655
 QY 660 FTNTPRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELEKVKYAKRLSDERNLLQDP 719
 Db 656 FTNTPRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELEKVKYAKRLSDERNLLQDP 715
 QY 720 NFTSINKQDPFISTNEOSNFTSIHQSEHGWSGSENIITIOEGNDVFKENYVTLPGTFNEC 779
 Db 716 NFTSINKQDPFISTNEOSNFTSIHQSEHGWSGSENIITIOEGNDVFKENYVTLPGTFNEC 775
 QY 780 YPTLYQKIGESLKVATRYQLRGYIEDSDQLLEIYLRYNKAKHETLDVPGTESVMPLSVE 839
 Db 776 YPTLYQKIGESLKVATRYQLRGYIEDSDQLLEIYLRYNKAKHETLDVPGTESVMPLSVE 835
 QY 840 SPIGRGCEPNRCAPHFENWPDLCSDRGKCAHSHHFSLDIDIGCTDLHENLGVWVVF 899
 Db 836 SPIGRGCEPNRCAPHFENWPDLCSDRGKCAHSHHFSLDIDIGCTDLHENLGVWVVF 895
 QY 900 KIKTOEGHARLGNLEFIEEPLGEGALSRVKRAEKKWRDKREKLOLETKRVYVTEAKEVD 959
 Db 896 KIKTOEGHARLGNLEFIEEPLGEGALSRVKRAEKKWRDKREKLOLETKRVYVTEAKEVD 955
 QY 960 ALFVDSQYNRLQADTNIGMHAADKLVRIRREAYLSLSVPGVNAEIPFEEGRITAI 1019
 Db 956 ALFVDSQYNRLQADTNIGMHAADKLVRIRREAYLSLSVPGVNAEIPFEEGRITAI 1015
 QY 1020 SLYDARNVVKNGDFNGLACNVNKGHVDVQOSSHRSVLVPIPEWAEVQAVRVCPCGYI 1079
 Db 1016 SLYDARNVVKNGDFNGLTCWNVKGHVDVQOSSHRSVLVPIPEWAEVQAVRVCPCGYI 1075
 QY 1080 LRVYAYKEGEGCVTHETENNTDELKPKNCEEEVYPTDGTCDNYTAHQGTA---V 1135
 Db 1076 LRVYAYKEGEGCVTHETENNTDELKPKNCEEEVYPTDGTCDNYTAHQGTA---V 1135
 QY 1136 CENRAGYEDAYEVDTTASVNYKPTVEEYTDVRRDNHCEYDRGVYVNPPLPAGYMTKE 1195
 Db 1136 CENRAGYEDAYEVDTTASVNYKPTVEEYTDVRRDNHCEYDRGVYVNPPLPAGYMTKE 1195
 QY 1196 LEYFPETDKVIBIGETEGKFIVDSEVLLMEE 1228
 Db 1196 LEYFPETDKVIBIGETEGKFIVDSEVLLMEE 1228

RESULT 2
 A:Experimental source: subsp. gallieriae HD29
 A:Note: sequence extracted from NCBI backbone (NCBI:129672, NCBI:129675)
 C:Superfamily: parasporal crystal protein
 C;Keywords: delta-endotoxin

Query Match 58.5%; Score 3791; DB 2; Length 1176;
 Best Local Similarity 62.3%; Pred. No. 3.9e-233;
 Matches 762; Conservative 125; Mismatches 241; Indels 96; Gaps 16;

QY 40 CIAEGNNINPLVSAVTVQIG---INTAGRLGLV---GVPPAQIASFVSFLVGLGLWPRG 93
 Db 14 CLSNPEEI--LLDGERISTGSSIDISLSIVQLLVGNFVPGGGLVGLLDFVWGVIGVP-- 69
 QY 94 RDOMEIPLFHEVQLINQOITENARNALARLOGLGDSFRAYQOSLSDLENRDRDARTSV 153
 Db 70 -SPWDAFLVQIEQILINERIAAARSAAISNLEGLGNFNIIYEAFAKWEADPNPVRTR 128
 QY 154 LTYQYTALELDLFNANPLFAIRNOEVPLLMVYAAANLHLLLRDASLSEFGLTSQEI 213
 Db 129 VVDRFRILQGLLERDIPSPRIAGFEVPLLSVYAAANLHLLLRDSSIFGARWGLTINV 188
 QY 214 QRYERQVQTRDYSDYCVWVNTGLNSLRGTNAASWRYNQPRDLITGLVLDLVALFPS 273
 Db 189 NENYELIRHIDEYANHCADTYNRGLNLPKSTYQDWITYNRLRDLTLTLVDIAAFAFPS 248
 QY 274 YDRTYTPINTSAOLTRVYTDALGATGVMAWNNWNNAPSPAETAVIRSHLLDL 333
 Db 249 YDNRYPISQVGLTREIYTDPLTFNPQOSV---AQLTFNVMSNAIRTPHLDVL 304
 QY 334 EQTIESTSRMSATRHMTYWRGHTIQSRPIGGLNTSTHGTNTSINPVRISFFSRDYV 393
 Db 305 NNLTITFD---WFSGRNFYWGHRVYSNRIGGNTSPYIGREANQEPSPRSTFNGPVF 361
 QY 394 WTESYAGVLLWGLYLPPIHGVPTVR-----FN-----FRNTQTFE---RGT 432
 Db 362 RTLSN-----PTFRPLQPPWAPPENLRGVGEVEFSTPLNSTFYRGRGT 405
 QY 433 ANYSQPVESPGQLKDSLETLPETTERPNVSYSHRSLHIGLISQSRVHV---PVYSW 488
 Db 406 V-----DSLTELPPEDNSVPEPRGYSHRLCHATFVQSRGTPTFTTGVFSW 451
 QY 489 THRSADRTNTISDSITQIPLVKSFNLNSGTSVSGPGTGGDIIRTNVNGSVLSMGLNF 548
 Db 452 THRSADRTNTIIPDVINQIPLVKAFNLTSQTSVVRGPGTGGDIIRTNVNGSVLSMGLNF 511
 QY 549 NNTSLQRYRVRYAASQTMVLRTVTVGGSTTFDQGPSTMSANESLTSQSRFAEPVGI 608
 Db 512 SNTTLQRYRVRYAASQTMVMSVTVGGSTTGNQGFPTMSANGALTSQSRFAEPVGI 571
 QY 609 SASGQTAGISISNAGROTFFHFKIEPIPTATFEAYDYDLERAQEAVALFTNTNPRRL 668
 Db 572 SASGQTAGISISNAGROTFFHFKIEPIPTATFEAYDYDLERAQEAVALFTNTNPRRL 631
 QY 669 KTDVTDYHIDQVSNLVACLSDEFCLDEKRELEKVKYAKRLSDERNLLQDPNFTSINKQ 728
 Db 632 KTDVTDYHIDQVSNLVACLSDEFCLDEKRELEKVKYAKRLSDERNLLQDPNFTSINKQ 691
 QY 729 DFISTNEQSNFTSIHQSEHGWSGSENIITIOEGNDVFKENYVTLPGTFNECPTYLYQKI 788
 Db 692 D-----RGMWGSTDTITIQGGDDVFKENYVTLPGTFNECPTYLYQKI 733
 QY 789 GSELSKAYRYOLRGYIEDSDQLLEIYLRYNKAKHETLDVPGTESVMPLSVESPIGRGCEP 848
 Db 734 DESKLSYRYELRGYIEDSDQLLEIYLRYNKAKHETLDVPGTESVMPLSVESPIGRGCEP 793
 QY 849 NRCAPHEWNPDLDCSDRGKCAHSHHFSLDIDIGCTDLHENLGVWVVFVFKIKTQEGHA 908
 Db 794 NRCAPHEWNPDLDCSDRGKCAHSHHFSLDIDIGCTDLHENLGVWVVFVFKIKTQEGHA 853
 QY 909 RLGNEFIEKDLIGALSRLVKRAEKKWRDKREKLOLETKRVYVTEAKEVDALFVDSQYN 968
 Db 854 RLGNEFIEKDLIGALSRLVKRAEKKWRDKREKLOLETKRVYVTEAKEVDALFVDSQYN 913

A:Experimental source: subsp. gallieriae HD29
 A:Note: sequence extracted from NCBI backbone (NCBI:129672, NCBI:129675)
 C:Superfamily: parasporal crystal protein
 C;Keywords: delta-endotoxin

Query Match 58.5%; Score 3791; DB 2; Length 1176;
 Best Local Similarity 62.3%; Pred. No. 3.9e-233;
 Matches 762; Conservative 125; Mismatches 241; Indels 96; Gaps 16;

QY 421 FRNPONTFERGTANYSPQYBSPGLQKDSLETLPETTERPNVSYSHRSLHIGLISQSR 480
 Db 416 FTNPQNSDRGTANYSPQYBSPGLQKDSLETLPETTERPNVSYSHRSLHIGLISQSR 475
 QY 481 VHPVYVSWTHRSADRTNTISDSITQIPLVKSFNLNSGTSVSGPGTGGDIIRTNVNGS 540
 Db 476 VNPVYVSWTHRSADRTNTIGPNRITQIPMKASLPGTIVVRGPGTGGDILLRNTTGG 535
 QY 541 VLSGLNPNNTSQRVRYRYAASQTMVLRTVTVGGSTTFDQGPSTMSANESLTSQSR 600
 Db 536 FGIIRTVNGLTQRYRIGRYASTVDFDFVSRGGTIVNFRFLRTMNSGDELKYGNFV 595
 QY 601 FAFEPVIGSAGSG--TAGISISNAGQTFHFKIEPIPTATFEAYDYDLERAQEAVAL 659
 Db 596 RRAFTPTFTTQDIIRTSIQGLSGNGEYIYDIEIIPVATFEAYDYDLERAQEAVAL 655
 QY 660 FTNTPRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELEKVKYAKRLSDERNLLQDP 719
 Db 656 FTNTPRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELEKVKYAKRLSDERNLLQDP 715
 QY 720 NFTSINKQDPFISTNEOSNFTSIHQSEHGWSGSENIITIOEGNDVFKENYVTLPGTFNEC 779
 Db 716 NFTSINKQDPFISTNEOSNFTSIHQSEHGWSGSENIITIOEGNDVFKENYVTLPGTFNEC 775
 QY 780 YPTLYQKIGESLKVATRYQLRGYIEDSDQLLEIYLRYNKAKHETLDVPGTESVMPLSVE 839
 Db 776 YPTLYQKIGESLKVATRYQLRGYIEDSDQLLEIYLRYNKAKHETLDVPGTESVMPLSVE 835
 QY 840 SPIGRGCEPNRCAPHFENWPDLCSDRGKCAHSHHFSLDIDIGCTDLHENLGVWVVF 899
 Db 836 SPIGRGCEPNRCAPHFENWPDLCSDRGKCAHSHHFSLDIDIGCTDLHENLGVWVVF 895
 QY 900 KIKTOEGHARLGNLEFIEEPLGEGALSRVKRAEKKWRDKREKLOLETKRVYVTEAKEVD 959
 Db 896 KIKTOEGHARLGNLEFIEEPLGEGALSRVKRAEKKWRDKREKLOLETKRVYVTEAKEVD 955
 QY 960 ALFVDSQYNRLQADTNIGMHAADKLVRIRREAYLSLSVPGVNAEIPFEEGRITAI 1019
 Db 956 ALFVDSQYNRLQADTNIGMHAADKLVRIRREAYLSLSVPGVNAEIPFEEGRITAI 1015
 QY 1020 SLYDARNVVKNGDFNGLACNVNKGHVDVQOSSHRSVLVPIPEWAEVQAVRVCPCGYI 1079
 Db 1016 SLYDARNVVKNGDFNGLTCWNVKGHVDVQOSSHRSVLVPIPEWAEVQAVRVCPCGYI 1075
 QY 1080 LRVYAYKEGEGCVTHETENNTDELKPKNCEEEVYPTDGTCDNYTAHQGTA---V 1135
 Db 1076 LRVYAYKEGEGCVTHETENNTDELKPKNCEEEVYPTDGTCDNYTAHQGTA---V 1135
 QY 1136 CENRAGYEDAYEVDTTASVNYKPTVEEYTDVRRDNHCEYDRGVYVNPPLPAGYMTKE 1195
 Db 1136 CENRAGYEDAYEVDTTASVNYKPTVEEYTDVRRDNHCEYDRGVYVNPPLPAGYMTKE 1195
 QY 1196 LEYFPETDKVIBIGETEGKFIVDSEVLLMEE 1228
 Db 1196 LEYFPETDKVIBIGETEGKFIVDSEVLLMEE 1228

RESULT 2
 A:Experimental source: subsp. gallieriae HD29
 A:Note: sequence extracted from NCBI backbone (NCBI:129672, NCBI:129675)
 C:Superfamily: parasporal crystal protein
 C;Keywords: delta-endotoxin

Query Match 58.5%; Score 3791; DB 2; Length 1176;
 Best Local Similarity 62.3%; Pred. No. 3.9e-233;
 Matches 762; Conservative 125; Mismatches 241; Indels 96; Gaps 16;

Qy 969 RLQADTNIGMHAADKLVRHIREAYLSELVSGVNAEIEELEGRIITAIISLYDARNVV 1028
 Db 914 RLQADTNIAIHAADKRVHIREAYLSELVSGVNAEIEELEGRIITAIISLYDARNVI 973
 Qy 1029 KNGDFNGLACVNVKGVHDV-QQSHRSVLVPEWEAEVQAVRVCPCRGYILRVYAYKE 1087
 Db 974 KNGDFNGLACVNVKGVHDV-QQSHRSVLVPEWEAEVQAVRVCPCRGYILRVYAYKE 1033
 Qy 1088 GYEGCVTIHEIENNTDELKPKCEBEVYPTDTGTCTNDVTAHQ---GTAVCNRSNAGYE 1144
 Db 1034 GYEGCVTIHEIENNTDELKPKCEBEVYPTDTGTCTNDVTAHQ---GTAVCNRSNAGYE 1092
 Qy 1145 DAYEVDITASVNYKPTVEETTYDVRDNHCEYDGRGVNYPPLPAGVMTKELEYFPETDK 1204
 Db 1093 KSYESSVQADYASVYKADYDGRDNHCEYDGRGVNYPPLPAGVMTKELEYFPETDK 1152
 Qy 1205 VWEIETEGETKFIIVDSVELLMEE 1228
 Db 1153 VWEIETEGETKFIIVDSVELLMEE 1176

RESULT 3
 S00944
 Parasporal crystal protein crylCal - Bacillus thuringiensis (strain entomocidus 60.5)
 C;Species: Bacillus thuringiensis
 C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
 C;Accession: S00944
 R;Honee, G.; van der Salm, T.; Visser, B.
 Nucleic Acids Res. 16, 6240, 1988
 A;Title: Nucleotide sequence of crystal protein gene isolated from B. thuringiensis subsp. entomocidus
 A;Reference number: S00944; MUID:88289380; PMID:3399402
 A;Accession: S00944
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-1189 <HON>
 A;Cross-references: UNIPROT:P05518; EMBL:X07518; NID:g40293; PIDN:CAA30396.1; PID:g40294
 C;Superfamily: parasporal crystal protein
 C;Keywords: delta-endotoxin

Query Match 53.8%; Score 3484.5; DB 2; Length 1189;
 Best Local Similarity 56.8%; Pred. No. 1.4e-213;
 Matches 715; Conservative 143; Mismatches 291; Indels 109; Gaps 20;

Qy 7 NENEII--NALSTPAVNSHSTQMDLSPARIESLCIAEGNNINPLVASSTVGTGINAG 64
 Db 5 NONQCIPTNCLSD-----NPEVLLDGERISTGN-----SSIDISLSLVQ 43
 Qy 65 RIILGVLPVPGAGIASFYSFLVGLWPRGRDOWEIFLEHVLEQLINQOITENANTALRL 124
 Db 44 FLVSNF-VPGGFLVGLIDFVWGVGP---SQMDAFLVQIEQLINERIAEFARNAAIL 99
 Qy 125 QGLGDSFRAYQOGLDLENRDDARTSVLYTOYIALELOFLNAMPULFARNQOEVLPMV 184
 Db 100 EGLONNFIVYFAKWEEDPNPETHRVIDRILDGLLERDIPFRISGEVPLLSV 159
 Qy 185 YAAQANLHLLLDASLFGSEFGITSOEIQRYXERQVEQTRDYSYCVWYNTGLNSLRG 244
 Db 160 YAAQANLHLLLDASLFGSEFGITSOEIQRYXERQVEQTRDYSYCVWYNTGLNSLRG 219
 Qy 245 TNAASVRYNQFRDLTLGLVDLVALPSPYDTRTYPTINTSAQLTREYVTDIAGTGNMA 304
 Db 220 STYQDMWYVNRRLDLTLGLVDLVALPSPYDTRTYPTINTSAQLTREYVTDIAGTGNMA 275
 Qy 305 SMWYNNNAPSFAETAVIRSHLLDLFLQTLTFTSSRWASRTHMYWRGHTIOGRPI 364
 Db 276 PQIQSAQLPTFNWESSRIRNPHLDLNNLTFTD---WFSVGRNFYGGHVRVSSLI 332
 Qy 365 GGGINTSTHGSNTSINPVLSPFSRDVYWTESYAGVLL---WGIYLEPIHGVPYVRFN 420
 Db 333 GGGNITSPIYGRANQEPSPFSFNGVFRVFTLSNPTLRLLQQWPAPPPNLRGVEGVEFS 392
 Qy 421 FRNPQNTFE---RGATANYQSPYSPGLQDKDSELTPEPTTERPNRYSYSHRLSHGLIS 477

Db 393 --TPTNSFTYRGRTV-----DSLTELPPEDNSVPPREGYSHRLCHATFVQ 436
 Qy 478 QSRVHV----PVYSWTHRSADRTNTISSDITQIPLVKSFNLSNGTSSVSGPGTGDII 533
 Db 437 RSGTPFLTITGWFSWTDRTSATLTNTIDPERINQIPLVKGFRVMGTSVITGPGTGDII 496
 Qy 534 RTVNGSVLSMGLNFNTSLQRYRVRVRYAASQ-----TMVLRTVTVGSGTTFDQGFPS 586
 Db 497 RRNTFGDVSLSQVNIINSIPITQRYRLFRYASSRDARVILVTGAAGTGGVQSVNMPLOK 556
 Qy 587 TMSANESLTSQSFRFAEFP-----VGISASGSQTAGISISNNAAGRTQPHFKIE 635
 Db 557 TMEIGENLTSRTYTDSPNPFPRANPDIIIGISEQLFCAG-SISGS-----ELYIDKIE 611
 Qy 636 FIPITATFEAYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDSEFCLE 695
 Db 612 IILADATFEAESDLERAQKAVNALFTSSNQIGLKTVDVTDYHIDQVSNLVACLSDSEFCLE 671
 Qy 696 KRELLEKVKYAKELSDERNLLQDPNFTSINKQDPFISTNEQSNFTSIHEQSEHGWMGSEN 755
 Db 672 KRELSEKVKHAKELSDERNLLQDPNFRGINRQPD-----RGRWGSTD 713
 Qy 756 ITIQGNDFVKENYVTLPGTFNECYPTLYQKIGESLKYTRYQLRGYIEDSDQLIYL 815
 Db 714 ITIQGDDVFKENYVTLPGTFNECYPTLYQKIDESKLKYTRYELRGYIEDSDQLIYL 773
 Qy 816 IRYNAKHETLDVPGTESVWPLSVESPIGRCEPNRCAPHFEPWPDLDSCDCRDGKCAHHS 875
 Db 774 IRYNAKHETLDVPGTESVWPLSVESPIGRCEPNRCAPHFEPWPDLDSCDCRDGKCAHHS 833
 Qy 876 HHSFLDIDGCTDLHENLGVVWVFKIQTQGHARLGNLEFIEEKLPLGEALSRVRAEKK 935
 Db 834 HHSFLDIDGCTDLHENLGVVWVFKIQTQGHARLGNLEFIEEKLPLGEALSRVRAEKK 893
 Qy 936 WRDKREKLQLETKRVYVTEAKEADVALFVDSQYNRLOADTNIGMHAADKLVRHIREAYLS 995
 Db 894 WRDKREKLQLETKRVYVTEAKEADVALFVDSQYNRLOADTNIGMHAADKLVRHIREAYLS 953
 Qy 996 ELSVIPGVNAEIEELEGRIITAIISLYDARNVKNVNGDFNNGLACVNVKGVHDV-QQSHHR 1054
 Db 954 ELSVIPGVNAEIEELEGRIITAIISLYDARNVKNVNGDFNNGLACVNVKGVHDV-QQSHHR 1013
 Qy 1055 SVLVPEWEAEVQAVRVCPCRGYILRVYAYKEGYEGCVTIHEIENNTDELKPKCEEE 1114
 Db 1014 SVLVPEWEAEVQAVRVCPCRGYILRVYAYKEGYEGCVTIHEIENNTDELKPKCEEE 1073
 Qy 1115 EYVPTDTGTCTNDVTA---HOGTAVCNRSNAGYEDAYEDVTASVNYKPYEETTYDVR 1170
 Db 1074 EYVPTDTGTCTNDVTA---HOGTAVCNRSNAGYEDAYEDVTASVNYKPYEETTYDVR 1131
 Qy 1171 RDNHCEYDGRGVNYPPLPAGVMTKELEYFPETDKVWIEIGETGKFIIVDSVELLMEE 1228
 Db 1132 RENPCESNRGYDGYTPLPAGVMTKELEYFPETDKVWIEIGETGKFIIVDSVELLMEE 1189

RESULT 4
 S11446
 Parasporal crystal protein crylDal - Bacillus thuringiensis
 N;Alternate names: parasporal crystal protein cryID
 C;Species: Bacillus thuringiensis
 C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
 C;Accession: S11446
 R;Hoefte, H.; Soetaert, P.; Janssens, S.; Peferoen, M.
 Nucleic Acids Res. 18, 5545, 1990
 A;Title: Nucleotide sequence and deduced amino acid sequence of a new Lepidoptera-specific
 A;Reference number: S11446; MUID:91016842; PMID:2216728
 A;Accession: S11446
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1165 <HOE>
 A;Cross-references: UNIPROT:P19415; EMBL:X54160; NID:g40279; PIDN:CAA38099.1; PID:g40280
 C;Superfamily: parasporal crystal protein
 C;Keywords: delta-endotoxin

[illegible]

57	VLGULIDWGVGP----	SQMDAFVLQIEQLISQIBIEFARNQALISRLBGLNLUVOIYAEA	111
138	LEDWLENRRDARTSVLYTQVIALEDFLNPAMPLFAIRNOEVPFLMVMYQAANLHLLLR	197	
114	PREWEADPTPALREEMRIQFNDMNSALTTAIPLFTVQYQVPLLSVVYQAVNLHLSVL	173	
198	DASLFGSEFGLTSGEIQRYTERQVEQTRDYSDYCVWYNTGNSRGTNAAASWRYNQFR	257	
174	DVSYFGQRWGLDVATINSRYNDLTRLTGTVDYAVRWYNTGLERWGPDSRWDWRYNQFR	233	
258	RDLTLGLVLDLVALPPSYDTRTYPTNTSAQLTREYVYDAIGATGVNMAWMNNAPFS	317	
234	RELTLTLVDLVSLEPNVDSRTYPIRTVSQLTREIYT-----NPVLENDFGSPRGSQAQ	285	
318	AIETAVIRSPHLPLDLBQLTIFSTSRWSATRHMTYWRGHTIQSRPIGGG---LWTSHTG	374	
286	RIEQS--IRSPHMLDIILNSITIYT-----DAHGGYVYMSGHQIMASPVGFSGPETFFPLYG	339	
375	STWTSINPVL--SPFSRDVWYTES---YAGVLLWGLYILEPIHGVTYVRFNFRNPONTEER	430	
340	TMGNAAPQQRIVAOGLQGVKRTLSSSTFYRNPFIIGINNQRUSVLDTGTEFAYGSSNL---	396	
431	GTANYSQVPSGPIQLKDSELTPEPETERPNERNYESYSHRLSHIGLI-----SOSRVHV	483	
397	----PSAVYRKSG--TVDSLDEIIPQDNVPPROGFSHRLSHVSMFRSGFNSSVSIIRA	450	
484	PVYSWTHRSADRTWTISDSISITQIPLVKFSFNLNGSTSVVSGPGTGGDIIRTNVNGSVLS	543	
451	PMFSWIHRSAEFNNIIIPSSQITQIPLTKSTNLGSGTSSVVGPGTGGDILARTSPGOJST	510	
544	MGLNFNNTSLQRYVRVRYAASQTMVLRTVTVGGSTTDDQGPSPMTSMANESLTSOSFRAE	603	
511	LRVNITAPLQRYKRVIRIYASTTNLQFHTSIDGRPIQGNFSATMSSCGNLQSGSFRTVG	570	
604	FPVGIS--ASGSQTAGISIS--NNAGROTTFHFDKIEFIPITATFEAYDILERAQEAVALFT	661	
571	FTTFFNFSNGSVFTLSAHVFNSGNEVY--IDRIEFVPAEVTFEABYDLERAQEAVALFT	629	
662	NTNPRRLKTDVTDYHIDQVSNLACLSDPEFLCDREKRELLEKVKYAKRLSDERNLLQDNF	721	
630	SPNOIGLTKTDVTDYHIDQVSNLVCLESDPEFLCDREKRELSEKVKHAKRLSDERNLLQDNF	689	
722	TSINKQPDFISTNEQSNFTSIIHQSEHGWMGSENIITIQEGNDVFKENVTVLPGTFNECVP	781	
690	RGINRQPD-----RGWRGSTDITIQGGDDVFKENVTVLPGTFDECYP	731	
782	TYLYQKIGESLKATRYQLRGYIEDSQDLLEYILIRYNAKHETLDPGCTESWPLSVESP	841	
732	TYLYQKIDESLKATRYELRGYIEDSQDLLEYILIRYNAKHETVNVPGTGLWPLSPSS	791	
842	IGRCGFENRCAPEHNPDLDCSRDEKCAHHSHHPSLDDICTDLHENLGVVWVFKI	901	
792	IGKCGFENRCAHLEWNPDLDCSRDEKCAHHSHHPSLDDVGCIDLNEGLVWVVIKFI	851	
902	KTOBCHARLGNLEPIEKLPLGEALSRVKRAEKKWRDKREKLQLETKRVYTEAKEAVDAL	961	
852	KTOQCHARLGNLEPIEKLPLVGEALARVKRAEKKWRDKREKLQLETNIVYKEAKESVDAL	911	
962	FVDSQYNRLQADTNIGMIHAADKULVHRIREAYLSLSLSESVIPGVNAEIPPELGRITL	1021	
912	FVNSQYDQLQADTNIAIMHTADKRVHRIQEAYLPELSVIPGVNAGIPELEGRIFTAYSL	971	
1022	YDARNVVKNGDFNNGLACWNVKGHDV--QQSHHRSVLVIPEWEAEVSQAVRCPGRGYIL	1081	
972	YDARNVVKNGDFNNGLSCWNVKGHDVVEEQNNHRSVLVVPWEAEVSQEVRCVPGRGYIL	1031	
1081	RVYAYKEGYGEGCVYTHEIENNTDELAKFNCEBEVYPTDTGTCNDYTAHQ---GTAYCN	1131	
1032	RVYAYKEGYGEGCVYTHEIENNTDELAKFNCVBEVYPNNVTVCNEYTANOEYGGAY-T	1091	
1138	SRNAGYEDAYEVDTTASVNYKPTVEETYTVDVRDNDHCEYDRGVYNYPPPLPAGYMWKLE	1191	

578 RIAEELPIRGELIYDIKIELILADATPEBEYDLERAQKAVNALFTSTNQGLGLKTDVTDYH 637
677 IDQVSNLVACLSDPEFCLDEKRELLEKVKAKRLSDERNLLQDNFTSINKQPDFISTNEQ 736
638 IDQVSNLVECLSDPEFCLDEKRELSEKVKAKRLSDERNLLQDNFNGINRQPD----- 690
737 SNFTSTHSESHGHWGSENIITQEGNDVFKENYVTLPGTFNECYPYLYQKIGESLKAY 796
691 -----RGWRGSTDTITIQGGDDVFKENYVTLPGTFDECYPTYLYQKIDESLKAY 739
797 TRYQLRGYIEDSODLIEYLIRYNNAKHETLDVPGTESVWPLSVESPIGRCEPNRCAPHPE 856
740 TRYELRGYIEDSQDLIEYLIRYNNAKHETVNPVGTGSLWPLSAQSPIGKCGEPNRCAPHLE 799
857 WNPDLDCSCEGKCAHSHHPSLSDIDIGCTDLHENLGVWVFKITQBGHARLGNLEFI 916
800 WNPDLDCSCEGKCAHSHHPSLSDIDVGCTDLNEDLGWVTFPKITQGYARLGNLEFL 859
917 EEKPLLGEALSRVKRAEKKWRDKREKLQLETRKRVYTEAKEAVDALFVDSQYNRLQADTNI 976
860 EENPLLGEALARVKRAEKKWRDKCELEWETNIVYKEAKESVDALFVNSQYDLQADTNI 919
977 GMIHAADKLVRIREAYLSELSVIPGVNAAIEFEELEGRIITAILSLYDARNVVKNGDFNNG 1036
920 AMTHAADKRVHSIREAYLPELSIVIPGVNAAIEFEELEGRIFTAFSLYDARNVVKNGDFNNG 979
1037 LACWNVKGHDV-QQSHHRSVLVIPWEAEVSOAVRVCPRGVYILRVATYKEGYGEGCVT 1095
980 LSCWNVKGHDVVEEQNNHRSVLVPPWEAEVSOEVRVCPRGVYILRVATYKEGYGEGCVT 1039
1096 IHEIENNTDELKFKNCEEVEVYPTDTGTGTCNDYTA----HQGTAVCNRSNAGYEDAYEVD 1151
1040 IHEIEDNTDELKFSNCEEVEVYPNNTVTCNNYTAQOEHEGT--YTSRNRGYDEAVESNS 1097
1152 TASVNYKPYBEETVDRDNHCEYDRGVYVNPPLPAGYMTKELEYFPETDKVWIEIGE 1211
1098 SV----HASVYEEKSYTDRRNPENPCSNRNGYDTPLPAGYVTKLEYFPETDKVWIEIGE 1154
1212 TEGKFTVDSVELLMEE 1228
1155 TEGTFTVDSVELLMEE 1171

RESULT 8
S32649
parasoral crystal protein cryIpa3 - Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S32649
R;Lambert, B.
submitted to the EMBL Data Library, April 1993
A;Reference number: S32645
A;Accession: S32649
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1174 <LAW>
A;Cross-references: UNIPROT:Q45749; EMBL:Z22512; NID:G235865; PIDN:CAA80235.1; E
C;Superfamily: parasoral crystal protein
C;Keywords: delta-endotoxin

Query Match 52.7%; Score 3413.5; DB 2; Length 1174;
Best Local Similarity 57.3%; Pred. No. 4.5e-209;
Matches 685; Conservative 139; Mismatches 264; Indels 107; Gaps 19;

72 VPFAGQIASFYSFLVGEIWPGRGDQWEIPLFHVQILNQIITENARNTALARLOGIGDSF 131
49 VPGVGVAFLFLIWGFITP---SEWSFLQLQIEQRIETLERNRAITTLRGIADSY 105
132 RAYQOSLEDLENRDARTSVLYTQYIALELDFLNAMPLFAIRNQEVPLMYAQAANL 191
106 EYVLEALREWEENPNNAQLQDRVIRFPAITDALLTAINNFTLTSTFEIPLSVYVQAANL 165
192 HULLLRDASLFGSEFGLTSQEIQRYYERQVEOTRDSYCYVEWYNTGLNSLRGTNAASWV 251

Db 681 NLQDPNFRGINRQLD-----RGMWGSDTIITIQGGDDVFKENYVTL 722
Qy 774 GTFNECYPTLYQKIGESLAKAYTRYQYRGVIEDSDLEIYLYIRYNAKHETLDVPGTESV 833
Db 723 GTFDECTPTLYQKIDSKLAKAYTRYQYRGVIEDSDLEIYLYIRYNAKHETVNVPGTGS 782
Qy 834 WPLSVESPIGRGPNRCAPHEFNPDLDCSCRDGKCAHSHHFSLDIDIGCTDLHENL 893
Db 783 WPLSAQSPIGKCGPNRCAPHEFNPDLDCSCRDGKCAHSHHFSLDIDVGCCTDLNEDL 842
Qy 894 GVVVFKITQEGHARLGNLEFIEBKPLGLBALSRVRAEKAKKWDKREKQLETKRYVTE 953
Db 843 GVVVFKITQEGHARLGNLEFIEBKPLGLBALSRVRAEKAKKWDKREKLEWETNIVKE 902
Qy 954 AKEAVDALFVDSQYRLQADTNIGMHAADKLVRIRREAYLSELSVPGVNAIFEELEG 1013
Db 903 AKESVDALFVNSQYDQADTNIGMHAADKVRHSIRREAYLSELSVPGVNAALFEELEG 962
Qy 1014 RIITAFSLYDARNVYKNGDFNNGLACWNVKGHDV-QQSHRSVLVPIPEWAEVSOAVRV 1072
Db 963 RIITAFSLYDARNVYKNGDFNNGLACWNVKGHDVQESQNNQSVLVVPEWAEVSOAVRV 1022
Qy 1073 CPGRGYILRVYAYKEGEGCVTHIENNTDELKFKNCBEEVYPTDGTCTNDYTAHQ- 1131
Db 1023 CPGRGYILRVYAYKEGEGCVTHIENNTDELKFKNCBEEVYPTDGTCTNDYTAHQ- 1082
Qy 1132 --GTAVCNRSNAGYEDAYEDVTTASVNVKPYEETVTDVRRDNHCEYDRGVNYPPLPA 1189
Db 1083 EYGGAY-TSRNRYNEAPSV----PASYVSEKSYTDORRENPCBFRNGRYDTPLPV 1137
Qy 1190 GYMTKELEYPPETDKVWIEIGETSGKFIIVDSVELLMEE 1228
Db 1138 GYVTKLEYPPETDKVWIEIGETSGKFIIVDSVELLMEE 1176

RESULT 10
A42459
parasporal crystal protein cryIaI - Bacillus thuringiensis (strain aizawai)
N;Alternate names: parasporal crystal protein cryIa
C;Species: Bacillus thuringiensis
C;Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 09-Jul-2004
C;Accession: A42459
R;Chambers, J.A.; Jelen, A.; Gilbert, M.P.; Jany, C.S.; Johnson, T.B.; Gawron-Burke, C.
J. Bacteriol. 173, 3966-3976, 1991
A;Title: Isolation and characterization of a novel insecticidal crystal protein gene fcd
A;Reference number: A42459; MUID:91286178; PMID:2061280
A;Accession: A42459
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1174 <CHA>
A;Cross-references: UNIPROT:Q03746; GB:M63897; NID:g142757; PIDN:AAA22348.1; PID:g142758
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin

Query Match 52.7%; Score 3412.5; DB 2; Length 1174;
Best Local Similarity 58.4%; Pred. No. 5.2e-209;
Matches 693; Conservative 132; Mismatches 271; Indels 91; Gaps 21;
Qy 72 VPAGQIASFYSFLVGLWPRGRDWEIIEHVEQLINQOITENARTALRLOGLGDSF 131
Db 49 VPGVGVAFLDILWGFIIP--SDSLFLLQIEQLIEQRIETLERNRATITLUGLADSY 105
Qy 132 RAYQQSLDELNRDARTSRVLYTOYIALDELFLNAPLFAIRNOEVPMLLVYAAANL 191
Db 106 EIVIEALREWEANPNNAQLREDVIRPANTDDALITAINNFTLTSFEIPLSVYVQAANL 165
Qy 192 HLLLRDASLFGSEFGLTSQEIQRYERQVEQTRDYSYDCEVWNTGLNSLRGTNAASV 251
Db 166 HLLSLRDASVFGQGLDIAVNVHNRNLNLRHYTKHCLDTYNQGLNLRGTNTROWA 225
Qy 252 RYQNRDLTLGLVLDLVALPSPDYTRYPINTSAQITREYVTDATGATGVNMAWMWYNN 311
Db 226 RFNQFRDLTLVLDLVALFPNDVTRYPYQTSQITREYTSVIEDSPVSA----- 278

Qy 312 NAPS-FSAIETAVIRSPHLLDFLEQLTIESTSRWSATRHMTYWRGHTIOSRPIGGG-LN 369
Db 279 NIPNGFNRAEFGV-RPHLMDFMNSL--FVTA---ETVRSQTWGGHLVSSRNTAGNRIN 332
Qy 370 TSHGSTNTINPVRSLFFS----RDVYWTESYAGVLLMGVILEPIHGVTVPVFNFRNPQ 425
Db 333 FPSVG----VPFGGAIWIADEPRFPYRTLS-----DVPF---VRGGFGNPH 373
Qy 426 N-----TPERTANYSQYSPESGQLQKDSSETPELTPETTERPNYESYSHRLSHI----- 473
Db 374 YVLGLRGVAFQQTGHTNTRTFRNSG--TIDSLDEIPQDNGSGAPWNDYSHLVNHTVFRV 431
Qy 474 -GLISQS-RVHVYVYVSWTHRSADRTNITSSDSTOIPLVKSFNLNGSTSVVSGPGTGGD 531
Db 432 PGISGSDSWRAPMFWSWTHRSATPTNIDPERITQPLVKAHTLQSGTTVVRGPGTGGD 491
Qy 532 IIRTNVNGSVLSLGLNPNNTSLQYRVRYAASQTMVLRVTVGGSTTFDQGFPTMSAN 591
Db 492 ILRRTSGPPAYTIVNINQQLPQYRARIRYASTTNLRIVYTVAGERIFAGQFNKTMDTG 551
Qy 592 ESLSQSFRPAEPVGVISAGSGQTAGISISNNAGROTFF-----HPDKIEFIPITATFEA 645
Db 552 DPLTFQSFSYATINTAFTFPMSQS-----SFTVGADTFSSGNEVYIDRFELIPVATFEA 606
Qy 646 EYDLERAQEAVALFNTNPRRLKTDVTDVHIDQVNLVACLSDDEFCLDEKRELLKVKY 705
Db 607 EYDLERAQKAVNALFTSIQIGIKTVDVHIDQVNLVACLSDDEFCLDEKRELLKVKY 666
Qy 706 AKELSDERNLLOPNFTSINKQPDFISTNEQSNFTSIHQSEHGMWGSNITIQEGDNVF 765
Db 667 AKELSDERNLLOPNFNGINRQLD-----RGMWGSDTIITIQGGDDVF 708
Qy 766 KENYVTLPGTFNECYPTLYQKIGESLAKAYTRYQYRGVIEDSDLEIYLYIRYNAKHETL 825
Db 709 KENYVTLPGTFNECYPTLYQKIGESLAKAYTRYQYRGVIEDSDLEIYLYIRYNAKHETV 768
Qy 826 DVPGTESVWPLSVESPIGRGPNRCAPHEFNPDLDCSCRDGKCAHSHHFSLDIDIG 885
Db 769 NVLGTGSLWPLSVQSPIRKCGPNRCAPHEFNPDLDCSCRDGKCAHSHHFSLDIDVG 828
Qy 886 CTDLHENLGVVVFVKITQEGHARLGNLEFIEBKPLGLBALSRVRAEKAKKWDKREKQL 945
Db 829 CTDLNEDLVVVFVKITQEGHARLGNLEFIEBKPLGLBALSRVRAEKAKKWDKREKLE 888
Qy 946 ETKRVYTEAKEAVDALFVDSQYRLQADTNIGMHAADKLVRIRREAYLSELSVPGVNA 1005
Db 889 ETNIVYKEAKESVDALFVNSQYDQADTNIGMHAADKVRHSIRREAYLSELSVPGVNV 948
Qy 1006 EIFEELGRIITAFSLYDARNVYKNGDFNNGLACWNVKGHDV-QQSHRSVLVPIPEWEA 1064
Db 949 DIFEELKGRITAFSLYDARNVYKNGDFNNGLACWNVKGHDVVEEQNNHRSVLVPEWEA 1008
Qy 1065 EYSQAVRVCGRGYILRVYAYKEGEGCVTHIENNTDELKFKNCBEEVYPTDGTG 1124
Db 1009 EYSQAVRVCGRGYILRVYAYKEGEGCVTHIENNTDELKFKNCBEEVYPTDGTG 1068
Qy 1125 NDYTAHQ---GTAVCNRSNAGYEDAYEDVTTASVNVKPYEETVTDVRRDNHCEYDRGY 1181
Db 1069 NDYTAHQEYGGAY-TSRNRYNEAPSV----PASYVSEKSYTDORRENPCBFRNGRY 1127
Qy 1182 VNPPLPAGYMTKELEYPPETDKVWIEIGETSGKFIIVDSVELLMEE 1228
Db 1128 GDYTPLPAGYMTKELEYPPETDKVWIEIGETSGKFIIVDSVELLMEE 1174

RESULT 11
S32647
parasporal crystal protein cryIaI - Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S32647
R;Lambert, B.

submitted to the EMBL Data Library, April 1993

A;Reference number: S32645

A;Accession: S32647

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1160 <LAW>

A;Cross-references: UNIPROT:Q45747; EMBL:Z22511; NID:g295963; PIDN:CAA80234.1; PID:g2958

C;Superfamily: parasporal crystal protein

C;Keywords: Delta-endotoxin

Query Match 52.6%; Score 3411; DB 2; Length 1160;

Best Local Similarity 56.3%; Pred. No. 6.3e-209;

Matches 695; Conservative 145; Mismatches 288; Indels 108; Gaps 21;

Qy 22 NHSTQMDLSPDARIEDSLCIAEGNNINP---LVSASTVOTGINTAGRIGLVGLG-----V 72
Db 4 NHQNO-----CIPYNCLSPDAILLDAERLETGTVADISLGLINFLYSNFV 50

Qy 73 PFAGQIASFYSFLVGLWPRGRDQWEIFLEHVEQLINQOITENARNATALRQLGDSFR 132
Db 51 PGGGFIVGLLELWFGVP---SQWEIFLAQIEQLISQRIEFAFARNOAISREGLSNYE 107

Qy 133 AYQOSLEDWLENRRDARTSRVLYTQYIALELDLFLNAPLFAIRNOEVPFLMVAQAANLH 192
Db 108 IYETFPANKEKDPSPALREMRTPQVMSALIAAIPLLLRVNYEVALLSVYVQAANLH 167

Qy 193 LLLRLDASLFGSEFGLTSQRIQRYRQVEQTRDYSYCVYEWNTGLNLRGTNAASVVR 252
Db 168 LSVLRDVSVYQWRGPDPAATVNSRYSDLTRLIHVYTDHCVDTYNDGLKLEGRSLDWWV 227

Qy 253 YNQRRDLTLGLDLVALFSDYTRTPINTSAQLTRVYTD---ICATGVNMAAMWYN 310
Db 228 YNFRRLTLISVLDIIAFFFNYDTEAYPIQTASQLTRVYLDLFPVNETLSPASY---- 283

Qy 311 NNAPSFAGIETAVRSRPHLLDFLQLTFTSSRSWATRMVYWRGHTIOSRPIGGGLN- 369
Db 284 ---PTFSAAESAILRSPLHVDLNFSTIYDUS-----LASVYMGHLLVNSFRGTGTTNL 335

Qy 370 --TSTHGSTNTSINPVRLSFF--SRDVTWYTESYAGVLLWGI--YLEPIHGVTVPFRNPNQ 425
Db 336 IRSPLYGREGNTERPVVISASPSVPIFRTLSTY-----FTGLNNNPVAGIEGVF-----Q 386

Qy 426 NTERGTANTSQPVESGLQKDSLETLPETTERPNYESYSHRLSH---IGLISQSRVH 482
Db 387 NTISRSIYRKSGPI-----DSFSELPQDVSVSPAIGYSHRLCHATEFLERISGPRIA 438

Qy 483 VPVYSWTHRSADRNTWISSDITQIPLVKSNLNSGTSVVGCGFTGCDIIRTVNVSGL 542
Db 439 GTVFSWTHRSASPINEVSPSRITQIPWKAKHTLASGASVINGPGFTGCDILTRNSMGDLG 498

Qy 543 SMGLNFNTSLQRYRVRVRYA--ASQTMVLRVTVGSGTTFDGPPPTWSANESLTSQSR 600
Db 499 ALRVTFTGRLPQSYIIPRVASVANRSGTFYSQPPS--YGISFPKMDAGEALTSRSPA 556

Qy 601 FAEFPVGISAGSQ-----TAGISNNAGROTTFHDKIEFTIPATFEAEVDLERAQ 653
Db 557 HTTLFTPTTSRAQEEFDLYTQSGV-----YIDRIETFPVDATFESEINLERAQ 605

Qy 654 EAVNALFTNTPRELKTDVTDYHLDVSNLVACLSDEFCLDEKELKEVKYAKRLSDER 713
Db 606 KAVNALFTSNQLGKTDVTDYHLDVSNLVACLSDEFCLDEKELKEVKYAKRLSDER 665

Qy 714 NLLQDPNFTSINKQDPFISTNEQSNFTSIHQSHGHWGSENITIQSGNDVDFKENYVTL 773
Db 666 NLLQDPNFRGINRQPD-----RGMWGSTDTITIQGGDDVDFKENYVTLT 707

Qy 774 GTFNECYPTLYQKIGSELKAYTRYQLRGVIEDSQBLEIYLIRYNAKHETLDVPGTESV 833
Db 708 GTFDECYPTLYQKIDESKLKAYTRYQLRGVIEDSQBLEIYLIRYNAKHETLVNVPGTSL 767

Qy 834 WPLSVESPIGCEGPNRCAPHEFWNPDLDCSCRGEKCAHSHHSHFDIDIGCTDLHENL 893
Db 768 WPLSVQSPIGKCEGPNRCAPHEWNPDLDCSCRDEKCAHSHHSHFDIDIVGCTDLNEDL 827

Qy 894 GVMVVFKIKTQGBHARLGNLEFIEEKPLLGREALSRVRAEKKWRDKREKLOLETQKRVYTE 953
Db 828 GVMVIFKIKTQDGBHARLGNLEFIEEKPLVGEALSRVRAEKKWRDKREKLELETNIVYKE 887

Qy 954 AKCAVDALFVDSQYNRLQADTNIGMHAADKLVHRIEAYLSLSLVIPIGVNAEIPFEELG 1013
Db 888 AKESVDALFVNSQYDQLQADTNIAHHAADKRVHSIREAYLPUSLVIPIGVNAGIPFEELG 947

Qy 1014 RIITAIISLYDARNVVKNGDFNNGLACWNVKGHDV--QOSHHRSVLVPIPEWAEYSQAVRV 1072
Db 948 RITATSLYDARNVVKNGDFNNGLSWNVKGHDVVEQNHRSLVLPWEAEYSQAVRV 1007

Qy 1073 CPGGYILRVAYKEGEGCVTIHEIENNTDELKFNKCEEEVYPTDTGTGTCNDYTAHQ 1132
Db 1008 CPGGYILRVAYKEGEGCVTIHEVDNNTDELKFSNCEKEQYYPGNTVACNDYNKNHG 1067

Qy 1133 TAVCNSNAGVEADAYEVDTTASVNYKPTVEETVTVDRDNHCEYDRGVNYPPLPAGYM 1192
Db 1068 ANACSSNRNGYDESYSNISPADIAPVYBEEAYTDGQRNCPCEFNRGHT---PLPAGYV 1124

Qy 1193 TKLEYEPETDKVMIEIGETEGKPIVDSVELLMEE 1228
Db 1125 TAELEYEPETDVWVEIGETEGTPIVDSVELLMEE 1160

RESULT 12

JC2219

parasporal crystal protein cryIAa - Bacillus thuringiensis

C;Species: Bacillus thuringiensis

C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004

C;Accession: JC2219

R;Udayasuriyan, V.; Nakamura, A.; Mori, H.; Masaaki, H.; Uozumi, T.

Biosci. Biotechnol. Biochem. 58, 830-835, 1994

A;Title: Cloning of a new cryIA(a) gene from Bacillus thuringiensis strain FU-2-7 and an

A;Reference number: JC2219; MUID:94289859; PMID:7764972

A;Accession: JC2219

A;Molecule type: DNA

A;Residues: 1-1176 <DA>

A;Cross-references: UNIPROT:Q45736; DDBJ:D17518; NID:g506190; PIDN:BAA04468.1; PID:g53571

C;Genetics:

A;Gene: cryIA(a)

C;Superfamily: parasporal crystal protein

C;Keywords: Delta-endotoxin

Query Match 52.6%; Score 3405.5; DB 2; Length 1176;

Best Local Similarity 56.3%; Pred. No. 1.5e-208;

Matches 697; Conservative 149; Mismatches 293; Indels 100; Gaps 24;

Qy 27 MDLSPDARIEDSLCIAEGNNINP---LVSASTVOTG---INIAGRILGVL---GVFPAGQ 77
Db 1 MDNNPNI---NECIPYNCLSNPEVEVLGGERIETGVTPIDSLSTQFLLSSEFVPGAG- 55

Qy 78 IASFYSFLVGLWLP--RGDQWEIFLEHVEQLINQOITENARNATALRQLGDSFRAYQQ 136
Db 56 ---FVLGLVDIIWGIQFGPSQWDAFLVQIQIEQINQRIEFAFARNOAISREGLSNLYQIYAE 112

Qy 137 SLEDWLENRRDARTSRVLYTQYIALELDLFLNAPLFAIRNOEVPFLMVAQAANLHLL 196
Db 113 SPFEWEADPTNPALREMRIOFNDMNSALITATPALLAVQVQVPLLSVYVQAANLHLSVL 172

Qy 197 RDASLFGSEFGLTSQRIQRYRQVEQTRDYSYCVYEWNTGLNLRGTNAASVRYNQF 256
Db 173 RDVSFQGRWGFDAATINSRYNDLTRIGNVTDYAVRWYNTGLERVNGPDSRDWRVYNQF 232

Qy 257 RRDITGLVDLVALFSDYTRTPINTSAQLTRVYTD---ICATGVNMAAMWYNNAAPSF 316
Db 233 RRELTLVLDLVALFSDYTRTPINTSAQLTRVYTD---ICATGVNMAAMWYNNAAPSF 280

Qy 317 SALETAV---IRSPHLLDFLEQLTIFSTSRWSATRMVYWRGHTIOSRPIGGG---LNT 370
Db 281 RGMARQEQINRQPHLMDILNSTIYI---DVHRGFNWSHQITASPVGFGSPGPEAF 335

Qy 954 AKEAVDALFVDSOVNRLQADTNIGMIIHAADKLVRIRREAYLSLSVPGVNAEIFELEG 1013
Db 903 AKESVDALFVNSQYDQLOADTNIAHIAADKRVHSIREAYLPESLVIPGVNAALFELEG 962
Qy 1014 RIITAIISLYDARNVVKNGDFNGLACWNVKGHDV-QQSHRSVLVPEWEAEVSQAVRV 1072
Db 963 RIITAFSLYDARNVVKNGDFNGLSCWNVKGHDVVEQNNQSVLVVPEWEAEVSQAVRV 1022
Qy 1073 CPGRGYILRTAYKEGEGCVTTHIEINNTDELKFNCEBEEVYPTDTGTCNDYTAHQ- 1131
Db 1023 CPGRGYILRTAYKEGEGCVTTHIEINNTDELKFNCEBEEVYPTDTGTCNDYTNQE 1082
Qy 1132 --GTAVCNSRNAGYEDAYEDVTTASVNYKPYEETVTVRRDNHCYDRCGVNYPPLPA 1189
Db 1083 EYGGAY-TSRNRGYNAPS-----PADYASVYEKSYTDGRRENPCFNRGYRDTPLPV 1137
Qy 1190 GYMTKELEYPPETDKVWIEIGETEGTFIVDSVELLMEE 1228
Db 1138 GYVTKELYPEPDKVWIEIGETEGTFIVDSVELLMEE 1176

RESULT 14
A22617
parasporal crystal protein cry1Aa1 - Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 09-Jul-2004
C;Accession: A22617
R;Schnepp, H.E.; Wong, H.C.; Whiteley, H.R.
J. Biol. Chem. 260, 6264-6272, 1985
A;Title: The amino acid sequence of a crystal protein from Bacillus thuringiensis deduced from the complementary DNA sequence
A;Reference number: A22617; MUID:85207613; PMID:2581950
A;Molecule type: DNA
A;Residues: 1-1176 <SCH>
A;Cross-references: UNIPROT:P02965; GB:M11250; NID:g142764; PIDN:AAA22353.1; PID:g142765
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin

Query Match 52.5%; Score 3399.5; DB 2; Length 1176;
Best Local Similarity 56.2%; Pred. No. 3.5e-208;
Matches 696; Conservative 149; Mismatches 294; Indels 100; Gaps 24;

Qy 27 MDLSPDARIEDSLCIAGNNINP---LVSASTVOTG---INIAIRIGVL---GVPPAGQ 77
Db 1 MDNNPNIT---NECIPYCNLSNPEVEVLGGRIETGTPIDISLSLQFLLSFEPVPGAG- 55
Qy 78 IASFYSFLVGLWP-RGRDQWEIIFLEHVEQLINQOITENARTALARLQGLGDSFRAYQQ 136
Db 56 ---FVLGLVDIIGFIPGSDQWDAFPVQIEQLINQRIEFARNOAISRLGLSNLYQIYAE 112
Qy 137 SLEDWLENRDDARTSRVLYTQYIALELDFLNAMPFAIRNOEVLPMVYQAANLHLLLL 196
Db 113 SFREWEADPTNPALREEMRQFNDMSALTTAIFLLAVQYQVPLSVYQAANLHLSVL 172
Qy 197 RDAISLFGSEFLTSQEIQRYRVEQTRDYSDYCEWYNTGLNSLRTNAAGSVRYNQF 256
Db 173 RDVSFVGORGFDAATINSRYNDLTRLIGNYTDYAVRWNTGLERVWGPDSRDWRVYNQF 232
Qy 257 RBDLTGLVDLVALFPSTYDTPINTSAQLTREYVTDATGATGVNWMNWNNAAPSF 316
Db 233 RRELTLVLDLVALFNSYDSSRRYPIRTVSQLTREIYNPV-----LENFDGSPF 280
Qy 317 SATETAV---IRSPHLLADEQLTIFSTSSKWSATRMWYRGHTIQSRPIGGG---LNT 370
Db 281 RGAQRTEQINRQPHLMDLINSITIT---DVHRGFNTWSGHQITASVFGSGPPEFAP 335
Qy 371 STHGSTNTSINPRLSFSDRVYWTES---YAGVLLW-GIYLEPIHGVPVTRFNFRN--- 423
Db 336 PLFGNAGNAAPPVLVSLTGLGIFPRLSSPLRYRIILGSGPNQELFVLDGTERFSASLT 395
Qy 424 --PONTF-ERGTANOSYPSPGLQKDSLETLPPTTERPNVYESYSHRLSHGLISQS- 479

Db 396 NLPSTIYRQGTGTV-----DSLDDVIPPQDNSVPPRAGFSHRLSHVTMLSOAA 441
Qy 480 ----RVHVPYVSMTHRSADRNTNTISSDSITQIPLVKFSNLSNGTSVVGPGFTGCDIIRT 535
Db 442 GAVVTLRAPTFSMQHRSAEFNIIIPSSQITQIPLTKSTNLGSGTSVVGPGFTGCDILRR 501
Qy 536 NVNGSVLSMGLNFNTSLORYRVRVAAQSQTWVLRVTVCGSTTFFDOGFSPMTSANESELT 595
Db 502 TSPQISTLRVNTAPLSQRYRVRIRYASTNLFQHTSIDGRPINQGNFSAATSSGSLNQ 561
Qy 596 SQSPRFAEFVPGIS-ASGQTAGISIS-NNAGROTFHDKIEFIPITATPAEAYDLERAQ 653
Db 562 SGSPRTVGTFTFPNFGSSSVFTLSAHVFNSEVY-IDRIEFVPAEVPFAEYDLERAQ 620
Qy 654 EAVNALFTNTNRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELEKLVKAKRLSDER 713
Db 621 KAVNELFTSSNGIKLTKDVTDYHIDQVSNLVACLSDEFCLDEKRELEKLVKAKRLSDER 680
Qy 714 NLLQDNRFTSINKQPDPISTNEQSNFTSIHQSEHGHWSSENIITIQSGNDVFKENYVTL 773
Db 681 NLLQDNPFRGINRQLD-----RGRGSTDITIQGGDDVFKENYVTL 722
Qy 774 GTFNECYPTLYOKIGSELKAVTRYQYLGIEDSQDLEIYLIRYNAKHETLDVPGTESV 833
Db 723 GTFDECYPTLYOKIDESKAVTRYQYLGIEDSQDLEIYLIRYNAKHETVNVPGTSL 782
Qy 834 WPLSVESPIGRCEPNRCAPHFENWPDLCSCRDGKCAHSHHFSLDIDIGCTDLHENL 893
Db 783 WPLSAQSPICGKCEPNRCAPHLEWNPDLCSCRDGKCAHSHHFSLDIDVGCTDLNEDL 842
Qy 894 GVVVFKIKTQEGHARLGNLEFTEEPKLLGELASRVRAEKKWRDKREKLOLETKRYVTE 953
Db 843 GVVVFKIKTQEGHARLGNLEFTEEPKLLGELASRVRAEKKWRDKREKLEWETNIVYKE 902
Qy 954 AKRAVDALFVDSOVNRLQADTNIGMIIHAADKLVRIRREAYLSLSVPGVNAEIFELEG 1013
Db 903 AKESVDALFVNSQYDQLOADTNIAHIAADKRVHSIREAYLPESLVIPGVNAALFELEG 962
Qy 1014 RIITAIISLYDARNVVKNGDFNGLACWNVKGHDV-QQSHRSVLVPEWEAEVSQAVRV 1072
Db 963 RIITAFSLYDARNVVKNGDFNGLSCWNVKGHDVVEQNNQSVLVVPEWEAEVSQAVRV 1022
Qy 1073 CPGRGYILRTAYKEGEGCVTTHIEINNTDELKFNCEBEEVYPTDTGTCNDYTAHQ- 1131
Db 1023 CPGRGYILRTAYKEGEGCVTTHIEINNTDELKFNCEBEEVYPTDTGTCNDYTNQE 1082
Qy 1132 --GTAVCNSRNAGYEDAYEDVTTASVNYKPYEETVTVRRDNHCYDRCGVNYPPLPA 1189
Db 1083 EYGGAY-TSRNRGYNAPS-----PADYASVYEKSYTDGRRENPCFNRGYRDTPLPV 1137
Qy 1190 GYMTKELEYPPETDKVWIEIGETEGTFIVDSVELLMEE 1228
Db 1138 GYVTKELYPEPDKVWIEIGETEGTFIVDSVELLMEE 1176

RESULT 15
USBSXH
parasporal crystal protein cry1Aci [validated] - Bacillus thuringiensis subsp. kurstaki
C;Species: Bacillus thuringiensis subsp. kurstaki
C;Date: 18-Apr-1984 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: A23962; A03489
R;Adang, M.J.; Staver, M.J.; Rocheleau, T.A.; Leighton, J.; Barker, R.F.; Thompson, D.V.
Gene 36, 289-300, 1985
A;Title: Characterized full-length and truncated plasmid clones of the crystal protein of
A;Reference number: A91526; MUID:86083171; PMID:3000881
A;Accession: A23962
A;Molecule type: DNA
A;Residues: 1-1178 <ADA>
A;Cross-references: UNIPROT:P05069; GB:M11068; NID:g142721; PIDN:AAA22331.1; PID:g142722
A;Experimental source: strain HD-73
A;Note: the authors translated the codon ATT for residue 11 as Leu
R;Wong, H.C.; Schnepp, H.E.; Whiteley, H.R.
J. Biol. Chem. 258, 1960-1967, 1983

A;Title: Transcriptional and translational start sites for the Bacillus thuringiensis cp
 A;Reference number: A92410; MUID:83109004; PMID:6296116
 A;Accession: A03489
 A;Molecule type: DNA
 A;Residues: 1-76, 'P', 78-147, 'L', 149-247, 'S', 249-282, 'M', 284-285, 'R', 287-288, 'QN', 291-292
 A;Experimental source: strain HD-1
 C;Comment: This protein is present in crystalline form as a component of the spore coat.
 C;Superfamily: parasporal crystal protein
 C;Keywords: delta-endotoxin

Query Match 52.5%; Score 3399.5; DB 1; Length 1178;
 Best Local Similarity 56.7%; Pred. No. 3.5e-208;
 Matches 704; Conservative 148; Mismatches 287; Indels 102; Gaps 26;

Qy	27	MDLSPDARIEDSLCIAENNINP---LVSASTVQTG---INIAGRIILGVL---GVPEAGQ 77
Db	1	MDNNFNI---NECIPYNCISNPEVEVLGGRIETGYTPIIDISLUTQFLLSBFVPGAG- 55
Qy	78	IAGFYSPLVGELWP-RGRDQWEIFLEHVEQLINQIITENARNTALARLOGLGDSFRAYQQ 136
Db	56	--FVLGLVDIIWGIFGPSQMDAFLVQIEQLINQRIEFAFNQAISEGLSNLYQIYAE 112
Qy	137	SLEDWLENRDARTSRVLYTQYIALEDLFLNAPLFAIRNOEVPPLMVYAAANLHLLLL 196
Db	113	SFEWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQYQVPLLSVYVQAANLHLSVL 172
Qy	197	RDASLFGSEFGLTSQEIQRVYRQVEQTRDYDVCVEMWNTGLNSLRGTNAASWVRYNQF 256
Db	173	RDVSFQQRGFDAATNSRYNDLTRLIGNYTDYAVRWYNTGLERWGPDSRDRWRYNQF 232
Qy	257	RDRLTLGLVDLVALFPSTYTRTPINTSAQLTREVTYDAIGATGVNMASNMWYNNAPSF 316
Db	233	RRELTLVLDIVLFPNYDSRRYPPIRVSQLTREIYT-----NPVLENFDGSRGSA 284
Qy	317	SAIETAVIRSHLLDFLEQLTIFSTSRWSATHMTWRGHTIQSRPIGG---LNTSTH 373
Db	285	QGIERS-IRSPHMLDIILNSITIVT-----DAHRGYYWSGHQIMASPVGSGPEFTPLY 338
Qy	374	GSTNTSINPVL-SFFSRDVTWTESYAGVLLGYLEPIHGVPTRVFNPNPO-----N 426
Db	339	GTWGNAAPOQRIVAQLCGGYRILSST-----LYRRPFN-----IGINNQQLSVLDGT 386
Qy	427	TFERGTYN--SOPYESPGQLKDSLETPEPPERPNYESYSHRLSHIGLI-----S 477
Db	387	EFAYGTSNLPNAVYRKSQ--TVDSLDEIIPPNNVPPRQGFSHRLSHVSMFRSGFSNS 444
Qy	478	QSRVHVPIVSWTHRSADRTNTISDSITQIPLVKSNLNSGTSVSGPGFTGGDIIRTNV 537
Db	445	VSIRAPMFWSIHRSAFNNIIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNS 503
Qy	538	NGS-----VLSMGLNFNTSLORYRVRYAASQTMVLRTVTVGGSTTDPQFPSTMSAN 591
Db	504	SGNNIQNRGYIEVPIHPPTS-TRYRVRYASVTPIHNVNNGNSIFSNVTVPATATSL 562
Qy	592	ESLTSQSFRAEPFVGISASGQTAGISIGNNAGROTTFHDKIEFIPITATFEAEYDLER 651
Db	563	DNLQSSDFGYFESANAFSTSLGNIUG--VRNPSGTAGVIIDREFIPVATLEAYNLER 620
Qy	652	AQAVNALFTNTNPRRLKTDVTDYHDQVSNLVACLSDPECLDEKRELLKVKYAKRLSD 711
Db	621	AQAVNALFTSNQLGLKTNVTDYHDQVSNLVYLSDEFCLDEKRELSKVKHAKRLSD 680
Qy	712	ERNLQDPNFTSINKOPDFISTNEQSNFTSIHQSHGHWGWSNITIOEGNDVFKENYVT 771
Db	681	ERNLLQDSNFKDINRQ-----ERWGGSGTGIITQGGDDVFKENYVT 722
Qy	772	LPGTTFNECYTYLYQKIGESLKYATRYQLRGYIEDSQDLEIYLIRYNKAKHETLDVPGTE 831
Db	723	LSGTFDECYTYLYQKIDESKLKAFTRYQLRGYIEDSQDLEIYLIRYNKAKHETVNVPGTG 782
Qy	832	SWNPLSVESPIGRGEPNRCAPHFENWPDLDCCSRGEEKCAHSHHSFLDIDIGCTDLHE 891
Db	783	SLWPLSAQSPIGKGEPNRCAPHLWNPDLDCCSRGEEKCAHSHHSFLDIDVGCITDLNE 842

Search completed: April 21, 2005, 04:17:21
 Job time : 59 secs

Qy	892	NLGVWVFKIKTOEGHARLGNLEFIEKPLLGALSRVKRAEKKWRDKREKLOLETKRVY 951
Db	843	DLGVWVFKIKTKODGHRARLGNLEFLEKPLVGLALARKRAEKKWRDKREKLEWETNIVY 902
Qy	952	TEAKEAVDALFVDSQYNRLQADTNIGMIHAADKLVHRIEAYLSLSVIPGVNAEIFEEL 1011
Db	903	KEAKESVDALFVNSQYDQLQADTNIAIHAADKRVHSIREAYLPESLVIPGVNAEIFEEL 962
Qy	1012	EGRIITAIISLYDARNVVKNGDFNGLACNVKGHVDV-QQSHHRSVLVIPWEAEVSQAV 1070
Db	963	EGRIITAFSLYDARNVIKNGDFNGLSCNVKGHVDVEEQNORSVLVVPWEAEVSQEV 1022
Qy	1071	RVCPGRGYTLRVYAKGYGEGCVTTHEENNTDELKFKNCEEEVYPTDTGTCNDYTAH 1130
Db	1023	RVCPGRGYTLRVYAKGYGEGCVTTHEENNTDELKFSNCEEEYPPNNTVTCNDYTVN 1082
Qy	1131	Q---GTAVCNRSNAGYEDAYEDVDTTASVNVYKPTYEBEETDVRDHNCEYDRGYVNYPP 1187
Db	1083	QBEYGGAY-TSRNRGYNEAPSV---PADYASVYEEKSYTDGRRENPCFENRGYRDYTPL 1137
Qy	1188	PAGYMTKELEYPPETDKWIEIGETEGKFIIVDSVELLLMEE 1228
Db	1138	PVGVTKELEYPPETDKWIEIGETEGTFIIVDSVELLLMEE 1178

61 NTAGILGVLGVPFAGQIASFYSLVGLWPRGRDQWEIFLEHVEQLINQOITENARNTA 120
 121 LARLOGLGDSFRAYQOSLEDWLENDDARTSVLYTQYIALELDPLNAMPFAIRNQVEP 180
 121 LARLOGLGDSFRAYQOSLEDWLENDDARTSVLYTQYIALELDPLNAMPFAIRNQVEP 180
 181 LLMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYRQVEQTRDYSYCVVWYNTGLN 240
 181 LLMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYRQVEQTRDYSYCVVWYNTGLN 240
 241 SLRGTAASWVRYNQFRDLTLGVLDLVALFPSYDTRTPINTSAQLTREVVYDAIGATG 300
 241 SLRGTAASWVRYNQFRDLTLGVLDLVALFPSYDTRTPINTSAQLTREVVYDAIGATG 300
 301 VNMASMNWYNNAPSALETAIVIRSPHLLDFLEQLTIFSTSRWSATRHMTYWRGHTIQ 360
 301 VNMASMNWYNNAPSALETAIVIRSPHLLDFLEQLTIFSTSRWSATRHMTYWRGHTIQ 360
 361 SRPIGGLNTSTHGSTNTSINPRLSFFGRDVTWTSYAGVLLWGLYLPBPIHGVPTVRFN 420
 361 SRPIGGLNTSTHGSTNTSINPRLSFFGRDVTWTSYAGVLLWGLYLPBPIHGVPTVRFN 420
 421 FRNPQTFERGTAANYQSPYESPGLQKDSSETLPPTTERPNYESYSHLSHIGLISQSR 480
 421 FRNPQTFERGTAANYQSPYESPGLQKDSSETLPPTTERPNYESYSHLSHIGLISQSR 480
 481 VHPVYVSWTHRSADRNTTSSDSITQIPLVKSFNLSGTSVSGPGFTGGDIIRTNVNGS 540
 481 VHPVYVSWTHRSADRNTTSSDSITQIPLVKSFNLSGTSVSGPGFTGGDIIRTNVNGS 540
 541 VLSMGLNFNTSLQRYRVRVRYAASQTMVLRTVVGSTTFDQGFPTMSANESLTSQSR 600
 541 VLSMGLNFNTSLQRYRVRVRYAASQTMVLRTVVGSTTFDQGFPTMSANESLTSQSR 600
 601 FAFPPVIGISAGSQTAGISINNAGQTHFDKIEPIPTATPEAYDILERAQEAVALP 660
 601 FAFPPVIGISAGSQTAGISINNAGQTHFDKIEPIPTATPEAYDILERAQEAVALP 660
 661 TTNPRRLKTDVTDYHIDQVSNLAVCLDSEFCLDEKRELLKVKYAKRLSDERLLQDPN 720
 661 TTNPRRLKTDVTDYHIDQVSNLAVCLDSEFCLDEKRELLKVKYAKRLSDERLLQDPN 720
 721 FTSINKQPDFISTNEOSNFTSIHQSEHGWGSENITIQEGNDVFKENYVTLPGTFNECY 780
 721 FTSINKQPDFISTNEOSNFTSIHQSEHGWGSENITIQEGNDVFKENYVTLPGTFNECY 780
 781 PTLYQKIGESSELKATRYQOLRGYIEDSQDLEIYLIRYNAKHETLDVPGTESVWPLSVES 840
 781 PTLYQKIGESSELKATRYQOLRGYIEDSQDLEIYLIRYNAKHETLDVPGTESVWPLSVES 840
 841 PIGRCGEPNRCAPHFENWPDLCSCRDGEKCAHSHHFLDIDIGCTDLHENIGVWVFK 900
 841 PIGRCGEPNRCAPHFENWPDLCSCRDGEKCAHSHHFLDIDIGCTDLHENIGVWVFK 900
 901 IKTQEGHARLGNLEFIEEKPLLEALSRVRAEKWKDRKEKLEKRYVTEAKEAVDA 960
 901 IKTQEGHARLGNLEFIEEKPLLEALSRVRAEKWKDRKEKLEKRYVTEAKEAVDA 960
 961 LFVDSQYRNLQADTNGIHAADKLVRHIREAYLSELVTPGVNAEIFEELGRIITAIS 1020
 961 LFVDSQYRNLQADTNGIHAADKLVRHIREAYLSELVTPGVNAEIFEELGRIITAIS 1020
 1021 LYDARNVVKNGDFNGLACVWNVXGHDVQSHRSVLVPEWEAEVSQAVRVCPRGYIL 1080
 1021 LYDARNVVKNGDFNGLACVWNVXGHDVQSHRSVLVPEWEAEVSQAVRVCPRGYIL 1080
 1081 RVYAYKEGYGEGCVTHIEIENNTDELKFKNCEBEEVYPTDGTGNDYTAHQGTAVCNRSN 1140
 1081 RVYAYKEGYGEGCVTHIEIENNTDELKFKNCEBEEVYPTDGTGNDYTAHQGTAVCNRSN 1140
 1200 AGYEDVDTTASVNNKPYTEEBEYTDVRRDNHCEYDRGYVNPPLPAGYMTKELEYFP

Db 1141 AGYEDVDTTASVNNKPYTEEBEYTDVRRDNHCEYDRGYVNPPLPAGYMTKELEYFP 1200
 QY 1201 ETDKWIIEIGTEGKFIIVDSVELLMEE 1228
 Db 1201 ETDKWIIEIGTEGKFIIVDSVELLMEE 1228
 RESULT 2
 US-10-428-961-38
 ; Sequence 38, Application US/10428961
 ; Publication No. US20030237111A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baum, James A.
 ; APPLICANT: Chu, Chih-Wei
 ; APPLICANT: Donovan, William P.
 ; APPLICANT: Gilmer, Mark J.
 ; APPLICANT: Rupar, Amy J.
 ; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
 ; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
 ; FILE REFERENCE: MECO201--1
 ; CURRENT APPLICATION NUMBER: US/10/428,961
 ; CURRENT FILING DATE: 2003-05-02
 ; PRIOR APPLICATION NUMBER: 09/661,322
 ; PRIOR FILING DATE: 2000-09-13
 ; PRIOR APPLICATION NUMBER: 60/153,995
 ; PRIOR FILING DATE: 1999-09-15
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 38
 ; LENGTH: 1228
 ; TYPE: PRT
 ; ORGANISM: Bacillus thuringiensis
 ; US-10-428-961-38
 Query Match 99.8%; Score 6464; DB 15; Length 1228;
 Best Local Similarity 99.7%; Pred No. 0;
 Matches 1224; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 LTSNRKNEIINALSIPAVSNHSTQMDLSPARDIEDSLCIAEGNNINPLVSASTVQTGI 60
 Db 1 LTSNRKNEIINALSIPAVSNHSTQMDLSPARDIEDSLCIAEGNNINPLVSASTVQTGI 60
 QY 61 NTAGILGVLGVPFAGQIASFYSLVGLWPRGRDQWEIFLEHVEQLINQOITENARNTA 120
 Db 61 NTAGILGVLGVPFAGQIASFYSLVGLWPRGRDQWEIFLEHVEQLINQOITENARNTA 120
 QY 121 LARLOGLGDSFRAYQOSLEDWLENDDARTSVLYTQYIALELDPLNAMPFAIRNQVEP 180
 Db 121 LARLOGLGDSFRAYQOSLEDWLENDDARTSVLYTQYIALELDPLNAMPFAIRNQVEP 180
 QY 181 LLMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYRQVEQTRDYSYCVVWYNTGLN 240
 Db 181 LLMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYRQVEQTRDYSYCVVWYNTGLN 240
 QY 241 SLRGTAASWVRYNQFRDLTLGVLDLVALFPSYDTRTPINTSAQLTREVVYDAIGATG 300
 Db 241 SLRGTAASWVRYNQFRDLTLGVLDLVALFPSYDTRTPINTSAQLTREVVYDAIGATG 300
 QY 301 VNMASMNWYNNAPSALETAIVIRSPHLLDFLEQLTIFSTSRWSATRHMTYWRGHTIQ 360
 Db 301 VNMASMNWYNNAPSALETAIVIRSPHLLDFLEQLTIFSTSRWSATRHMTYWRGHTIQ 360
 QY 361 SRPIGGLNTSTHGSTNTSINPRLSFFGRDVTWTSYAGVLLWGLYLPBPIHGVPTVRFN 420
 Db 361 SRPIGGLNTSTHGSTNTSINPRLSFFGRDVTWTSYAGVLLWGLYLPBPIHGVPTVRFN 420
 QY 421 FRNPQTFERGTAANYQSPYESPGLQKDSSETLPPTTERPNYESYSHLSHIGLISQSR 480
 Db 421 FRNPQTFERGTAANYQSPYESPGLQKDSSETLPPTTERPNYESYSHLSHIGLISQSR 480
 QY 481 VHPVYVSWTHRSADRNTTSSDSITQIPLVKSFNLSGTSVSGPGFTGGDIIRTNVNGS 540
 Db 481 VHPVYVSWTHRSADRNTTSSDSITQIPLVKSFNLSGTSVSGPGFTGGDIIRTNVNGS 540

seq id no 63 in the previous file

This Page Blank (uspto)

QY 541 VLSMGLNFNTSLQRYRVRVRYAASQTMVLRTVTVGGSTTDFDQGPSTMSANESLTSQSPR 600
DB 541 VLSMGLNFNTSLQRYRVRVRYAASQTMVLRTVTVGGSTTDFDQGPSTMSANESLTSQSPR 600
QY 601 FAEFPVGISASGOTAGISINNAAGROTFFDKIEPIPTATPEAEYDLERAOEAVNALF 660
DB 601 FAEFPVGISASGOTAGISINNAAGROTFFDKIEPIPTATPEAEYDLERAOEAVNALF 660
QY 661 TTNPRRLKTDVTDYHIDQVSNLVACLSDFCLDEKRELEKVKYAKRLSDERNLLQDPN 720
DB 661 TTNPRRLKTDVTDYHIDQVSNLVACLSDFCLDEKRELEKVKYAKRLSDERNLLQDPN 720
QY 721 FTSINQKPDISTNEQSNFTSIHQSEHGHWGSENITIQEGNDVFKENYVTLPGTFNECY 780
DB 721 FTSINQKPDISTNEQSNFTSIHQSEHGHWGSENITIQEGNDVFKENYVTLPGTFNECY 780
QY 781 PTLYQKIGESSELKAYTRYQLRGVIEDSQDLEIYLIRYNAKHETLDVPGTESVWPLSVES 840
DB 781 PTLYQKIGESSELKAYTRYQLRGVIEDSQDLEIYLIRYNAKHETLDVPGTESVWPLSVES 840
QY 841 PIGRCGEPNRCAPHFENWPDLDSCRDGKCAHSHHFSLDIDIGCTDLHENLGVWVVKF 900
DB 841 PIGRCGEPNRCAPHFENWPDLDSCRDGKCAHSHHFSLDIDIGCTDLHENLGVWVVKF 900
QY 901 IKTOEGHARLGNLEFTEEPKLLGEALSRVRAEKKWRDKREKLOLETKRYVYTAKEAVDA 960
DB 901 IKTOEGHARLGNLEFTEEPKLLGEALSRVRAEKKWRDKREKLOLETKRYVYTAKEAVDA 960
QY 961 LFDVDSQVNRLOADTNIGMIHAADKLVHRIEAYLSELVTPGVNAEIPFELEGRIITAIS 1020
DB 961 LFDVDSQVNRLOADTNIGMIHAADKLVHRIEAYLSELVTPGVNAEIPFELEGRIITAIS 1020
QY 1021 LYDARNVKNMGDFNGLACVNNVKGHVQVQSHRSVLVPEWEAEVSQAVRVCPCRGYIL 1080
DB 1021 LYDARNVKNMGDFNGLACVNNVKGHVQVQSHRSVLVPEWEAEVSQAVRVCPCRGYIL 1080
QY 1081 RVTAYKEGEGCVTTHEINNTDELKFNCEBEEVPTDTGTCNDYTAHQGTAVCNERN 1140
DB 1081 RVTAYKEGEGCVTTHEINNTDELKFNCEBEEVPTDTGTCNDYTAHQGTAVCNERN 1140
QY 1141 AGYEDAYEVDVTTASVNNKPYEETVTVDRDNHCEYDRGVNYPPLPAGYVTKLEYFP 1200
DB 1141 AGYEDAYEVDVTTASVNNKPYEETVTVDRDNHCEYDRGVNYPPLPAGYVTKLEYFP 1200
QY 1201 ETDKWIEIGETEGTFIVDSVLELLMEE 1228
DB 1201 ETDKWIEIGETEGTFIVDSVLELLMEE 1228

RESULT 3

US-10-428-961-63
; Sequence 63, Application US/10428961
; Publication No. US2003023711A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupa, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; FILE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
; FILE REFERENCE: MECO201-1
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/153,995
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
; LENGTH: 1227

; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
; US-10-428-961-63

Query Match 91.3%; Score 5912.5; DB 15; Length 1227;
Best Local Similarity 91.6%; Pred. No. 0;
Matches 1127; Conservative 36; Mismatches 62; Indels 5; Gaps 3;

QY 1 LTSNRKNEEIIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI 60
DB 1 LTSNRKNEEIIINALSIPAVSNHSAQMNLSLDARIEDSLCIAEGNNIDPPVSASTVQTGI 60
QY 61 NIAGRILGVLPVFPAGQIASFYSLVGLMELPRGRDQWEIFLEHVQLINOQIITENARNTA 120
DB 61 NIAGRILGVLPVFPAGQIASFYSLVGLMELPRGRDQWEIFLEHVHLIRQOVTENTRDTA 120
QY 121 LARLOGLGDSFRAYQOSLEDWLENRDDARTSRVLYTQYIALELDLFLNAMPFLAIRNOEVP 180
DB 121 LARLOGLGDSFRAYQOSLEDWLENRDDARTSRVLYTQYIALELDLFLNAMPFLAIRNOEVP 180
QY 181 LLMVYAAANLHLLLRDASLFGSEFGLTSQEIQRYRYERQVEQTRDYSYCVWEYNTGLN 240
DB 181 LLMVYAAANLHLLLRDASLFGSEFGLTSQEIQRYRYERQVEKTRYSYCARWYNTGLN 240
QY 241 SLRGTVAAWRYNQPRDLITGLVLDLVALFPSYDTRTPINTSAQLTREYVTDATGATG 300
DB 241 NLRGTVAAWRYNQPRDLITGLVLDLVALFPSYDTRTPINTSAQLTREYVTDATGATG 300
QY 301 V--NMAWNNVNNAPSPSAIETAVIRSPLHLDLFLQLTIESSTSSSWSATHTMYRGT 358
DB 301 APSGFATWNNFNNAPSPSAIETAVIRSPLHLDLFLQLTIESSTSSSWSATHTMYRGT 358
QY 359 IQSRPIGGGLNTSTHGSTNTSINPVLSPFSDVYVYTESYAGVLLMGVILEPIHGVTVR 418
DB 361 LBSRTIRGSLTWTGNTSINPVLSPFSDVYVYTESYAGVLLMGVILEPIHGVTVR 418
QY 419 FNRUPQNTFERTGANYSQPYSPGLQKDSLETLPETTERPNYESYSHRSLHGLISQ 478
DB 419 FNRWNPNSL-RGSLYITGTVGTGVTGQTFDSELPETTERPNYESYSHRSLHGLISQ 477
QY 479 SRVHPVYVSWTHRSADRTNTISSDSITQIPVKSFNLSGTSVWSGPGTGGDIITNVN 538
DB 478 NTLRAPVYVSWTHRSADRTNTISSDSITQIPVKSFNLSGTSVWSGPGTGGDIITNVN 537
QY 539 GSVLWGLNFNTSLQRYRVRVRYAASQTMVLRTVTVGGSTTDFDQGPSTMSANESLTSQ 598
DB 538 GSVLWGLNFNTSLQRYRVRVRYAASQTMVLRTVTVGGSTTDFDQGPSTMSANESLTSQ 597
QY 599 FRPAEFPVGISASGOTAGISINNAAGROTFFDKIEPIPTATPEAEYDLERAOEAVNA 658
DB 598 FRPAEFPVGISASGOTAGISINNAAGROTFFDKIEPIPTATPEAEYDLERAOEAVNA 657
QY 659 LFTNTNPRRLKTDVTDYHIDQVSNLVACLSDFCLDEKRELEKVKYAKRLSDERNLLQD 718
DB 658 LFTNTNPRRLKTDVTDYHIDQVSNLVACLSDFCLDEKRELEKVKYAKRLSDERNLLQD 717
QY 719 PNFTSINKQPDISTNEQSNFTSIHQSEHGHWGSENITIQEGNDVFKENYVTLPGTFNE 778
DB 718 PNFTSINKQPDISTNEQSNFTSIHQSEHGHWGSENITIQEGNDVFKENYVTLPGTFNE 777
QY 779 CYPTLYQKIGESSELKAYTRYQLRGVIEDSQDLEIYLIRYNAKHETLDVPGTESVWPLSV 838
DB 778 CYPTLYQKIGESSELKAYTRYQLRGVIEDSQDLEIYLIRYNAKHETLDVPGTESVWPLSV 837
QY 839 ESPICRCGEPNRCAPHFENWPDLDSCRDGKCAHSHHFSLDIDIGCTDLHENLGVWVVK 898
DB 838 ESPICRCGEPNRCAPHFENWPDLDSCRDGKCAHSHHFSLDIDIGCTDLHENLGVWVVK 897
QY 899 FKIKTOEGHARLGNLEFTEEPKLLGEALSRVRAEKKWRDKREKLOLETKRYVYTAKEAV 958
DB 898 FKIKTOEGHARLGNLEFTEEPKLLGEALSRVRAEKKWRDKREKLOLETKRYVYTAKEAV 957
QY 959 DALFVDSQVNRLOADTNIGMIHAADKLVHRIEAYLSELVTPGVNAEIPFELEGRIITA 1018

This Page Blank (uspto)

Db 2161 TTCATCCATCAATAAGCAACAGAGCTTCATATCTACTAATGAGCAATCGAATTTTCCACA 2220
 QY 2221 TCTATCCATCAACCAATCTGACATGGAATGCTGGGAGTGGAGACATTAACAATCCAGGAA 2280
 Db 2221 TCTATCCATCAACCAATCTGACATGGAATGCTGGGAGTGGAGACATTAACAATCCAGGAA 2280
 QY 2281 GGAATGACGTATTTAAAGAGAAATACGTACACATACCGGGGACTTTTAATGAGTGTAT 2340
 Db 2281 GGAATGACGTATTTAAAGAGAAATACGTACACATACCGGGGACTTTTAATGAGTGTAT 2340
 QY 2341 CCGACGTATTTATCAAAAAATAGGAGAGTGGAAATTAAGCTTATATCTCGCTACCAA 2400
 Db 2341 CCGACGTATTTATCAAAAAATAGGAGAGTGGAAATTAAGCTTATATCTCGCTACCAA 2400
 QY 2401 TTAAGGGGTATATTGAAGATAGTCAAGATTTAGAGATATATTGATCTGTTAATGCG 2460
 Db 2401 TTAAGGGGTATATTGAAGATAGTCAAGATTTAGAGATATATTGATCTGTTAATGCG 2460
 QY 2461 AAACATGAAACATTTGATGTTCCAGGTACCGAGTCCGTATGGCGGCTTTTCAGTTGAAAGC 2520
 Db 2461 AAACATGAAACATTTGATGTTCCAGGTACCGAGTCCGTATGGCGGCTTTTCAGTTGAAAGC 2520
 QY 2521 CCAATCGAAGGTGCGGAGAACCGAATCGATGCGCACCAATTTTGAATGGAATCTCTGAT 2580
 Db 2521 CCAATCGAAGGTGCGGAGAACCGAATCGATGCGCACCAATTTTGAATGGAATCTCTGAT 2580
 QY 2581 CTAGATGTTCTCCGAGAGTGGAGAAATGCGCATCATTTCCCATCATTTCTCTTTG 2640
 Db 2581 CTAGATGTTCTCCGAGAGTGGAGAAATGCGCATCATTTCCCATCATTTCTCTTTG 2640
 QY 2641 GATATTGATATTGGATGTCACAGACTTGCATGAGAACTAGGCGGTGGGTGATTCAG 2700
 Db 2641 GATATTGATATTGGATGTCACAGACTTGCATGAGAACTAGGCGGTGGGTGATTCAG 2700
 QY 2701 ATTAAGACGAGGAGGTGATGCAAGACTAGGGAATCTGGAATTTATGAAGAGAAACCA 2760
 Db 2701 ATTAAGACGAGGAGGTGATGCAAGACTAGGGAATCTGGAATTTATGAAGAGAAACCA 2760
 QY 2761 TTATTAGGAGAGCACTGCTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2820
 Db 2761 TTATTAGGAGAGCACTGCTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2820
 QY 2821 GAAAACTCAATTTGAAACAAACAGATATACAGAGGCAAAAGAGCTGGATGCT 2880
 Db 2821 GAAAACTCAATTTGAAACAAACAGATATACAGAGGCAAAAGAGCTGGATGCT 2880
 QY 2881 TTATTGATAGTTCTCAATATATAGATTACAGCGGATACAAACATTTGGCATGATTCAT 2940
 Db 2881 TTATTGATAGTTCTCAATATATAGATTACAGCGGATACAAACATTTGGCATGATTCAT 2940
 QY 2941 GCGGAGATAAATCTGTTTCATCGAATTCGAGAGGCTTATCTGTCAGAAATATCTGTATC 3000
 Db 2941 GCGGAGATAAATCTGTTTCATCGAATTCGAGAGGCTTATCTGTCAGAAATATCTGTATC 3000
 QY 3001 CCGGTGTAATTCGGAATTTTGAAGATTTAGAGGTCGCAATTCATCTGCAATCTCC 3060
 Db 3001 CCGGTGTAATTCGGAATTTTGAAGATTTAGAGGTCGCAATTCATCTGCAATCTCC 3060
 QY 3061 CTATACGATCGGAGAAATGCTGTTAAATGTTGATTTTAAATGATTTAGCATGCTCG 3120
 Db 3061 CTATACGATCGGAGAAATGCTGTTAAATGTTGATTTTAAATGATTTAGCATGCTCG 3120
 QY 3121 AATGTAAGGCGCATGTAGATGTACAAAGAGGCTTATCTGCTGCTGTTATCCCA 3180
 Db 3121 AATGTAAGGCGCATGTAGATGTACAAAGAGGCTTATCTGCTGCTGTTATCCCA 3180
 QY 3181 GAATGGAGAGAGTGTACAGAGAGTTCGGTCTGTCGGGGGCTGGCTATATCTC 3240
 Db 3181 GAATGGAGAGAGTGTACAGAGAGTTCGGTCTGTCGGGGGCTGGCTATATCTC 3240
 QY 3241 CGTGTACAGAGGTACAAAGAGGATATGAGAGGTTGTTAAGCATCCATCAATCCAG 3300
 Db 3241 CGTGTACAGAGGTACAAAGAGGATATGAGAGGTTGTTAAGCATCCATCAATCCAG 3300

QY 3301 AACATACAGAGCACTAAATTTTAAATCTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3360
 Db 3301 AACATACAGAGCACTAAATTTTAAATCTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3360
 QY 3361 ACAGGAACGTGTAAATGATATATCTGCACCAAGGTACAGCAGTATGTAATTTCCCGTAAT 3420
 Db 3361 ACAGGAACGTGTAAATGATATATCTGCACCAAGGTACAGCAGTATGTAATTTCCCGTAAT 3420
 QY 3421 GCTGGATATGAGATGATATGATATGATATGATATGATATGATATGATATGATATGATATG 3480
 Db 3421 GCTGGATATGAGATGATATGATATGATATGATATGATATGATATGATATGATATGATATG 3480
 QY 3481 TATGAAG 3540
 Db 3481 TATGAAG 3540
 QY 3541 TATGTGAATTTATCCACACTTACAGCTGCTTATATGACAAAAGAAATAGAAATTTCCCA 3600
 Db 3541 TATGTGAATTTATCCACACTTACAGCTGCTTATATGACAAAAGAAATAGAAATTTCCCA 3600
 QY 3601 GAAACCGATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3660
 Db 3601 GAAACCGATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3660
 QY 3661 GTGGATTTACTCTTATGAGAGAGATAG 3687
 Db 3661 GTGGATTTACTCTTATGAGAGAGATAG 3687

RESULT 2
 US-10-428-961-37
 ; Sequence 37, Application US/10428961
 ; Publication NO. US20030237111A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baum, James A.
 ; APPLICANT: Chu, Chih-Rei
 ; APPLICANT: Donovan, William P.
 ; APPLICANT: Gilmer, Amy J.
 ; APPLICANT: Rupar, Mark J.
 ; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
 ; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
 ; FILE REFERENCE: MECO201--1
 ; CURRENT APPLICATION NUMBER: US/10/428,961
 ; PRIOR FILING DATE: 2003-05-02
 ; PRIOR APPLICATION NUMBER: 09/661,322
 ; PRIOR FILING DATE: 2000-09-13
 ; PRIOR APPLICATION NUMBER: 60/153,995
 ; PRIOR FILING DATE: 1999-09-15
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 37
 ; LENGTH: 4173
 ; TYPE: DNA
 ; ORGANISM: Bacillus thuringiensis
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(3687)
 US-10-428-961-37

Query Match 99.4%; Score 3666.2; DB 17; Length 4173;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 3674; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 TTGACTTCAATAG 60
 Db 1 TTGACTTCAATAG 60
 QY 61 TCGAATCAATTCACAAATGAGATCTATCAGCAGATGCTCGTATTTAGAGATTTCTTTTGT 120
 Db 61 TCGAATCAATTCACAAATGAGATCTATCAGCAGATGCTCGTATTTAGAGATTTCTTTTGT 120
 QY 121 ATAGCCGAGGGGAGATATATCAATCCACTTTGTAGGAGATCAACAGTCCAAACCGGATATT 180

This Page Blank (uspto)

121 ATAGCCGAGGGAATAATCAATCACTTTGATGCGATCAACAGTCCAAACGGGTATT 180
181 AACATAGCTGGTGAATACTAGTGTATATAGCGGTACCGTTTGGTGGCAAAATAGCTAGT 240
181 AACATAGCTGGTGAATACTAGTGTATATAGCGGTACCGTTTGGTGGCAAAATAGCTAGT 240
241 TTTTATAGTTTCTTGTGGTGAATATAGCGGCGCGGCGGAGATCACTGGGAAATTTTC 300
241 TTTTATAGTTTCTTGTGGTGAATATAGCGGCGCGGCGGAGATCACTGGGAAATTTTC 300
301 CTAGAACATGTCGAACAACTTAAATCAACAAATAACAGAAATGCTAGGAATACGGCA 360
301 CTAGAACATGTCGAACAACTTAAATCAACAAATAACAGAAATGCTAGGAATACGGCA 360
361 CTTGCTCGAATCAAGGTTTAGAGATTCCTTTAGAGCCTATCAACAGTCACTTGAAGAT 420
421 TGGCTAGAAAACCGTGATGATCAAGAGAGAGAGTGTCTTTATACCCCAATATATAGCC 480
421 TGGCTAGAAAACCGTGATGATCAAGAGAGAGAGTGTCTTTATACCCCAATATATAGCC 480
481 TTAGAACTTTGATTTCTTAATCGATGCGCGCTTTTTCGCAATTAGAAACCAAGAGTTCCA 540
481 TTAGAACTTTGATTTCTTAATCGATGCGCGCTTTTTCGCAATTAGAAACCAAGAGTTCCA 540
541 TTATTAATGGTATATGCTCAAGCTGCAAAATTAACCTTATTAATTTAGAGATGCTCT 600
541 TTATTAATGGTATATGCTCAAGCTGCAAAATTAACCTTATTAATTTAGAGATGCTCT 600
601 CTTTGTGTAGTGAATTTGGCTTACATCGCAGGAATTCAGAGTATTTATGCGGCCAA 660
601 CTTTGTGTAGTGAATTTGGCTTACATCGCAGGAATTCAGAGTATTTATGCGGCCAA 660
661 GTGGAAACAAAGAGATTAATCCGACTATGCGTAGAATGGTATTAATACAGGTCTAAAT 720
661 GTGGAAACAAAGAGATTAATCCGACTATGCGTAGAATGGTATTAATACAGGTCTAAAT 720
721 AGCTTGAGAGGGAACAAATGCGCAAGTGGGTGCTTATAATCAATTCGGTAGAGATCTA 780
721 AGCTTGAGAGGGAACAAATGCGCAAGTGGGTGCTTATAATCAATTCGGTAGAGATCTA 780
781 ACCTTAGGGGTATAGATCTAGTGGCACTATCCCAAGCTATGACACTCGCACTTATCCA 840
781 ACCTTAGGGGTATAGATCTAGTGGCACTATCCCAAGCTATGACACTCGCACTTATCCA 840
841 ATAAATACAGTCTCAGTTTAAACAGGGAAGTTTATACAGACCAATTTGGAGCAACAGGG 900
841 ATAAATACAGTCTCAGTTTAAACAGGGAAGTTTATACAGACCAATTTGGAGCAACAGGG 900
901 GTAAATATGCAAGTATGAATTTGGTATTAATTAATTAATTAATTTCCGCTATAGAG 960
901 GTAAATATGCAAGTATGAATTTGGTATTAATTAATTAATTAATTTCCGCTATAGAG 960
961 ACTGCGGTATCCGAAGCCGCACTACTTGTATTTCTAGAACAACTTAACTTATTTAGC 1020
961 ACTGCGGTATCCGAAGCCGCACTACTTGTATTTCTAGAACAACTTAACTTATTTAGC 1020
1021 ACTTTCATCAGATGGAGTGTCTAGGCAATGACTTACTTGGCGGGGCAACAAATTTCAA 1080
1021 ACTTTCATCAGATGGAGTGTCTAGGCAATGACTTACTTGGCGGGGCAACAAATTTCAA 1080
1081 TCTCGGCAATAGAGGCGGATTAATTAATTAATTAATTAATTTAGCAATCTTCTATT 1140
1081 TCTCGGCAATAGAGGCGGATTAATTAATTAATTAATTAATTTAGCAATCTTCTATT 1140
1141 AATCCTGTAAAGATTAATTAATTTCTCTCGAGAGCGTATTTGGAGTGAATCATATAGCAGGA 1200
1141 AATCCTGTAAAGATTAATTAATTTCTCTCGAGAGCGTATTTGGAGTGAATCATATAGCAGGA 1200
1201 GTGCTTCTATGGGGAATTTACCTTGAACCTTATTCATGCTGTCCTTCTGTTAGATTTAAT 1260

1201 GTGCTTCTATGGGGAATTTACCTTGAACCTTATTCATGCTGTCCTTCTGTTAGATTTAAT 1260
1261 TTTTAGGAACCTCAGAAATCTTTTGAAGAGGTACTGCTAACTATAGTCAACCCCTATGAG 1320
1261 TTTTAGGAACCTCAGAAATCTTTTGAAGAGGTACTGCTAACTATAGTCAACCCCTATGAG 1320
1321 TCACCTGGGCTTCAATTTAAAGATTGAAATCTGAATTAACACAGAAACCAACAGGCA 1380
1321 TCACCTGGGCTTCAATTTAAAGATTGAAATCTGAATTAACACAGAAACCAACAGGCA 1380
1381 CCAATTTATGAATCATATAGTATCATAGGCTTCTCAATAGGCTCAATTTCAATCTAGG 1440
1381 CCAATTTATGAATCATATAGTATCATAGGCTTCTCAATAGGCTCAATTTCAATCTAGG 1440
1441 GTGATGTACCCAGTATATTTCTTGACCGCAGCGTAGTCAGATCGTACAAATACCAATAGT 1500
1441 GTGATGTACCCAGTATATTTCTTGACCGCAGCGTAGTCAGATCGTACAAATACCAATAGT 1500
1501 TCAGATAGCATAAACAAATACCAATTTGGTAAATCATTTCAACCTTAAATTCAGGTACCTCT 1560
1501 TCAGATAGCATAAACAAATACCAATTTGGTAAATCATTTCAACCTTAAATTCAGGTACCTCT 1560
1561 GTAGTCAGTGGCCCGAGGATTTACAGGAGGGGATATAATCCGAACTTAACGTTAAATGGTAGT 1620
1561 GTAGTCAGTGGCCCGAGGATTTACAGGAGGGGATATAATCCGAACTTAACGTTAAATGGTAGT 1620
1621 GTACTAGTATGGGTCTTTAAATTTTAAATAATACATCATTTACAGCGGTATCGCGTAGAGTT 1680
1621 GTACTAGTATGGGTCTTTAAATTTTAAATAATACATCATTTACAGCGGTATCGCGTAGAGTT 1680
1681 CGTTATGCTGCTTCTCAAAATGCTGAGGGTAACTGTCGAGGGAGTACTACTTTT 1740
1681 CGTTATGCTGCTTCTCAAAATGCTGAGGGTAACTGTCGAGGGAGTACTACTTTT 1740
1741 GATCAAGATTTCCCTAGTACTATGAGTCAAAATGAGTCTTTTGACATCTCAATCATTTAGA 1800
1741 GATCAAGATTTCCCTAGTACTATGAGTCAAAATGAGTCTTTTGACATCTCAATCATTTAGA 1800
1801 TTTGACAGAAATTTCCCTAGTACTATGAGTCAAAATGAGTCTTTTGACATCTCAATCATTTAGA 1860
1801 TTTGACAGAAATTTCCCTAGTACTATGAGTCAAAATGAGTCTTTTGACATCTCAATCATTTAGA 1860
1861 AGTAATAATGCAAGTATGACAAACGTTTTCACTTTGATAAAATTTGAATTTCAATTTACT 1920
1861 AGTAATAATGCAAGTATGACAAACGTTTTCACTTTGATAAAATTTGAATTTCAATTTACT 1920
1921 GCAACCTTTCGAGCAGAAATACGATTTAGAAAGGGCGCAAGAGCGGTGAATCTCTGTTT 1980
1921 GCAACCTTTCGAGCAGAAATACGATTTAGAAAGGGCGCAAGAGCGGTGAATCTCTGTTT 1980
1981 ACTAATACGAATTCGAAGAGATTGAAACAGATGTGACAGATTTATCATATTCATCAAGTA 2040
1981 ACTAATACGAATTCGAAGAGATTGAAACAGATGTGACAGATTTATCATATTCATCAAGTA 2040
2041 TCCAAATTTAGTGGCGTTTATCGGATGAAATTTCTGCTTAGATGAAAGAGAGATTTACTT 2100
2041 TCCAAATTTAGTGGCGTTTATCGGATGAAATTTCTGCTTAGATGAAAGAGAGATTTACTT 2100
2101 GAGAAAGTGAATATTCGAAACGACTTCAGTGTAGTGAAGAACTTACTCCAAAGATCCAAAC 2160
2101 GAGAAAGTGAATATTCGAAACGACTTCAGTGTAGTGAAGAACTTACTCCAAAGATCCAAAC 2160
2161 TTTCAATCCATCAATAGGCAACAGACTTTCATATCTTACTTAATGAGCAATCGAATTTTACA 2220
2161 TTTCAATCCATCAATAGGCAACAGACTTTCATATCTTACTTAATGAGCAATCGAATTTTACA 2220
2221 TCTATCCATGAACAAATCTGAAATGATGGTGGGAGTGTAGAACATTACAAATCCAGGAA 2280
2221 TCTATCCATGAACAAATCTGAAATGATGGTGGGAGTGTAGAACATTACAAATCCAGGAA 2280
2281 GGAATGAGCTATTTAAAGAGAAATTTACGTCACATCCGCGGACTTTTAAATGAGTGTAT 2340
2281 GGAATGAGCTATTTAAAGAGAAATTTACGTCACATCCGCGGACTTTTAAATGAGTGTAT 2340

This Page Blank (uspto)

Qy	3421	GCTGGATATGAGGATGCAATATGAAGTTTGATACATACAGCATCTGTTAATTAACAACCGACT	3480
Db	3421	GCTGGATATGAGGATGCAATATGAAGTTTGATACATACAGCATCTGTTAATTAACAACCGACT	3480
Qy	3481	TATGAGAGAAACGTCATACAGATGTACGAAAGAGATAATCATTTGTGAATATGACAGAGG	3540
Db	3481	TATGAGAGAAACGTCATACAGATGTACGAAAGAGATAATCATTTGTGAATATGACAGAGG	3540
Qy	3541	TATGTGAATTTATCCACCCTACCACTACCACTGGTGTATATGACAAAAGAAATTAGAAATACTTCCCA	3600
Db	3541	TATGTGAATTTATCCACCCTACCACTACCACTGGTGTATATGACAAAAGAAATTAGAAATACTTCCCA	3600
Qy	3601	GAACCCGATTAAGGTATGGAATGAGATGGAGAAACGGAAGGGAAGTTTATTTGTAGACAGC	3660
Db	3601	GAACCCGATTAAGGTATGGAATGAGATGGAGAAACGGAAGGGAAGTTTATTTGTAGACAGC	3660
Qy	3661	GTGGAATTACTCTTATGGAGGAATAG	3687
Db	3661	ATAGAATTACTCTTATGGGAAGAATAG	3687

RESULT 3

US-10-428-961-62

Sequence 62, Application US/10428961

Publication No. US20030237111A1

GENERAL INFORMATION:

APPLICANT: Baum, James A.

APPLICANT: Chu, Chih-Rei

APPLICANT: Donovan, William P.

APPLICANT: Galmer, Amy J.

APPLICANT: Rupar, Mark J.

TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin

TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amend)

FILE REFERENCE: MECO201--1

CURRENT APPLICATION NUMBER: US/10/428,961

CURRENT FILING DATE: 2003-05-02

PRIOR APPLICATION NUMBER: 09/661,322

PRIOR FILING DATE: 2000-09-13

PRIOR APPLICATION NUMBER: 60/153,995

PRIOR FILING DATE: 1999-09-15

NUMBER OF SEQ ID NOS: 63

SOFTWARE: Patent in version 3.2

SEQ ID NO 62

LENGTH: 3684

TYPE: DNA

ORGANISM: *Bacillus thuringiensis*

US-10-428-961-62

Query Match	88.4%	Score 3260.2;	DB 17;	Length 3684;
Best Local Similarity	93.3%;	Pred. No. 0;		
Matches 3445;	Conservative 0;	Mismatches 233;	Indels 15;	Gaps 3;

Qy	1	TTGACTTCAAAATAGGAAAAATGAGAATGAAATATAAATGCTTTATCGATTCCAGCTGTA	60
Db	1	TTGACTTCAAAATAGGAAAAATGAGAATGAAATATAAATGCTTTATCGATTCCAGCTGTA	60
Qy	61	TGGAATCATTCACACAAATGATCTATCACAGATGCTCGTATTGAGGATCTTTGTGCT	120
Db	61	TGGAATCATTCGCGACAAATGATCTTATCAACGATGCTCGTATTGAGGATAGCTTTGTG	120
Qy	121	ATAGCCGAGGGGAATAATATCAATCCATCTGTTAGCGCATCAACAGTCCAAACGGGTATT	180
Db	121	ATAGCCGAGGGGAACAAATATCGATCCATTTGTTAGGCGCATCAACAGTCCAAACGGGTATT	180
Qy	181	ACATAGCTGGTAGAATACCTAGGTGTAATTAGGCGTACCGTTTGTCTGGACAAATAGCTAGT	240
Db	181	AACATAGCTGGTAGAATACCTAGGTGTAATTAGGCGTACCGTTTGTCTGGACAAATAGCTAGT	240
Qy	241	TTTTATAGTTTCTTGTGTTGTCAAATTATGCGCCCGCGCAGAGATCAGTGGGAAATTTTC	300
Db	241	TTTTATAGTTTCTTGTGTTGTTGAAATTATGCGCCCGCGCAGAGATCCTTGGGAAATTTTC	300
Qy	301	CTAGAACATGTGCAACAACTTATAAATCAACAAATAACAGAAATATGCTAGGAATACGGCA	360

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 21, 2005, 03:37:54 ; Search time 58 Seconds
(without alignments)
1580.501 Million cell updates/sec

Title: US-10-614-524-2
Perfect score: 6479
Sequence: 1 LTSNRKNEIINALSIPAV.....IGTEGKFIVDSVELLMEE 1228

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6462	99.7	1228	4	US-09-661-322A-38
2	5926.5	91.5	1227	1	US-08-448-170-8
3	5926.5	91.5	1227	3	US-08-961-803-9
4	5912.5	91.3	1227	4	US-09-661-322A-63
5	5659.5	87.4	1207	1	US-07-951-715A-7
6	5659.5	87.4	1207	2	US-08-459-448A-7
7	5659.5	87.4	1207	3	US-08-459-595A-7
8	5659.5	87.4	1207	3	US-08-459-504B-7
9	5659.5	87.4	1207	3	US-08-459-444-7
10	5659.5	87.4	1207	3	US-09-053-549-8
11	5659.5	87.4	1207	3	US-09-547-422-7
12	5659.5	87.4	1207	4	US-09-988-462-7
13	5436.5	83.9	1227	3	US-09-053-549-2
14	5237.5	80.8	1229	1	US-08-100-709-4
15	5237.5	80.8	1229	1	US-08-176-865-4
16	5237.5	80.8	1229	1	US-08-474-038-4
17	5237.5	80.8	1229	2	US-08-779-046-4
18	5237.5	80.8	1229	2	US-08-881-340-4
19	5108	78.8	1186	3	US-09-178-252-23
20	5108	78.8	1186	4	US-09-826-660-23
21	3977.5	61.4	1174	1	US-08-040-751-3
22	3977.5	61.4	1174	1	US-08-291-368-2
23	3977.5	61.4	1174	2	US-08-962-190-2
24	3977.5	61.4	1174	5	PCT-US95-10310-2
25	3977.5	61.4	1174	6	5164180-4
26	3977.5	61.4	1174	6	5164180-4
27	3791	58.5	1176	1	US-08-434-823-2

```

28 3791 58.5 1176 1 US-08-457-366-2 Sequence 2, Appli
29 3579 55.2 1170 1 US-08-032-364-2 Sequence 2, Appli
30 3556 54.9 1167 1 US-08-100-709-2 Sequence 2, Appli
31 3556 54.9 1167 1 US-08-176-865-2 Sequence 2, Appli
32 3556 54.9 1167 1 US-08-474-038-2 Sequence 2, Appli
33 3556 54.9 1167 2 US-08-779-046-2 Sequence 2, Appli
34 3556 54.9 1167 2 US-08-881-340-2 Sequence 2, Appli
35 3502.5 54.1 1189 2 US-08-980-071-59 Sequence 59, Appl
36 3502.5 54.1 1189 3 US-09-314-093-59 Sequence 59, Appl
37 3502.5 54.1 1189 3 US-09-337-635-59 Sequence 59, Appl
38 3502.5 54.1 1189 4 US-09-337-280-59 Sequence 59, Appl
39 3502.5 54.1 1189 4 US-09-972-175-59 Sequence 59, Appl
40 3502.5 54.1 1189 4 US-10-200-522-59 Sequence 59, Appl
41 3500.5 54.0 1189 2 US-08-980-071-2 Sequence 2, Appli
42 3500.5 54.0 1189 2 US-08-757-536-2 Sequence 2, Appli
43 3500.5 54.0 1189 3 US-09-314-093-2 Sequence 2, Appli
44 3500.5 54.0 1189 3 US-09-250-848-2 Sequence 2, Appli
45 3500.5 54.0 1189 3 US-09-251-885-2 Sequence 2, Appli

```

ALIGNMENTS

RESULT 1

US-09-661-322A-38
; Sequence 38, Application US/09661322A
; Patent No. 6593293

; GENERAL INFORMATION:

; APPLICANT: Baum, James A.

; APPLICANT: Chu, Chih-Rei

; APPLICANT: Donovan, William P.

; APPLICANT: Gilmer, Amy J.

; APPLICANT: Rupar, Mark J.

; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Composi

; TITLE OF INVENTION: and Methods of Use

; FILE REFERENCE: MEC0201

; CURRENT APPLICATION NUMBER: US/09/661,322A

; CURRENT FILING DATE: 2000-09-13

; NUMBER OF SEQ ID NOS: 63

; SOFTWARE: Patentin version 3.0

; SEQ ID NO 38

; LENGTH: 1228

; TYPE: PRT

; ORGANISM: Bacillus thuringiensis

US-09-661-322A-38

```

Query Match          99.7%; Score 6462; DB 4; Length 1228;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1223; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 LTSNRKNEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MTSNRKNEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 NIAGRILGVLPFAGQIASFYSLGELWPRGRDQWEIFLEHVEQLINQOITENARNTA 120
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 NIAGRILGVLPFAGQIASFYSLGELWPRGRDQWEIFLEHVEQLINQOITENARNTA 120
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 LARLOGGDSFRAYQOSLEDWLENRDDARTSRVLYTQYIALELDFLNAPLFAIRNOEVP 180
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 LARLOGGDSFRAYQOSLEDWLENRDDARTSRVLYTQYIALELDFLNAPLFAIRNOEVP 180
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 181 LMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSYCVWYNTGLN 240
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 LMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSYCVWYNTGLN 240
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 241 SLRGTTNAASWVRVYNQFRDRDLTLGVLDLVALFPSTYDTRTYPINTSAQLTREYVTDAGTG 300
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 SLRGTTNAASWVRVYNQFRDRDLTLGVLDLVALFPSTYDTRTYPINTSAQLTREYVTDAGTG 300
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 301 VNMASMNWYNNNAPSFAISATVIRSHLLDFLEQLTIFSTSSRWSATRMTYWRGHTIQ 360
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 VNMASMNWYNNNAPSFAISATVIRSHLLDFLEQLTIFSTSSRWSATRMTYWRGHTIQ 360
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

361 SRPIGGLNTSTHGSTNTSINPVLRSFSDVYVWTSYAGVLLWGLIYLEPIHGVPTVRFN 420
361 SRPIGGLNTSTHGSTNTSINPVLRSFSDVYVWTSYAGVLLWGLIYLEPIHGVPTVRFN 420
421 FRNPQNTFERTANYSPYSPGLQKDSSTETLPPTTERPNYSYSHRLSHIGLISQSR 480
421 FRNPQNTFERTANYSPYSPGLQKDSSTETLPPTTERPNYSYSHRLSHIGLISQSR 480
481 VHVYVSWTHRSADRTNTISDSITQIPLVKSFNLSGTSVSGPGFTGGDIIRTNVGS 540
481 VHVYVSWTHRSADRTNTISDSITQIPLVKSFNLSGTSVSGPGFTGGDIIRTNVGS 540
541 VLSGLNFNNTSLQRYRVRVRYAASQTMVLRTVVGSTTFDQGPPTMSANESLTSQSPR 600
541 VLSGLNFNNTSLQRYRVRVRYAASQTMVLRTVVGSTTFDQGPPTMSANESLTSQSPR 600
601 FAEFPVGISASGQTAGISINNAGRTQPHFDKIEPIPTATFEAEYDLERAQEAVALNF 660
601 FAEFPVGISASGQTAGISINNAGRTQPHFDKIEPIPTATFEAEYDLERAQEAVALNF 660
661 TTNTPRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKLSDERNLLQDPN 720
661 TTNTPRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKLSDERNLLQDPN 720
721 FTSINKOPDFISTNEQSNFTSIHQSEHGWGSENITIQEGNDVFKENYVTLPGTFNECY 780
721 FTSINKOPDFISTNEQSNFTSIHQSEHGWGSENITIQEGNDVFKENYVTLPGTFNECY 780
781 PTLYQKIGSELKATRYQLRGYIEDSQDLIELYLRYNKAKHETLDVPGTESVWPLSVES 840
781 PTLYQKIGSELKATRYQLRGYIEDSQDLIELYLRYNKAKHETLDVPGTESVWPLSVES 840
841 PIGRCSEPNRCAPHFENPDLDCSDGCKEKAHSHHFSLDIDIGCTDLHENLGVWVVF 900
841 PIGRCSEPNRCAPHFENPDLDCSDGCKEKAHSHHFSLDIDIGCTDLHENLGVWVVF 900
901 IKTOEGHARLGNLEFTEKPLLEALSRVKRKAKKWRDKREKLOLETKRVYVTEAKEAVDA 960
901 IKTOEGHARLGNLEFTEKPLLEALSRVKRKAKKWRDKREKLOLETKRVYVTEAKEAVDA 960
961 LFVDSQVNRQADNTNIGMHAADKLVRIRIYALSELVPIGVNABIEFELEGRITTAIS 1020
961 LFVDSQVNRQADNTNIGMHAADKLVRIRIYALSELVPIGVNABIEFELEGRITTAIS 1020
1021 LYDARNVVKNGDFNGLACNVKGVHDVQOSHRSVLVIPWEAEYSQAVRVCGRGYIL 1080
1021 LYDARNVVKNGDFNGLACNVKGVHDVQOSHRSVLVIPWEAEYSQAVRVCGRGYIL 1080
1081 RVTAYKEGYEGCVTTHEIENNTDELKFKNCEEEVYPTDTGTCNDYTAHQGTAVCNRSN 1140
1081 RVTAYKEGYEGCVTTHEIENNTDELKFKNCEEEVYPTDTGTCNDYTAHQGTAVCNRSN 1140
1141 AGYEDAYEDVTTASVNYKPYEETVTDVRRDNHCEYDRGVNYPPLPAGYMTKELEYFP 1200
1141 AGYEDAYEDVTTASVNYKPYEETVTDVRRDNHCEYDRGVNYPPLPAGYMTKELEYFP 1200
1201 ETDKWIEIGETGKFIIVDSVELLMBE 1228
1201 ETDKWIEIGETGKFIIVDSVELLMBE 1228

```

RESULT 2

```

US-08-448-170-8
; Sequence 8, Application US/08448170
; Patent No. 5723758
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel
; APPLICANT: Cummings, David A.
; APPLICANT: Cannon, Raymond J.C.
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Stelman, Steve
; TITLE OF INVENTION: No. 5723758el Bacillus thuringiensis Isolate Denoted

```

```

; TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes
; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,170
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,902
; FILING DATE: 01-JUNE-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/S 102D.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1227 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-448-170-8

```

```

Query Match 91.5%; Score 5926.5; DB 1; Length 1227;
Best Local Similarity 91.8%; Pred. No. 0;
Matches 1129; Conservative 36; Mismatches 60; Indels 5; Gaps 3;

QY 1 LTSNRKNEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI 60
Db 1 LTSNRKNEIINALSIPAVSNHSAQMLSTDAIEDSLCIAEGNNIDPFVSASTVQTGI 60

QY 61 NIAGRILGLVGPFAQGIASFYFLVGLWPRGRDQWEIFLEHVEQLINQOITENARNTA 120
Db 61 NIAGRILGLVGPFAQGIASFYFLVGLWPRGRDQWEIFLEHVEQLINQOITENARNTA 120

QY 121 LARLOGLGDSFRAYQOSLEDWLENRDDARTSRVLYTOYIALELDFLNAMPLFAIRNQEVP 180
Db 121 LARLOGLGDSFRAYQOSLEDWLENRDDARTSRVLYTOYIALELDFLNAMPLFAIRNQEVP 180

QY 181 LLMVYAAANLHLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSYCVWEYNTGLN 240
Db 181 LLMVYAAANLHLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSYCVWEYNTGLN 240

QY 241 SLRGTHAASVWRYNQFRDLTLGLVDLVALFSDYDTRTYPTINTSAQITREYVTDATGATG 300
Db 241 SLRGTHAASVWRYNQFRDLTLGLVDLVALFSDYDTRTYPTINTSAQITREYVTDATGATG 300

QY 301 V--NMASMMWYNNAPSFSAIETAVIRSPHLLDFLEQLTIFSTSSRWSATRHMTYWRGHT 358
Db 301 APSGFATWFWNNAPSFSAIETAVIRSPHLLDFPEQLTIFSVLRWSNTQYNNYVWGH 360

QY 359 IQSRPTGGGLNTSTHGSTNTSINPVLRSFSDVYVWTSYAGVLLWGLIYLEPIHGVPTV 418
Db 359 IQSRPTGGGLNTSTHGSTNTSINPVLRSFSDVYVWTSYAGVLLWGLIYLEPIHGVPTV 418

```

```

Db 361 LESRTIRGSLSTSTHGTNTSINPVTQLQTSRDVVRTSPAGINI--LLTTPVNGVPEWAR 418
Qy 419 PNFRNPQNTFPGTANYSQPYESQGLQKQSETLPPETTERPNYESYSHRLSHGLISQ 478
Db 419 PNFRNPQNTFPGTANYSQPYESQGLQKQSETLPPETTERPNYESYSHRLSHGLISQ 477
Qy 479 SRVHPVYVSWTHRADRTNTISSDSITQIPLVKFNLNSGTSVVGPGFTGGDIIRTNVN 538
Db 478 NTLRAPVYVSWTHRADRTNTISSDSITQIPLVKFNLNSGTSVVGPGFTGGDIIRTNVN 537
Qy 539 GSVLSMGLNFNTSLQRYRVRVRYAASQTMVLRVTGSGTTFDDQGFPTSMANESLSQS 598
Db 538 GSVLSMGLNFNTSLQRYRVRVRYAASQTMVLRVTGSGTTFDDQGFPTSMANESLSQS 597
Qy 599 FRFAEPFVGISASGSGTAGISISNNAGROTFPHFKIEFIPITATFEAYDYLERAOEAVNA 658
Db 598 FRFAEPFVGISASGSGTAGISISNNAGROTFPHFKIEFIPITATFEAYDYLERAOEAVNA 657
Qy 659 LFTNTNPRRLKTDVTDYHIDOVSNLVAQLSDEFCLDEKRELLKVKYAKRLSDERNLLQD 718
Db 658 LFTNTNPRRLKTDVTDYHIDOVSNLVAQLSDEFCLDEKRELLKVKYAKRLSDERNLLQD 717
Qy 719 PNFTSINKQDPFISTNQSNFTSHEQSEHGWSGSENIITQEGNDVFKENYVILPGTFNE 778
Db 718 PNFTSINKQDPFISTNQSNFTSHEQSEHGWSGSENIITQEGNDVFKENYVILPGTFNE 777
Qy 779 CYPTLYQKIGESLKYATRYQLRGYIEDSGDLBIYLIRYNAXHETLDVPGTESVWPLSV 838
Db 778 CYPTLYQKIGESLKYATRYQLRGYIEDSGDLBIYLIRYNAXHETLDVPGTESVWPLSV 837
Qy 839 ESPIGRCGEPNRCAPHFEPWPDLDSCRDGKCAHSHHPSLDDIDGCTDLHENLGVWV 898
Db 838 ESPIGRCGEPNRCAPHFEPWPDLDSCRDGKCAHSHHPSLDDIDGCTDLHENLGVWV 897
Qy 899 FKIKTOGSHARLGNLEFIEBKPLGEALSRVKRAKKWRDKREKLQETKRVYTEAKEAV 958
Db 898 FKIKTOGSHARLGNLEFIEBKPLGEALSRVKRAKKWRDKREKLQETKRVYTEAKEAV 957
Qy 959 DALFVDSQYRNLQADTNGIMHAADKLVHRIREAYLSLSVPGVNAEIPFEELEGRITTA 1018
Db 958 DALFVDSQYRNLQADTNGIMHAADKLVHRIREAYLSLSVPGVNAEIPFEELEGRITTA 1017
Qy 1019 ISLYDARNVKNKGFNNGLACWYKGVHVDVQOSSHRSVLVPEWEAEVSQAVRVCPRGY 1078
Db 1018 ISLYDARNVKNKGFNNGLACWYKGVHVDVQOSSHRSVLVPEWEAEVSQAVRVCPRGY 1077
Qy 1079 ILRVTAYKEGEGECVTHIETENNDELKFNCEEEVYPTDCTCNDYTAHQCTAVCNS 1138
Db 1078 ILRVTAYKEGEGECVTHIETENNDELKFNCEEEVYPTDCTCNDYTAHQCTAVCNS 1137
Qy 1139 RNAGYEDAYEVDTTASVNYKPYEEETVTVRRDNHCEYDRGYVNYPPPLPAGYMTKELEY 1198
Db 1138 RNAGYEDAYEVDTTASVNYKPYEEETVTVRRDNHCEYDRGYVNYPPVPGYMTKELEY 1197
Qy 1199 PPETDKWIEIGETEGKFIIVDSVLLMEE 1228
Db 1198 PPETDKWIEIGETEGKFIIVDSVLLMEE 1227

```

RESULT 3

```

US-08-961-803-9
; Sequence 9, Application US/08961803
; Patent No. 6150589
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel
; APPLICANT: Cummings, David A.
; APPLICANT: Cannon, Raymond J.C.
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Stelman, Steve
; TITLE OF INVENTION: No. 6150589el Bacillus thuringiensis Isolate Denoted
; TITLE OF INVENTION: B.t. PS158C3, Active Against Lepidopteran Pests, and Genes
; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
; NUMBER OF SEQUENCES: 10

```

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Jay M. Sanders
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,803
FILING DATE: 31-OCT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/069,902
FILING DATE: 01-JUNE-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/759,247
FILING DATE: 13-SEPT-1991
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/448,170
FILING DATE: 23-MAY-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: M/S 102DCD1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1227 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-961-803-9

Query Match 91.5%; Score 5926.5; DB 3; Length 1227;
Best Local Similarity 91.8%; Pred. No. 0;
Matches 1129; Conservative 36; Mismatches 60; Indels 5; Gaps 3;

Qy 1 LTSNRKNEIINALSTIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI 60
Db 1 LTSNRKNEIINALSTIPAVSNHSAQMNLSLTDARIEDSLCIAEGNNIDPPFVSASTVQTGI 60
Qy 61 NIAGRILGLVGPAGQIASFYSLVGLWPRGRDOWEIFLEHVQQLINOQITENARNTA 120
Db 61 NIAGRILGLVGPAGQIASFYSLVGLWPRGRDPWEIFLEHVQQLIRQOVTENTRDTA 120
Qy 121 LARLQGLGDSFRAYQQSLEDWLENRRDARTSRVLYTQYIALELDLFLNAPLFAIRNQEVP 180
Db 121 LARLQGLGNSFRAYQQSLEDWLENRRDARTSRVLYTQYIALELDLFLNAPLFAIRNQEVP 180
Qy 181 LLMVYQAANLHLLLRDASLFGSEFGLTSQETQRYRQVEQTRDYSYCVHYNTGLN 240
Db 181 LLMVYQAANLHLLLRDASLFGSEFGLTSQETQRYRQVEQTRDYSYCVHYNTGLN 240
Qy 241 SLRGTNAASVRYNQPREDTLGLVLDLVALPPSVDTETYPINTSAQLTREVYTDATGATG 300
Db 241 NLRGTNAESWLRYNQFRDRTLGLVLDLVALPPSVDTETYPINTSAQLTREVYTDATGATG 300
Qy 301 V--NMASNNYNNNAPSFAIETAVIRSPHLLDFLEQLTIFSTSSRSRWSATRHMTYWRGHT 358
Db 301 APSGFASTNNFNNSAPSFAIEAAVIRPPHLLDFPEQLTIFSVLSRNSNTQYNNYVWYVHR 360
Qy 359 IQSRPIGGGLNTSTHGSTNTSINPVRSLFFSRDYYVWYTESVAGVLLWGLIYLEPIHGVTVR 418

```



```

Qy 899 FKIKTQCHARKLGNLEIEEKPLLEALSRVKRAEKKWRDKREKLOLETKRVYTEAKEAV 958
Db 898 FKIKTQCHARKLGNLEIEEKPLLEALSRVKRAEKKWRDKREKLOLETKRVYTEAKEAV 957
Qy 959 DALFVDSQYNRLQADTNGIMHAADKLVRIRREAYLSLSVPCVNAEIEEELGRIITA 1018
Db 958 DALFVDSQYNRLQADTNGIMHAADKLVRIRREAYLSLSVPCVNAEIEEELGRIITA 1017
Qy 1019 ISLYDARNVKNKGFNNGLACWNVKGVHVDVQOSSHRSVLVPIPEWAEVSAQVRVCPGRGY 1078
Db 1018 ISLYDARNVKNKGFNNGLACWNVKGVHVDVQOSSHRSVLVPIPEWAEVSAQVRVCPGRGY 1077
Qy 1079 ILRVATYKEGVGECVTHIEIENNTDELKFKNCBEEVYPTDTCNDYTAHQGTAVCNS 1138
Db 1078 ILRVATYKEGVGECVTHIEIENNTDELKFKNCBEEVYPTDTCNDYTAHQGTAVCNS 1137
Qy 1139 RNAGYEDAYEVDTTASVNYKPYEEYTVDRDNHCEYDRGVYVPPVAGYMTKSELEY 1198
Db 1138 RNAGYEDAYEVDTTASVNYKPYEEYTVDRDNHCEYDRGVYVPPVAGYMTKSELEY 1197
Qy 1199 FPETDKWIEIGETEGKFIVDSEVLLMEE 1228
Db 1198 FPETDKWIEIGETEGKFIVDSEVLLMEE 1227

```

RESULT 5

```

US-07-951-715A-7
; Sequence 7, Application US/07951715A
; Patent No. 5625136
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/951,715A
; FILING DATE: 25-SEP-1992
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP

```

TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: (919)541-8615
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1207 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-951-715A-7

```

```

Query Match 87.48; Score 5659.5; DB 1; Length 1207;
Best Local Similarity 89.48; Pred. No. 0;
Matches 1079; Conservative 34; Mismatches 89; Indels 5; Gaps 2;

```

```

Qy 27 MDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRILGVLPFAGQIASFYFLV 86
Db 1 MDLLPDARIEDSLCIAEGNNIDPVSASTVQTGINIAGRILGVLPFAGQIASFYFLV 60
Qy 87 GELWPRGRDQWEIFLEHVEQLINQOITENARNALTALRQGLGDSFRAYQOSLEWLENRD 146
Db 61 GELWPRGRDQWEIFLEHVEQLINQOITENARNALTALRQGLGDSFRAYQOSLEWLENRD 120
Qy 147 DARTSRVLYTQYIALELDFLNAMPFAIRNOEVPFLMVYAQAANLHLLLRDASLFGEF 206
Db 121 DARTSRVLYTQYIALELDFLNAMPFAIRNOEVPFLMVYAQAANLHLLLRDASLFGEF 180
Qy 207 GLTSQEIQRYYEQRVOTRQSDYCVWEYNTGLNSLRGTNAASWVRVYNQFRDRLTLGVLD 266
Db 181 GLTSQEIQRYYEQRVOTRQSDYCVWEYNTGLNSLRGTNAASWVRVYNQFRDRLTLGVLD 240
Qy 267 LVALFPSYDTRTYPINTSAQLTREVTYDAIGATGVNMAWNNVNNAPSFAITAVIRS 326
Db 241 LVALFPSYDTRTYPINTSAQLTREVTYDAIGATGVNMAWNNVNNAPSFAITAVIRS 300
Qy 327 PHLLDFLEQLTIFTSRWSATRHMTYWRGHTTQSRPIGGGLNTSTHGTNTSINPVRLS 386
Db 301 PHLLDFLEQLTIFTSRWSATRHMTYWRGHTTQSRPIGGGLNTSTHGTNTSINPVTLR 360
Qy 387 FFSRDVVTWTSYAGVLLWGIYLEPIHGVPTVRNFNPONTFERGTANYSPYSPGLQL 446
Db 361 FASRDVVTWTSYAGVLLWGIYLEPIHGVPTVRNFNPONTFERGTANYSPYSPGLQL 420
Qy 447 KDSETELPETTERPNYSEYSHRLSHIGLSQSRHVHPVYSWTHRSADRTNTISDSITQ 506
Db 421 KDSETELPETTERPNYSEYSHRLSHIGLSQSRHVHPVYSWTHRSADRTNTIGPNRITQ 480
Qy 507 IPLVKSFNLSGTSVSGPGFTGDDIIRTNVNGSVLSMGLNFNTSLQTRVRYRYAASQ 566
Db 481 IPVYKASELPQGTWVRGPGFTGDDILRRNTNTGCGPIRVTVNGPLTQRYRIGFYASTV 540
Qy 567 TMVLRTVTGGSTTFDQGFPTMSANESLTSQSRFAEFPPVGVISASGSQ-TAGISISNAG 625
Db 541 DFDFFVSRGGTTVNNPFLTMSNGDELKYNFRRRAFTPTPTQIQDIIRTSIQGLSG 600
Qy 626 RQTFHFDKIEFIPITATFEAEYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVA 685
Db 601 NGEVYIDKIEIIPWTATFEAEYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVA 660
Qy 686 CLSDEFCLDEKRELLEKVKYAKRLSDERNLLQPNFTSINKQDPFITNQSQNSFTSHEQ 745
Db 661 CLSDEFCLDEKRELLEKVKYAKRLSDERNLLQPNFTSINKQDPFITNQSQNSFTSHEQ 720
Qy 746 SEHGWMGSENIITQEGNDVFEKNYVTLPGTFNCEYPTLYOKYGESELKAYTRYQLRGYI 805
Db 721 SEHGWMGSENIITQEGNDVFEKNYVTLPGTFNCEYPTLYOKYGESELKAYTRYQLRGYI 780
Qy 806 EDSQDLIELYIRYNAKHETLDVPGTSEVWPLSVESPIGRCEPNRCAPHFEPWNPDLDCSC 865
Db 781 EDSQDLIELYIRYNAKHETLDVPGTSEVWPLSVESPIGRCEPNRCAPHFEPWNPDLDCSC 840
Qy 866 RDGEKCAHSHHFLSDIDICTDLHENLGVVWVFKIKTQGHARPLGNLEIEEKPLLEGEA 925

```

Db 841 RDGEKCAHSHHSFSLDIDVGTDLHENLGVWVFKIKTQBCHARLGNLEFIEEKPLLGEA 900
 QY 926 LSRVKRAEKKWRDREKLQLETKVYTEAEAVDALVDQSOYNRLQADTNIGMIHAADKL 985
 Db 901 LSRVKRAEKKWRDREKLQLETKVYTEAEAVDALVDQSOYNRLQADTNIGMIHAADKL 960
 QY 986 VHRIRAYLSLSVPGVNAEIPFEELGRITITAIISLYDARNVVKNGDFNNGLACWNVKGH 1045
 Db 961 VHRIRAYLSVPGVNAEIPFEELGHIITAIISLYDARNVVKNGDFNNGLTCWNVKGH 1020
 QY 1046 VDVOQSHRSVLVPEWEAEVSQAVRCPGRGYILRVYAYKEGEGCVTIHIEINNTDE 1105
 Db 1021 VDVOQSHRSVLVPEWEAEVSQAVRCPGRGYILRVYAYKEGEGCVTIHIEINNTDE 1080
 QY 1106 LKFKNCEEEVYPTDGTCDNDYTAHQCTA---VCNRSNAGYEDAVEVDFTASVNYKPTY 1161
 Db 1081 LKFKNCEEEVYPTDGTCDNDYTAHQCTACACACNSRNAGYEDAVEVDFTASVNYKPTY 1140
 QY 1162 EETTYTDVRDNDHCEYDRGVNYPPLPAGYMTKELEYFPETDKVWIEIGTEGKFIIVDSV 1221
 Db 1141 EETTYTDVRDNDHCEYDRGVNYPPLPAGYMTKELEYFPETDKVWIEIGTEGKFIIVDSV 1200
 QY 1222 ELLMEE 1228
 Db 1201 ELLMEE 1207

RESULT 6

US-08-459-448A-7
 ; Sequence 7, Application US/08459448A
 ; Patent No. 5859336
 ; GENERAL INFORMATION:
 ; APPLICANT: Koziel, Michael G.
 ; APPLICANT: Desai, Nalini M.
 ; APPLICANT: Lewis, Kelly S.
 ; APPLICANT: Kramer, Vance C.
 ; APPLICANT: Warren, Gregory W.
 ; APPLICANT: Evola, Stephen V.
 ; APPLICANT: Crossland, Lyle D.
 ; APPLICANT: Wright, Martha S.
 ; APPLICANT: Launis, Karen L.
 ; APPLICANT: Rothstein, Steven J.
 ; APPLICANT: Bowman, Cindy G.
 ; APPLICANT: Dawson, John L.
 ; APPLICANT: Dunder, Erik M.
 ; APPLICANT: Pace, Gary M.
 ; APPLICANT: Suttie, Janet L.
 ; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
 ; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
 ; NUMBER OF SEQUENCES: 94
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: No. 5859336artis Corporation
 ; STREET: Patent & Trademark Dept., 520 White Plains
 ; STREET: Rd., POB 2005
 ; CITY: Tarrytown
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10591-9005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentcin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/459,448A
 ; FILING DATE: 02-JUN-1995
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/951,715
 ; FILING DATE: 25-SEP-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/772,027

; FILING DATE: 04-OCT-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Pace, Gary M.
 ; REGISTRATION NUMBER: 40403
 ; REFERENCE/DOCKET NUMBER: CGC 1577/CLIP/DIV4
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (919) 541-8582
 ; TELEFAX: (919) 541-8689
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1207 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-459-448A-7
 ;
 ; Query Match 87.4%; Score 5659.5; DB 2; Length 1207;
 ; Best Local Similarity 89.4%; Pred. No. 0;
 ; Matches 1079; Conservative 34; Mismatches 89; Indels 5; Gaps 2;
 ;
 QY 27 MDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINAGTILGVLGVPPFAGQIASFYSELY 86
 Db 1 MDLLPDARIEDSLCIAEGNNIDFVSASTVQTGINAGTILGVLGVPPFAGQIASFYSELY 60
 QY 87 GELWPRGRDQWEIFLEHVEQLINQOITENARTALRQGLGDSFRAYQOQSLDLEWENRD 146
 Db 61 GELWPRGRDQWEIFLEHVEQLINQOITENARTALRQGLGDSFRAYQOQSLDLEWENRD 120
 QY 147 DARTRSVLYTQYIALELDFINAMPLFAIRNQEVPLLMVYAQAANLHLLLRDASLFGSEF 206
 Db 121 DARTRSVLYTQYIALELDFINAMPLFAIRNQEVPLLMVYAQAANLHLLLRDASLFGSEF 180
 QY 207 GLTSQEIORYYERQVETRDYSDYCVWYNTGLNSRGNTAASWVYVYQOFRDLITGLVLD 266
 Db 181 GLTSQEIORYYERQVETRDYSDYCVWYNTGLNSRGNTAASWVYVYQOFRDLITGLVLD 240
 QY 267 LVALFPSYDTRTYPINTSAQLTREVTYDAIGATGVNMAWNNYNNNAPSALJETAVIRS 326
 Db 241 LVALFPSYDTRTYPINTSAQLTREVTYDAIGATGVNMAWNNYNNNAPSALJETAVIRS 300
 QY 327 PHLLDFLEQLTIFSTSRWSATRHMTYWRGHTIQSRPIGGGLNTSTHGTSINTSINPVRLS 386
 Db 301 PHLLDFLEQLTIFSTSRWSATRHMTYWRGHTIQSRPIGGGLNTSTHGTSINTSINPVRLS 360
 QY 387 FESRDVYVWTESYAGVLLWGLYLEPHGVPTVRNENPONTPERGTANTYQVYESQGLQL 446
 Db 361 FASRDVYVWTESYAGVLLWGLYLEPHGVPTVRNENPONTPERGTANTYQVYESQGLQL 420
 QY 447 KDSETELPPTETTERPNYESYSHRLSHIGLISOSRVHPVYVSWTHRSADRTNITSSDITQ 506
 Db 421 KDSETELPPTETTERPNYESYSHRLSHIGLISOSRVHPVYVSWTHRSADRTNITSSDITQ 480
 QY 507 IPLVKSFLNLSGTSVVGPGFTGGDIIRTNVNGSVLSMGLNFNNTSLQRYVRVYVAAQS 566
 Db 481 IPMVKASELPQGTTVVVRGPGFTGGDILRRNTGFGPIRVTVNGPLTQRYRIGFYASTV 540
 QY 567 TMVLRYTVGSGTTFDQGFSTMSANESLTSQSFRFAEFPGVIGISASGSO-TAGTISINNAG 625
 Db 541 DEDFFVSRGGTIVNNFRFLRTMNSGDELKYGFRRAFTTPTFTTQIDIRTSIQGLSG 600
 QY 626 RQTFHFDEKIEFIPITATFEAEYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVNLVA 685
 Db 601 NGEVYIDKIEIIPVATATFEAEYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVNLVA 660
 QY 686 CLSDEFCLEKRELEKVKYAKRLSDERNLLQDPNFTSINKQDPDFTSTNEQSNFTSIHEQ 745
 Db 661 CLSDEFCLEKRELEKVKYAKRLSDERNLLQDPNFTSINKQDPDFTSTNEQSNFTSIHEQ 720
 QY 746 SEHGWWGSENIITQEGNDVFKENYVTLPGTFNECYPTLYQKIGESLKAITYQLRGYI 805
 Db 721 SEHGWWGSENIITQEGNDVFKENYVTLPGTFNECYPTLYQKIGESLKAITYQLRGYI 780
 QY 806 EDSQDLEIYLIRYNAKHETLDVPGTESVWPLSVESPIGRCEPNRCAPHFENPDLDCSC 865

Db 781 EDSQDLLEIYLRNAKHETLDVPGTESLWPLSVESPIGRGCEPNRCAPHFEWPPDDCSC 840
Qy 866 RDGEKCAHSHHFLSDIDIGCTDLHENLGVVWVFKIKTQEGHARLGNLEFIEBKPLLGEA 925
Db 841 RDGEKCAHSHHFLSDIDVGCCTDLHENLGVVWVFKIKTQEGHARLGNLEFIEBKPLLGEA 900
Qy 926 LSRVRAEKWRDKREKQLQLETRKRVYTEAKEAVDALFVDSQYNRLQADTNIGMHAADKL 985
Db 901 LSRVRAEKWRDKREKQLQLETRKRVYTEAKEAVDALFVDSQYNRLQADTNIGMHAADKL 960
Qy 986 VHRIRAYLSLSVPGVNAIEFEELBGRITITSLYDARNVKNKGDFNGLTCNNVKGH 1045
Db 961 VHRIRAYLSLPVPGVNAIEFEELBGRITITSLYDARNVKNKGDFNGLTCNNVKGH 1020
Qy 1046 VDQQSHHRSVLVPEWAEVSQAVRVCPCGRGYLRVTAYKEGVBGECVTIHIENNTDE 1105
Db 1021 VDQQSHHRSVLVPEWAEVSQAVRVCPCGRGYLRVTAYKEGVBGECVTIHIENNTDE 1080
Qy 1106 LKFNCEEEVYPTDTGTCNDYTAHQGTA----VCNSRNAGYEDAEVDTTASVNYKPTY 1161
Db 1081 LKFNCEEEVYPTDTGTCNDYTAHQGTA----VCNSRNAGYEDAEVDTTASVNYKPTY 1140
Qy 1162 EETTYDVRDNCEDRGVYVPPPLPAGYMTKELEYFPETDKWIEIGETGKFIUDSV 1221
Db 1141 EETTYDVRDNCEDRGVYVPPPLPAGYMTKELEYFPETDKWIEIGETGKFIUDSV 1200
Qy 1222 ELLMEE 1228
Db 1201 ELLMEE 1207

RESULT 7

US-08-459-595A-7

; Sequence 7, Application US/08459595A

; Patent No. 6018104

; GENERAL INFORMATION:

; APPLICANT: Koziel, Michael G.

; APPLICANT: Desai, Nalini M.

; APPLICANT: Lewis, Kelly S.

; APPLICANT: Kramer, Vance C.

; APPLICANT: Warren, Gregory W.

; APPLICANT: Evola, Stephen V.

; APPLICANT: Crossland, Lyle D.

; APPLICANT: Wright, Martha S.

; APPLICANT: Merlin, Ellis J.

; APPLICANT: Launis, Karen L.

; APPLICANT: Rothstein, Steven J.

; APPLICANT: Bowman, Cindy G.

; APPLICANT: Dawson, John L.

; APPLICANT: Dunder, Erik M.

; APPLICANT: Pace, Gary M.

; APPLICANT: Suttie, Janet L.

; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE

; NUMBER OF SEQUENCES: 94

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: No. 6018104artis Corporation

; STREET: Patent & Trademark Dept., 520 White Plains

; STREET: Rd., POB 2005

; CITY: Tarrytown

; STATE: New York

; COUNTRY: USA

; ZIP: 10591-9005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/459,595A

; FILING DATE: 02-JUN-1995

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40403
; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8582
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1207 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-459-595A-7

Query Match 87.4%; Score 5659.5; DB 3; Length 1207;

Best Local Similarity 89.4%; Pred. No. 0;

Matches 1079; Conservative 34; Mismatches 89; Indels 5; Gaps 2;

Qy 27 MDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRILGVLPFAGQIASFYSLV 86

Db 1 MDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRILGVLPFAGQIASFYSLV 60

Qy 87 GELWPRGROWEI FLEHVEQLINQQTENARNALTALRQLGDSFRAYQOSLEDWLENRD 146

Db 61 GELWPRGROWEI FLEHVEQLINQQTENARNALTALRQLGDSFRAYQOSLEDWLENRD 120

Qy 147 DARTSRVLYTQYIALELDFLNAMPFAIRNQEVPLLMVYAQAANHLHLLLRDASLFGSEF 206

Db 121 DARTSRVLYTQYIALELDFLNAMPFAIRNQEVPLLMVYAQAANHLHLLLRDASLFGSEF 180

Qy 207 GLTSQEIQRYERQVQTRDYSDYCVIEWYNTGLNSLRGTNAASWVRVYQFRDLTLGVLD 266

Db 181 GLTSQEIQRYERQVQTRDYSDYCVIEWYNTGLNSLRGTNAASWVRVYQFRDLTLGVLD 240

Qy 267 LVALPFSYDTRTYPINTSAQLTREVTDAIGATGVNMAWNNVNNAPSFALETAVIRS 326

Db 241 LVALPFSYDTRTYPINTSAQLTREVTDAIGATGVNMAWNNVNNAPSFALEAAAIRS 300

Qy 327 PHLLDFLEQLTIESTSRWSATRHMTYWRGHTTQSRPIGGGLNTSTHGSTNTSINPVRLS 386

Db 301 PHLLDFLEQLTIESTSRWSATRHMTYWRGHTTQSRPIGGGLNTSTHGSTNTSINPVTLR 360

Qy 387 FFSRDVYVTESYAGVLLWGIYLEPIHGVPVTRFNRPNQPTFERGTANYSQPYESPGQL 446

Db 361 FASRDVYVTESYAGVLLWGIYLEPIHGVPVTRFNRPNQPTFERGTANYSQPYESPGQL 420

Qy 447 KDSETELPETTERPNYESYSHRLSHIGLSQSRVHVVPVSWTHRSADRNTTSSDITQ 506

Db 421 KDSETELPETTERPNYESYSHRLSHIGLSQSRVHVVPVSWTHRSADRNTTGPNRITQ 480

Qy 507 IPLVKSFNLSGTSVVGSGPGTGGDIIRTNVNGSVLSMGLNFNNTSLQRYVRVRYAASQ 566

Db 481 IPWKASELPQGTIVVRGPGTGGDIIRTNVNGSGPPIRVTVNGPLTORVIRGFYASTV 540

Qy 567 TWVLRVTVGSTTTFDQGFPTMSANESLTSQSFRFAEPVVGISASGSQ-TAGISISNAG 625

Db 541 DFDFFVSRGGTTVNNFRFLRTMNSGDELKYGNFVRAFTTPTFTQIQDIIRTSIQGLSG 600

Qy 626 ROTFHKIEFIPITATFEAEYDLERAQEAVALFNNTNPRRLKTDVTDHIDQVSNLVA 685

Db 601 NGEVYDKIEIIPVATFEAEYDLERAQEAVALFNNTNPRRLKTDVTDHIDQVSNLVA 660

Qy 686 CLSDEFCLDEKRELLEKVKYAKELSDERNLLOPNFTSINKOPDFTSTNQSNTSITHEQ 745

Db 661 CLSDEFCLDEKRELLEKVKYAKELSDERNLLOPNFTSINKOPDFTSTNQSNTSITHEQ 720

```

QY 746 SEHGWSGSENIITQEGNDVFNKENVVILPGTFNECPTLYLQKIGESSELKAYTRYQLRGI 805
Db 721 SEHGWSGSENIITQEGNDVFNKENVVILPGTFNECPTLYLQKIGESSELKAYTRYQLRGI 780
QY 806 EDSQDLBIYLRINAKHETLDVPGTESVWPLSVESPIGRCEPNRCAPHFEMWPDLDSC 865
Db 781 EDSQDLBIYLRINAKHETLDVPGTESVWPLSVESPIGRCEPNRCAPHFEMWPDLDSC 840
QY 866 RDEKCAHSHHSLDIDIGCTDLHENLGVVWVFKIKTQGHARLGNLEFIEBKPLLGEA 925
Db 841 RDEKCAHSHHSLDIDIGCTDLHENLGVVWVFKIKTQGHARLGNLEFIEBKPLLGEA 900
QY 926 LSRVKRAEKWRDKREKLETKRKYVTEAEAVDALPVDQSYNRLQADTNIGMHAADKL 985
Db 901 LSRVKRAEKWRDKREKLETKRKYVTEAEAVDALPVDQSYNRLQADTNIGMHAADKL 960
QY 986 VHRIRAYLSLSVPGVNAEIEFEELBGRITITAIISLYDARNVVKNGDFNNGLACWNVKGH 1045
Db 961 VHRIRAYLSLSVPGVNAEIEFEELBGRITITAIISLYDARNVVKNGDFNNGLACWNVKGH 1020
QY 1046 VDVQOQSHRSVILVPEWAEVSQAVRVCPCGRGYILRVITAYKEGEGECVTIHEIENNTDE 1105
Db 1021 VDVQOQSHRSVILVPEWAEVSQAVRVCPCGRGYILRVITAYKEGEGECVTIHEIENNTDE 1080
QY 1106 LKFKNCEEEVYPTDGTCTNDYTAHQGTAT---VCNSRNAGYEDAEVDDTTASVNVKPTY 1161
Db 1081 LKFKNCEEEVYPTDGTCTNDYTAHQGTATACACNSRNAGYEDAEVDDTTASVNVKPTY 1140
QY 1162 EETTYDVRDNHCEYDRGVNYPPLPAGYMTKELEYFPFTDKWIBIGTEGKFIQVDSV 1221
Db 1141 EETTYDVRDNHCEYDRGVNYPVPPVAGYVTKLEYFPFTDVTWIBIGTEGKFIQVDSV 1200
QY 1222 ELLIMEE 1228
Db 1201 ELLIMEE 1207

```

RESULT 8

```

US-08-459-504B-7
; Sequence 7, Application US/08459504B
; Patent No. 6075185
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 6075185artis Corporation
; STREET: 3054 Cornwalis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,504B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/459,595
; FILING DATE: 02-JUN-1995
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1207 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-459-504B-7

Query Match 87.4%; Score 5659.5; DB 3; Length 1207;
Best Local Similarity 89.4%; Pred. No. 0;
Matches 1079; Conservative 34; Mismatches 89; Indels 5; Gaps 2;

QY 27 MDLSPDARTEDSLCIAEGNNINPLVSASTVQTGINIAGRILGVLGVFPFAGQIASFYSLV 86
Db 1 MDLLPDARTEDSLCIAEGNNIDPVSASTVQTGINIAGRILGVLGVFPFAGQIASFYSLV 60
QY 87 GELWPRGRDQWEIFLEHVEQLINQITENARNALTALRQLGSDSPRAYQQSLDLENRD 146
Db 61 GELWPRGRDQWEIFLEHVEQLINQITENARNALTALRQLGSDSPRAYQQSLDLENRD 120
QY 147 DARTSVLYTQYIALDELFINAMPLFAIRNOEVPILMVTAQAAANHLHLLLDASLFGSEF 206
Db 121 DARTSVLYTQYIALDELFINAMPLFAIRNOEVPILMVTAQAAANHLHLLLDASLFGSEF 180
QY 207 GLTSQBIQRYERQVETRDYSDYCVIEWNTGLNSRGNTAAASWVRYNPPRRDLTIGVLD 266
Db 181 GLTSQBIQRYERQVETRDYSDYCVIEWNTGLNSRGNTAAASWVRYNPPRRDLTIGVLD 240
QY 267 LVALFPSYDTRTYPIINTSAQLTREVTDAIGATGVNMAWNNWNNNAPSFAIETAVIRS 326
Db 241 LVALFPSYDTRTYPIINTSAQLTREVTDAIGATGVNMAWNNWNNNAPSFAIETAAIRS 300
QY 327 PHLLDFLEQLTIFSTSSRWASRTHMTYWRGHTIQSRPIGGGLNTSTHGSTNTSINPVRLS 386
Db 301 PHLLDFLEQLTIFPSASSRWSNRTHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLR 360
QY 387 FFSRDVVTWTSVAGVLLWGLYLEPIHGVTVPNPNPONTPERGNTANTSQPYESPGQLQ 446
Db 361 FASRDVVTWTSVAGVLLWGLYLEPIHGVTVPNPNPONTPERGNTANTSQPYESPGQLQ 420
QY 447 KQSETELPPTTERPNYESHRLSHIGLISQSRVHPVYVSWTHRSADRNTTSSDITQ 506
Db 421 KQSETELPPTTERPNYESHRLSHIGLISQSRVHPVYVSWTHRSADRNTTIGPNRITQ 480
QY 507 IPLVKSFNLSGTSVYSGFTGGDIIRTNVAGSVLSMGLNFNTSLQVRVAVRAASQ 566
Db 481 IPMVKASELPQGTVVVRGFTGGDIIRTNVAGSVLSMGLNFNTSLQVRVAVRAASQ 540
QY 567 TMVLRTVVGSTTFDQGFPTMSANESLTSQSFRFAEFVPGISASGSQ-TAGISISNNAG 625
Db 541 DFDFFVSRGGTTVNNFRFLRTMNSGDELKXGVFRAFTPTFTTQIIDIIRTSIQGLSG 600
QY 626 ROTFHFDKIEFIPITATFAEYDLERAQBAVNALFNTNPPRLKTDVTDYHIDQVNLVA 685

```

601 NGEVYIDKIELIIPVTATFEAYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVA 660
686 CLSDEFCLDEKRELEKVKYAKRLSDERNLLQDNFTSINKQPDFISTNEQSNFTSIHEQ 745
661 CLSDEFCLDEKRELEKVKYAKRLSDERNLLQDNFTSINKQPDFISTNEQSNFTSIHEQ 720
746 SEHCWGSNITIOEGNDVFNKENVTLPGTFNECYPTLYQKIGESLKYATRYQLRGYI 805
721 SEHCWGSNITIOEGNDVFNKENVTLPGTFNECYPTLYQKIGESLKYATRYQLRGYI 780
806 EDSQDLIYLIRYNAKHETLDVPGTESVWPLSVESPIGRCEPNRCAPHFENWPDLCSC 865
781 EDSQDLIYLIRYNAKHETLDVPGTESVWPLSVESPIGRCEPNRCAPHFENWPDLCSC 840
866 RDGEKCAHSHHFLSDIDIGCTDLHENLGVVWVFKIKTQEGHARLGNLEFIEEKPLGEEA 925
841 RDGEKCAHSHHFLSDIDIGCTDLHENLGVVWVFKIKTQEGHARLGNLEFIEEKPLGEEA 900
926 LSRVKRAEKKWRDKREKLOLETKREVTYEAKEAVDALFVDSQYNFLQADTWIGMHAADKL 985
901 LSRVKRAEKKWRDKREKLOLETKREVTYEAKEAVDALFVDSQYNFLQADTWIGMHAADKL 960
986 VHRIRAYLSLSVIPGVNAEIPFEELEGRIITALSIDARNVVKNGDFNNGLACWNVKGH 1045
961 VHRIRAYLSLSVIPGVNAEIPFEELEGRIITALSIDARNVVKNGDFNNGLACWNVKGH 1020
1046 VDVQSHRSVLVTPWEAEVQSVQAVRCPGCGYILRTVAYKEGVEGCVTIHEIENNTDE 1105
1021 VDVQSHRSVLVTPWEAEVQSVQAVRCPGCGYILRTVAYKEGVEGCVTIHEIENNTDE 1080
1106 LKPKNCEEEVYPTDTCNDYTAHQCTA----VCNSRNAGYEDAYEVDTTASVNYKPT 1161
1081 LKPKNCEEEVYPTDTCNDYTAHQCTA----VCNSRNAGYEDAYEVDTTASVNYKPT 1140
1162 EETTYDVRDNHCEYDRGVYVNPPLPAGYMTKELYFPFETDKWVIEIGTEGKFI VDSV 1221
1141 EETTYDVRDNHCEYDRGVYVNPPLPAGYMTKELYFPFETDKWVIEIGTEGKFI VDSV 1200
1222 ELLMEE 1228
1201 ELLMEE 1207

RESULT 9
US-08-459-444-7

Sequence 7, Application US/08459444
Patent No. 6121014

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lytle D.
Wright, Martha S.
Merlin, Ellis J.
Lauis, Karen L.

TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED

NUCLEIC ACID CODING SEQUENCE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,444A
FILING DATE: 02-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1207 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-08-459-444-7

Query Match 87.4%; Score 5659.5; DB 3; Length 1207;

Best Local Similarity 89.4%; Pred. No. 0;

Matches 1079; Conservative 34; Mismatches 89; Indels 5; Gaps 2;

QY 27 MDLSPDARIEDSLCIARGNINPLVSAVSTVQTGINIAGRILGVLPVFPAGQIASFYSLV 86
DB 1 MDLSPDARIEDSLCIARGNINPLVSAVSTVQTGINIAGRILGVLPVFPAGQIASFYSLV 60
QY 87 GELWPRGRDQWEIFLEHVEQLINQOITENARNALALQGLGDSFRAYQOSLEDWLENRD 146
DB 61 GELWPRGRDQWEIFLEHVEQLINQOITENARNALALQGLGDSFRAYQOSLEDWLENRD 120
QY 147 DARTSRVLYTQYIALELDLFLNAMPFAIRNQEVPLLMVYAQAANHLHLLRLDASLFGSEF 206
DB 121 DARTSRVLYTQYIALELDLFLNAMPFAIRNQEVPLLMVYAQAANHLHLLRLDASLFGSEF 180
QY 207 GLTSQEIQRVYERQVECTRDYSDYCVEMVNTGLNSLGTNAASWVRVYQNRDRDLTLGVLD 266
DB 181 GLTSQEIQRVYERQVECTRDYSDYCVEMVNTGLNSLGTNAASWVRVYQNRDRDLTLGVLD 240
QY 267 LVALFPSYDTRTYPIINTSAQLTREVTDAIGATGVNMAWNNYNNAPSAIETAVIRS 326
DB 241 LVALFPSYDTRTYPIINTSAQLTREVTDAIGATGVNMAWNNYNNAPSAIETAVIRS 300
QY 327 PHLLDFLEQLTIFTSRWSATRMVYWRGHTIQSRPIGGGLNTSTHGNTNTSINPVRLS 386
DB 301 PHLLDFLEQLTIFTSRWSATRMVYWRGHTIQSRPIGGGLNTSTHGNTNTSINPVRLS 360
QY 387 FFSRDVYVWTSYAGVLLWGIYLEPIHCVPTVRNFRNPONTFERGTANYQPYESGQLQ 446
DB 361 FASRDVYVWTSYAGVLLWGIYLEPIHCVPTVRNFRNPONTFERGTANYQPYESGQLQ 420
QY 447 KDSETELPPTTERPNYESYSHRLSHIGLSQSRVHVVPVSWTHRSADRNTNTSSDSITQ 506
DB 421 KDSETELPPTTERPNYESYSHRLSHIGLSQSRVHVVPVSWTHRSADRNTNTSSDSITQ 480
QY 507 IPLVKSPNLNGSVSGPGFTGGDIIRTNVNGSVLSMGLNFNNTSLQRYVRVRYAASQ 566
DB 481 IPWKASSELPGQITVVRGPGFTGGDILRLNTNTGGFPIRVTVANGPLTQRYRIGFRYASTV 540
QY 567 TMVLRTVVGSTTFDQGFPPSTMSANESLTSQSRFAEFPPVIGISASGSGQ-TAGISISNAG 625
DB 541 DFDFFVSRGCTTVNFRFLETMSGDELKYNFVRRAFTPTFTPTQDIIRTISIQGLSG 600
QY 626 RQTFHFKIEFIPITATFEAYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVA 685
DB 601 NGEVYIDKIELIIPVTATFEAYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVA 660

```

686 CLSDFCLDEKRELEKVKYAKRLSDERNLLQDPNFTSINKQDPFISTNEQSNFTSIHQ 745
661 CLSDFCLDEKRELEKVKYAKRLSDERNLLQDPNFTSINKQDPFISTNEQSNFTSIHQ 720
746 SEHGWSGSENIITQEGNDVFKENYVTLPGTFNECYPTLYQKIGESSELKAYTRYQLRGI 805
721 SEHGWSGSENIITQEGNDVFKENYVTLPGTFNECYPTLYQKIGESSELKAYTRYQLRGI 780
806 EDSQDLIYLIRYNAKHETLDVPGTESVWPLSVESPIGRCEPNRCAPHFENPDLDCSC 865
781 EDSQDLIYLIRYNAKHETLDVPGTESVWPLSVESPIGRCEPNRCAPHFENPDLDCSC 840
866 RDGEKCAHSHHFSLDIDIGCTDLHENLGVWVFKIKTQEGHARLGNLEFIEEKPILGEA 925
841 RDGEKCAHSHHFSLDIDIGCTDLHENLGVWVFKIKTQEGHARLGNLEFIEEKPILGEA 900
926 LSRVKRAEKKWRDKREKQLQLETKRVYTEAKEAVDALFVDSQYNRQLQADTNIGMHAADKL 985
901 LSRVKRAEKKWRDKREKQLQLETKRVYTEAKEAVDALFVDSQYNRQLQADTNIGMHAADKL 960
986 VHRIRAYLSLSVTPGNAEIPFELGRITITSLYDARNVKNQGNFNGLACVNVKGH 1045
961 VHRIRAYLSVTPGNAEIPFELGRITITSLYDARNVKNQGNFNGLACVNVKGH 1020
1046 VDVOQSHRSVLVTPWEAEVSQAVRVCPCRGYILRVTAKEGEGECVTHIEENNTDE 1105
1021 VDVOQSHRSVLVTPWEAEVSQAVRVCPCRGYILRVTAKEGEGECVTHIEENNTDE 1080
1106 LKFNCEEEVYPTDTCNDYTAHQGTA ---VCNSRNAGYEDAYEVDVTTASVNVKPTY 1161
1081 LKFNCEEEVYPTDTCNDYTAHQGTA ---VCNSRNAGYEDAYEVDVTTASVNVKPTY 1140
1162 EETTYDVRDNHCEYDRGVNPPPLPAGVMTKELEYFPETDKWIBIGTEGKFIYDSV 1221
1141 EETTYDVRDNHCEYDRGVNPPVPPVAGVYTKLEYFPETDVTWIBIGTEGKFIYDSV 1200
1222 ELLIMEE 1228
1201 ELLIMEE 1207

```

```

RESULT 10
US-09-053-549-8
; Sequence 8, Application US/09053549
; Patent No. 6121521
; GENERAL INFORMATION:
; APPLICANT: Desai, Nalini
; TITLE OF INVENTION: No. 6121521el Insecticidal Protein and Gene
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6121521artis Corporation
; STREET: 3054 Cornwalis Rd.
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/053,549
; FILING DATE: 01-APR-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40,403
; REFERENCE/DOCKET NUMBER: CGC 1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8582
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 8:

```

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 1207 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-053-549-8

Query Match. 87.4%; Score 5659.5; DB 3; Length 1207;
Best Local Similarity 89.4%; Pred. No. 0;
Matches 1079; Conservative 34; Mismatches 89; Indels 5; Gaps 2;

27 MDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRILGVLPFAQGIASFYSFLV 86
1 MDLSPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRILGVLPFAQGLASFYSFLV 60
87 GELWPRGRDQWEIFLBEHVEQLINQOITENARNALTALRQGLGDSFRAYQOSLEDWLENRD 146
61 GELWPRGRDQWEIFLBEHVEQLINQOITENARNALTALRQGLGDSFRAYQOSLEDWLENRD 120
147 DARTSRVLTQYIALDELDFLNAMPLFAIRNOEVPILMVYAQAANIHLILLRDLASLFGSEF 206
121 DARTSRVLTQYIALDELDFLNAMPLFAIRNOEVPILMVYAQAANIHLILLRDLASLFGSEF 180
207 GLTSQSIQRYRYERQVOTRDYSDYCVIEWYNTGLNSLRGTNAASWVRYNOFRRLDITLGVL 266
181 GLTSQSIQRYRYERQVOTRDYSDYCVIEWYNTGLNSLRGTNAASWVRYNOFRRLDITLGVL 240
267 LVALPFSYDTRTPINTSAQLTREVTDAIGATGVNMAWNNYNNNAPSFAIETAVIRS 326
241 LVALPFSYDTRTPINTSAQLTREVTDAIGATGVNMAWNNYNNNAPSFAIETAVIRS 300
327 PHLLDPLEOLTIFSTSSRSATRHMTYWRGHTIQSRPIGGGLNTSTHGTNTSINPVRLS 386
301 PHLLDPLEOLTIFSTSSRSATRHMTYWRGHTIQSRPIGGGLNTSTHGTNTSINPVRLS 360
387 FFSRDVYVYESVAGVLLWGIYLEPIHGVTVFNFNPQNTFERGTANTSQPYESPLQL 446
361 FASRDVYVYESVAGVLLWGIYLEPIHGVTVFNFNPQNTFERGTANTSQPYESPLQL 420
447 KQSETLPPETTERPNYESYSHRLSHIGLISQSRVHVVPVYVSWTHRSADRTNTISSIITQ 506
421 KQSETLPPETTERPNYESYSHRLSHIGLISQSRVHVVPVYVSWTHRSADRTNTIGPNRITQ 480
507 IPLVKSFNLSGTSVVGPGFTGGDIIRTNVNGSVLSMGLNFNNTSLQRYRVVRYAASQ 566
481 IPWVRASELPQGTIVVRGPGFTGGDIIRTNVNGSVLSMGLNFNNTSLQRYRVVRYAASQ 540
567 TWVLRVTVGGSTTFDQGFPTMSANESLTSQSFRFAEFVVGISASGSQ-TAGISISNNAG 625
541 DPDFVVSRGTTVNNFRPLRTWNSGDELYKGNFVRAFTTPFTTQIQDIIRTSIQLSG 600
626 RQTFHDKLEFIPITATPEAYDLEAQAVALFNTNPRKLKTDVTHHIDQVSNLVA 685
601 NGEVYIDKIEIIPVATPEAYDLEAQAVALFNTNPRKLKTDVTHHIDQVSNLVA 660
686 CLSDFCLDEKRELEKVKYAKRLSDERNLLQDPNFTSINKQDPFISTNEQSNFTSIHQ 745
661 CLSDFCLDEKRELEKVKYAKRLSDERNLLQDPNFTSINKQDPFISTNEQSNFTSIHQ 720
746 SEHGWSGSENIITQEGNDVFKENYVTLPGTFNECYPTLYQKIGESSELKAYTRYQLRGI 805
721 SEHGWSGSENIITQEGNDVFKENYVTLPGTFNECYPTLYQKIGESSELKAYTRYQLRGI 780
806 EDSQDLIYLIRYNAKHETLDVPGTESVWPLSVESPIGRCEPNRCAPHFENPDLDCSC 865
781 EDSQDLIYLIRYNAKHETLDVPGTESVWPLSVESPIGRCEPNRCAPHFENPDLDCSC 840
866 RDGEKCAHSHHFSLDIDIGCTDLHENLGVWVFKIKTQEGHARLGNLEFIEEKPILGEA 925
841 RDGEKCAHSHHFSLDIDIGCTDLHENLGVWVFKIKTQEGHARLGNLEFIEEKPILGEA 900
926 LSRVKRAEKKWRDKREKQLQLETKRVYTEAKEAVDALFVDSQYNRQLQADTNIGMHAADKL 985

```

Db 901 LSRVRAEKKRDKREKLOLETKREVTYKEAENVDALEFVDSQYDELQADTNIGMHAADKL 960
Qy 986 VHRIREAYLSVLPVGNNAEIEFELEGRITITAILSYDARNVVKNGDFNGLACWNVKGH 1045
Db 961 VHRIREAYLSVLPVGNNAEIEFELEGRITITAILSYDARNVVKNGDFNGLTCWNVKGH 1020
Qy 1046 VDVOQSHRSVLPVPEAEVSQARVCPGCGYILRTAYKEGCGCVTIHEIENNTDE 1105
Db 1021 VDVOQSHRSVLPVPEAEVSQARVCPGCGYILRTAYKEGCGCVTIHEIENNTDE 1080
Qy 1106 LKFKNEEEVYPTDTCNDYTAHQGTA----VCNSRNAGYEDAYEVDVTTASVNYKPT 1161
Db 1081 LKFKNEEEVYPTDTCNDYTAHQGTAACACACNSRNAGYEDAYEVDVTTASVNYKPT 1140
Qy 1162 EETVTDVDRDNCEYDRGVNYPPLPAGVNTKELEYFPETDKWIBIGTEGKFI VDSV 1221
Db 1141 EETVTDVDRDNCEYDRGVNYPPLPAGVNTKELEYFPETDKWIBIGTEGKFI VDSV 1200
Qy 1222 ELLMEE 1228
Db 1201 ELLMEE 1207

RESULT 11

US-09-547-422-7
; Sequence 7, Application US/09547422
; Patent No. 6320100
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; Desai, Nalini M.
; Lewis, Kelly S.
; Kramer, Vance C.
; Warren, Gregory W.
; Evola, Stephen V.
; Crossland, Lyle D.
; Wright, Martha S.
; Merlin, Ellis J.
; Lounis, Karen L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRES:
; ADDRESSEE: No. 6320100artis Agribusiness Biotechnology Research, Inc.
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/547,422
; FILING DATE: 11-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/459,595
; FILING DATE: 02-JUN-1995
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-18805H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:

; ; LENGTH: 1207 amino acids
; ; TYPE: amino acid
; ; TOPOLOGY: linear
; ; MOLECULE TYPE: protein
; ; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-547-422-7
Query Match 87.4%; Score 5659.5; DB 3; Length 1207;
Best Local Similarity 89.4%; Pred. No. 0;
Matches 1079; Conservative 34; Mismatches 89; Indels 5; Gaps 2;
Qy 27 MDLSPDARIEDSCIAEGNNINPLVSASTVQTGINTAGRIILGVLPFAGQIASFYFLV 86
Db 1 MDLSPDARIEDSCIAEGNNIDFVSASTVQTGINTAGRIILGVLPFAGQIASFYFLV 60
Qy 87 GELWPRGRDQWEIFLEHVEQLINQOITENARNALTALRQLGDSFRAYQOSLEDWLNRD 146
Db 61 GELWPRGRDQWEIFLEHVEQLINQOITENARNALTALRQLGDSFRAYQOSLEDWLNRD 120
Qy 147 DARTSVLYTQYIALELDLFLNAMPFLFAIRNQEVPLLMVYAAQANLHLLLRDASLFGSEF 206
Db 121 DARTSVLYTQYIALELDLFLNAMPFLFAIRNQEVPLLMVYAAQANLHLLLRDASLFGSEF 180
Qy 207 GLTSQEIORYERQVEQTRDYSYCVWEYNTGLNSLRGTNAASWVRVNOFRDRLTLGLD 266
Db 181 GLTSQEIORYERQVEQTRDYSYCVWEYNTGLNSLRGTNAASWVRVNOFRDRLTLGLD 240
Qy 267 LVALFPSYDTRTYPIINTSAQLTREVTDAIGATGVNMAWNNYNNAPSAIETAVIRS 326
Db 241 LVALFPSYDTRTYPIINTSAQLTREVTDAIGATGVNMAWNNYNNAPSAIETAAIRS 300
Qy 327 PHLLDFLEQLTIFSTSRMSATRMHTYWRGHTIQSRPIGGGLNTSTHGSTNTSINPVRLS 386
Db 301 PHLLDFLEQLTIFSASSRWSNTRHTMYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLR 360
Qy 387 FFSRDVYWTESYAGVLLWGIYLEPIHGVPVTFNFPNPTFERTGANYSQYESPGQL 446
Db 361 FASRDVYTESYAGVLLWGIYLEPIHGVPVTFNFPNPTFQISDRGTANYSQYESPGQL 420
Qy 447 KQSETELPETTERPNVYESYSHRLSHIGLISQSRVHVVPVSWTHRSADRNTNITSSDSITQ 506
Db 421 KQSETELPETTERPNVYESYSHRLSHIGLISQSRVHVVPVSWTHRSADRNTNITGPNRITQ 480
Qy 507 IPIVKGFNLSGTSVSGPGFTGDIIRTNVNGSVLSMGLFNNTSLQRVVRVRYAASQ 566
Db 481 IPWKASLPQGTTVVRGPGFTGDIIRTNVNGSVLSMGLFNNTSLQRVVRVRYASTV 540
Qy 567 TMVLRYTVCGSTTFDQGFSTMSANESLTSQSRFAEPFVGISASGQ-TAGISISNAG 625
Db 541 DFDFVSRGGTTVNNFRFLRTMNSGDELKYGNVFRAFTTPTFTQIDITISQISL 600
Qy 626 RQTFHFDKIEFIPITATFAEYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVA 685
Db 601 NGEVYIDKIEIIPVATFAEYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVA 660
Qy 686 CLSDEFCLDEKRELLEKVKYAKELSDERNLLOPNFTSINKQPDFISTNQSNFTSHEQ 745
Db 661 CLSDEFCLDEKRELLEKVKYAKELSDERNLLOPNFTSINKQPDFISTNQSNFTSHEQ 720
Qy 746 SEHWGNGSENITIOEGNDVFKENYVTLPGTFNFCYPTLYLQKIGESLKYATRYQLRGI 805
Db 721 SEHWGNGSENITIOEGNDVFKENYVTLPGTFNFCYPTLYLQKIGESLKYATRYQLRGI 780
Qy 806 EDSQDLEIYLIRYNAKHETLDVPGTESVPLSVESPIGRGCEPNRCAPHFEMWPDLDSC 865
Db 781 EDSQDLEIYLIRYNAKHETLDVPGTESVPLSVESPIGRGCEPNRCAPHFEMWPDLDSC 840
Qy 866 RDGEKCAHSHHFLDIDIGCTDLHENLGVVYVFKIKTQEGHARLGNLEFIEEKLGEA 925
Db 841 RDGEKCAHSHHFLDIDIGCTDLHENLGVVYVFKIKTQEGHARLGNLEFIEEKLGEA 900
Qy 926 LSRVRAEKKRDKREKLOLETKREVTYKEAENVDALEFVDSQYDELQADTNIGMHAADKL 985

901 LSRVRAEKKWRDKLEQLTKRVTYEAKEAVDALFVDSQYDRLQADTWIGMHAADKL 960
 986 VHRIRAYLSLSVTPGNAEIPFELSGRIITAIISLYDARNVVKNGDFNGLACWNKGH 1045
 961 VHRIRAYLSLPIPGNAEIPFELSGRIITAIISLYDARNVVKNGDFNGLTCWNKGH 1020
 1046 VDVOQSHRSVLVPEWAEVSQAVRVCPCGRGYILRTAYKEGEGCVTHIETENNTE 1105
 1021 VDVOQSHRSVLVPEWAEVSQAVRVCPCGRGYILRTAYKEGEGCVTHIETENNTE 1080
 1106 LKFKNCBEEVYPTDTCNDYTAHQSTA----VCNSRNAGYEDAYEVDVTTASVNYKPTY 1161
 1081 LKFKNCBEEVYPTDTCNDYTAHQSTA----VCNSRNAGYEDAYEVDVTTASVNYKPTY 1140
 1162 EEEYTDVRDNCEYDRGVNYPPLPAGYMTKELEYFPEPTDKWIBIGTEGKFIVDSV 1221
 1141 EEEYTDVRDNCEYDRGVNYPPLPAGYMTKELEYFPEPTDKWIBIGTEGKFIVDSV 1200
 1222 ELLIMEE 1228
 1201 ELLIMEE 1207

RESULT 12

US-09-988-462-7
 ; Sequence 7, Application US/09988462
 ; Patent No. 6720488
 ; GENERAL INFORMATION:

APPLICANT: Kozziel, Michael G.
 Desai, Nalini M.
 Lewis, Kelly S.
 Kramer, Vance C.
 Warren, Gregory W.
 Evola, Stephen V.
 Crossland, Lytle D.
 Wright, Martha S.
 Merlin, Ellis J.
 Launis, Karen L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
 INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: Syngenta Biotechnology, Inc.
 STREET: 3054 Cornwallis Road
 CITY: Research Triangle Park
 STATE: NC
 COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/988,462
 FILING DATE: 20-No. 6720488-2001
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/547,422
 FILING DATE: 11-APR-2000
 APPLICATION NUMBER: US 08/459,504
 FILING DATE: 02-JUN-1995
 APPLICATION NUMBER: US 07/951,715
 FILING DATE: 25-SEP-1992
 APPLICATION NUMBER: US 07/772,027
 FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy
 REGISTRATION NUMBER: 38,241
 REFERENCE/DOCKET NUMBER: S-188051
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (919)541-8587
 TELEFAX: (919)541-8689

; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1207 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 US-09-988-462-7

Query Match 87.4%; Score 5659.5; DB 4; Length 1207;
 Best Local Similarity 89.4%; Pred. No. 0;
 Matches 1079; Conservative 34; Mismatches 89; Indels 5; Gaps 2;

QY	27	MDLSPARIEDSLCIAEGNNINPLVSASTVTCINAGRIILGVLPFAQIASFSFLV	86
DB	1	MDLLPARIEDSLCIAEGNNIDPFVSASTVTCINAGRIILGVLPFAQIASFSFLV	60
QY	87	GELWPRGRDQWEIFLHVQQLINQOITENARNTALARLOGLGDSFRAYQOSLEDWLENRD	146
DB	61	GELWPRGRDQWEIFLHVQQLINQOITENARNTALARLOGLGDSFRAYQOSLEDWLENRD	120
QY	147	DARTRSVLYTQYIALBELDFLNAMPLFAIRNQEVPLLMVYAQAANLHLLLRDASLFGSEF	206
DB	121	DARTRSVLYTQYIALBELDFLNAMPLFAIRNQEVPLLMVYAQAANLHLLLRDASLFGSEF	180
QY	207	GLTSQEIQRYYEROVETRDYSDYCVWEYNTGLNSLRGTNAASWVRYNQRFRDLTIGVLD	266
DB	181	GLTSQEIQRYYEROVETRDYSDYCVWEYNTGLNSLRGTNAASWVRYNQRFRDLTIGVLD	240
QY	267	LVALPFSYDTRTYPIINTSAQLTREVTDAIGATGVNMAWMNNAPSAIETAVIRS	326
DB	241	LVALPFSYDTRTYPIINTSAQLTREVTDAIGATGVNMAWMNNAPSAIETAVIRS	300
QY	327	PHLLDFLEQLTTFSTSRWSATRHMTYWRGHTIQSRPICGGLNTSHGTSNTSINPRLS	386
DB	301	PHLLDFLEQLTTFSTSRWSATRHMTYWRGHTIQSRPICGGLNTSHGTSNTSINPRLS	360
QY	387	PFSDRVVTESYAGVLLWGIYLEPIHGVPTVFPNPNPONTFERGTANYSQVPESGLQL	446
DB	361	PFSDRVVTESYAGVLLWGIYLEPIHGVPTVFPNPNPONTFERGTANYSQVPESGLQL	420
QY	447	KDSETELPETTERPNYESYSHRLSHIGLISQSRHVVPVYVSWTHRSADRNTSSDITQ	506
DB	421	KDSETELPETTERPNYESYSHRLSHIGLISQSRHVVPVYVSWTHRSADRNTSSDITQ	480
QY	507	IPLVKSFNLNSGTSVVGSGFTGGDIIRTNVNGSVLSMGLNPNNTSLQRYRVRVRAAQ	566
DB	481	IPLVKSFNLNSGTSVVGSGFTGGDIIRTNVNGSVLSMGLNPNNTSLQRYRVRVRAAQ	540
QY	567	TWVLRVTGSGTTFDQGPSTMSANESLTSQSFRAEFPPVGISASGQ-TAGISISNAG	625
DB	541	DDDFVSRGCTVNNPFRFLRTMNSGDELKYGIVRAFTPTFTQIQDIIRTSIOGLSG	600
QY	626	ROTFHFKIEFIPITATFEAYDLERAQAVNALFTNTNPRKLKTDVTDYHIDQVSNLVA	685
DB	601	NGEVYDKIEIIPVTATFEAYDLERAQAVNALFTNTNPRKLKTDVTDYHIDQVSNLVA	660
QY	686	CLSDREPCLDKELKVKYAKRLSDERNLLODPNFTSINKQDPDFTSTNEQSNFTSIHQ	745
DB	661	CLSDREPCLDKELKVKYAKRLSDERNLLODPNFTSINKQDPDFTSTNEQSNFTSIHQ	720
QY	746	SEHGWMGSENITIQEGNDVFKENYVTLPGTFNECYPTYLYQKIGSELKAYTRYQLRGYI	805
DB	721	SEHGWMGSENITIQEGNDVFKENYVTLPGTFNECYPTYLYQKIGSELKAYTRYQLRGYI	780
QY	806	EDSQDLEIYLIRYNAKHETLDVPGTESVWPLSVESPIGRGCEPNRCAPHEWNPDLDCSC	865
DB	781	EDSQDLEIYLIRYNAKHETLDVPGTESVWPLSVESPIGRGCEPNRCAPHEWNPDLDCSC	840
QY	866	RDEKCAHSHHFSLDIDIGCTDLHENLGVWVFKIKTQEGHARLGNLFIEKPLLGEA	925
DB	841	RDEKCAHSHHFSLDIDIGCTDLHENLGVWVFKIKTQEGHARLGNLFIEKPLLGEA	900

QY 926 LSRVRAEKWRDREKLEQLQETKRVYTEAKEAVDALFVDSQYNRLQADTNIGMHAADKL 985
DB 901 LSRVRAEKWRDREKLEQLQETKRVYTEAKEAVDALFVDSQYNRLQADTNIGMHAADKL 960
QY 986 VHRIRAYLSLSVPGVNAEIPFELGRITITSLYDARNVKNVGNGLACWNVKGH 1045
DB 961 VHRIRAYLSLPIVPGVNAEIPFELGRITITSLYDARNVKNVGNGLACWNVKGH 1020
QY 1046 VDQOQSHRSVLPIPEWAEVSQAVRVCPCGRGYLRVTAYKEGEGCVTIHEIENNTDE 1105
DB 1021 VDQOQSHRSVLPIPEWAEVSQAVRVCPCGRGYLRVTAYKEGEGCVTIHEIENNTDE 1080
QY 1106 LKFKNCBEEVYPTDTCNDYTAHQGTA----VCNSRNAGYEDAYEVDVTASVNYKPT 1161
DB 1081 LKFKNREEEYVPTDTCNDYTAHQGTAHQGTAHQGTAHQGTAHQGTAHQGTAHQGTA 1140
QY 1162 EETITDVRDNHCEYDRGVYVNPPLPAGVYMTKELEYFPETDKWIBIGTEGKFI VDSV 1221
DB 1141 EETITDVRDNHCEYDRGVYVNPPLPAGVYMTKELEYFPETDKWIBIGTEGKFI VDSV 1200
QY 1222 ELLLMEE 1228
DB 1201 ELLLMEE 1207

RESULT 13

US-09-053-549-2
; Sequence 2, Application US/09053549
; Patent No. 6121521
; GENERAL INFORMATION:
; APPLICANT: Desai, Nalini
; TITLE OF INVENTION: No. 6121521el Insecticidal Protein and Gene
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: No. 6121521artie Corporation
; STREET: 3054 Cornwallis Rd.
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/053,549
; FILING DATE: 01-APR-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40,403
; REFERENCE/DOCKET NUMBER: CGC 1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8582
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1227 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-053-549-2

Query Match 83.9%; Score 5436.5; DB 3; Length 1227;
Best Local Similarity 84.3%; Pred. No. 0;
Matches 1040; Conservative 63; Mismatches 118; Indels 13; Gaps 5;
QY 1 LTSNRKNEEINIALSIPVNSHSTOMDLSDPARIEDSLCTAEGNNINPLVSASTVOTGI 60
DB 1 MTSNRKNEEINIL-----AVSNHQAQMDLLDPARIEDSLCTAEGNNIDPPVSASTVOTGI 55
QY 61 NIAGRILGLVGPVFPAGQIASFYSFLVGLWPRGRDQWEIFLEHVEQLINQOITENARNTA 120

DB 56 NIAGRILGLVGPVFPAGQIASFYSFLVGLWPRGRDQWEIFLEHVEQLINQOITENARNTA 115
QY 121 LARLOGLGDSFRAYQOQSLDWNLENRDDARTSRVLYTQYIALELDFLNAMEPLFAIRNOEVP 180
DB 116 LARLOGLGDSFRAYQOQSLDWNLENRDDARTSRVLYTQYIALELDFLNAMEPLFAIRNOEVP 175
QY 181 LLMVYAQAANLHLLLRDASLFGSEBGLTSQETQRYRQVQVQETRDYSDYCVIEWYNTGLN 240
DB 176 LLMVYAQAANLHLLLRDASLFGSEBGLTSQETQRYRQVQVQETRDYSDYCVIEWYNTGLN 235
QY 241 SLRGTAASVWRVYNQPRDRLTGLVDLVALFSPVDTRTYPINTSAQLTREVYTDAGATG 300
DB 236 SLRGTAASVWRVYNQPRDRLTGLVDLVALFSPVDTRTYPINTSAQLTREVYTDAGATG 295
QY 301 VNMASNMVYNNAPSFSAIETAVIRSPHLLDFLEQLTIFSTSRWSATRMHTYWRGHTIQ 360
DB 296 VNMASNMVYNNAPSFSAIETAVIRSPHLLDFLEQLTIFSTSRWSATRMHTYWRGHTIQ 355
QY 361 SRPIGGGLNTSTHGSTNTSINPVRSLFFSRDVTWTSYAGVLLWGIYLEPIHGVPTVRFN 420
DB 356 SRPIGGGLNTSTHGATNTTINPVTLPASRDVYRTESYAGVLLWGIYLEPIHGVPTVRFN 415
QY 421 FRNPQNTFERGTANYSQPYESPGQLKDSLTPPETTERPNYSEYSHRLSHIGLISQSR 480
DB 416 FTNPQNISDRGTANYSQPYESPGQLKDSLTPPETTERPNYSEYSHRLSHIGLISQSR 475
QY 481 VHVYVSWTHRSADRTNTISSDITQIPLVKSFNLMSGTSVWSGPGTGGDIIRNTNNGS 540
DB 476 VHVYVSWTHRSADRTNTIGPNRITQIPMVKASELPQGTTVVRGPGTGGDILARTTNGG 535
QY 541 VLSMGLNFNTSLQRYRVRYAASQTMVLRVTGSGSTTFDQGPSTMSANESLTSQSPR 600
DB 536 FGPIRVTVNGPLTQRYRIGRYASTVDFDFVSRGGTTVNNFRFLRTMNSGDELKYGNEV 595
QY 601 FAEFPVGISASGQT-AGISINNAGRQTFHFKIEPIPTATPEAYDILERAQEVNAL 659
DB 596 RRAFTPTFTQITQIRTSIQGLSNGEYVTDKIEIIPVTATPEAYDILERAQEVNAL 655
QY 660 FTNTNPRRLKTDVYHIDQVSNLVACLSDFCLDEKRELLEKVKYAKRLSDERNLLQDP 719
DB 656 FTNTNPRRLKTDVYHIDQVSNLVACLSDFCLDEKRELLEKVKYAKRLSDERNLLQDP 715
QY 720 NFTSINKQPDFISTNEQSNFTSIHEQSEHGWGSENITIOEGNDVFKENYVTLPGTNEC 779
DB 716 NFTSINKQPDFISTNEQSNFTSIHEQSEHGWGSENITIOEGNDVFKENYVTLPGTNEC 775
QY 780 YPTVLYOKIGESLKAATRYOLRGYTEDSODLEIYLRYNKAKHETLDVPGTESLWPLSVE 839
DB 776 YPTVLYOKIGESLKAATRYOLRGYTEDSODLEIYLRYNKAKHETLDVPGTESLWPLSVE 835
QY 840 SPIGRCEPNRCAPHPEWNPDLDCSCRDGKCAHSHHFLDIDIGCTDLHENLGVWVVF 899
DB 836 SPIGRCEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFLDIDVGTDLNEDLGVWVIF 895
QY 900 KIKTOEGHARLGNLEFIEEKPLLEALSRVKRAKWRDKREKLQLETKRYVTEAKSAVD 959
DB 896 KIKTOEGHARLGNLEFIEEKPLLEALSRVKRAKWRDKREKLQLETKRYVTEAKSAVD 955
QY 960 ALFVDSQYNRLQADTNIGMHAADKLVHRTREAYLSLSVTPGVNAEIPFEELEGRITAI 1019
DB 956 ALFVNSQYDLQADTNIAMHAADKRVHSIREAYLPESLVPVNAEIPFEELEGRITAF 1015
QY 1020 SLVDARNVKNVGNGLACWNVKGVHDV-QQSHRSVLPIPEWAEVSQAVRVCPCGRGY 1078
DB 1016 SLVDARNVKNVGNGLACWNVKGVHDVQEQNNHRSVLVPEWAEVSQAVRVCPCGRGY 1075
QY 1079 ILRVATYKEGEGCVTIHEIENNTDELKPKNCEEEVYPTDTCNDYTA----HOGTA 1134
DB 1076 ILRVATYKEGEGCVTIHEIENNTDELKPKNCEEEVYPTDTCNDYTA----HOGTA 1134
QY 1135 VCNRSNAGYEDAYEVDVTASVNYKPTBETTYDVRDNHCEYDRGVYVNPPLPAGVYMTK 1194

Db 1135 -YTSRNRGYDGAYESNSVPADYASAEYKAYTDGRDNPCESNRGYGDYTLPGAGVTK 1193

Qy 1195 ELEYFPETDKWIEIGETEGKFIIVDSVELLMEE 1228

Db 1194 ELEYFPETDKWIEIGETEGKFIIVDSVELLMEE 1227

RESULT 14

US-08-100-709-4

Sequence 4, Application US/08100709

Patent No. 5322687

GENERAL INFORMATION:

APPLICANT: Donovan, William P.

APPLICANT: Tan, Yiping

APPLICANT: Jan, Christine S.

APPLICANT: Gonzalez Jr., Jose M.

TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5

TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.

STREET: 1601 Market Street, 36th Floor

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: U.S.A.

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/100,709

FILING DATE: 19930729

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Egolf, Christopher

REGISTRATION NUMBER: 27633

REFERENCE/DOCKET NUMBER: 7205-49

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-757-1590

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 1229 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-100-709-4

Query Match 80.8%; Score 5237.5; DB 1; Length 1229;

Best Local Similarity 79.9%; Pred. No. 0;

Matches 983; Conservative 94; Mismatches 149; Indels 5; Gaps 3;

Qy 1 LTSNRKNEIINALSIPAVNSHSTQMDLSPDARIEDSLCIAEANNINPLVASTVQTGI 60

Db 1 LTSNRKNEIINALSIPVSNSTQMDLSPDARIEDSLCIAEANNINPLVASTVQTGI 60

Qy 61 NIAGRILGVLPFAGQIASFYFLVCELWPRGRDOWEIEFLEHVEQLINQOITENARNTA 120

Db 61 NIAGRILGVLPFAGQIASFYFLVCELWPRGRDOWEIEFLEHVEQLINQOITENARNTA 120

Qy 121 LARLOGLGDSFRAYQQSLEDWLENRDARTSRVLYTQYIALELDFLNAPLFAIRNQVEP 180

Db 121 IARLEGLRGYRSVQQALETWLDNRNDARSIIILERYVALELDITTAIPLFIRNEEP 180

Qy 181 LMVYAQAANLHLLLDASLFSSEFLGTSQETQRYRQYERQVQTRDYSYCVWEYNTGLN 240

Db 181 LMVYAQAANLHLLLDASLFSSEGMASSDVNNQYQEQIRYTBYSNHCYQVNTGLN 240

Qy 241 SLRGTNAASVRYNQFRDRLTLGLVDLVALFPSPYDTRTYPINTSAOLTREVVYTDALGATG 300

Db 241 NLRGTNAESWLRNQFRDRLTLGLVDLVALFPSPYDTRTYPINTSAOLTREIYTDPIRTN 300

Qy 301 V--NMASMMWNNNAPSFAIETAVIRSPHLLDFLEOLTIFSTSSRWSATRHMTYWGHT 358

Db 301 APSGFASSTWNNNAPSFAIETAVIRSPHLLDFLEOLTIFSTSSRWSATRHMTYWGHT 360

Qy 359 IQSRPIGGGLNTSTHGST-NTSINPVRSLSPFSDRVVWYTESYAGVLLWGLYLEPIHGVPY 417

Db 361 LNFPRPIGGTLNTSTQGLTNTSINPVTQFTSRDVRVYTESNAGTNI--LFTTPVNGVPA 418

Qy 418 RENFRPQNTFERGTANYSPYESPGLQKDSSTELPPETTERPNYESYSHRLSHIGLIS 477

Db 419 RFNFPQNTYERGATTYSQYQGVGQLFDSSTELPPETTERPNYESYSHRLSHIGLII 478

Qy 478 QSRVHVPSWTHRSADRTNTISSDSITQPLVKSNLNSGTSVVSQPGTGGDIIRTNV 537

Db 479 GNTLRAPVPSWTHRSADRTNTIGPNRIQTPIPVKALNLHSGVTVVGPGTGGDILRTN 538

Qy 538 NGSVLSGLNFNTSILQRYRVRYAAQTMVLRTVVGSTTDFDQGPSPMSANESITSQ 597

Db 539 TGTFGDIRLINVPLSQRYRVRYASTTDLQFTTRINGTTVNIQNFRTMNRGDNLEYR 598

Qy 598 SFRFAEPFVIGISASGSQTAGISISNAGRQTFHFDKIERIPITATREAEVDLERAQAVN 657

Db 599 SFRTAGFTFNFNAQSTFTLGAQSFNSQEVYIDRVFVPAEVTFEAEVDLERAQAVN 658

Qy 658 ALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELEKVKYAKRLSDERNLLQ 717

Db 659 ALFTSNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELEKVKYAKRLSDERNLLQ 718

Qy 718 DPNFTSINKQDPFISTNBNQSFTHSQSHGHWGSENITIQEGNDVFKENYVTLPGTFN 777

Db 719 DPNFTSISQSPASIDGOSNFPISNELSHGHWGSAVNTIQEGNDVFKENYVTLPGTFN 778

Qy 778 ECVPTLYOKIGESLKAQRYQRCYIEDSOLYLIRYNKAKHETLDVPGESVWPLS 837

Db 779 ECVPTLYOKIGESLKAQRYQRCYIEDSOLYLIRYNKAKHETLDVPGESVWPLS 838

Qy 838 VESPIGRCEPNRCAPHFENWPDLCSCRDGKCAHSHHFLSDIDIGCTDLHENLGVWV 897

Db 839 VESPIGRCEPNRCAPHFENWPDLCSCRDGKCAHSHHFLSDIDIGCTDLHENLGVWV 898

Qy 898 VFKIQTQEGHARLGNLEFIEEKLGEALSRVGAQKWRDKREKLOLETKRYVYTAKEA 957

Db 899 VFKIQTQEGHARLGNLEFIEEKLGEALSRVGAQKWRDKREKLOLETKRYVYTAKEA 958

Qy 958 VDALLFVDSQVNRLOADTNIGMHAADKLVRHIREAVLSLSVIPGVNAEIELEGRIT 1017

Db 959 VDALLFVDSQVNRLOADTNIGMHAADKLVRHIREAVLSLSVIPGVNAEIELEGRIT 1018

Qy 1018 AISLYDARNVVKNGDFNNGLCNNVKGHVQVQSHHRSVLVIPWEBAEVSQAVRVCPRG 1077

Db 1019 AMSLYDARNVVKNGDFNNGLCNNVKGHVQVQSHHRSVLVIPWEBAEVSQAVRVCPRG 1078

Qy 1078 YILRVYAYKEGEGCVTHIEENTDELKFNCEEEVYPTDGTCTNDYTAHQGTAVCN 1137

Db 1079 YILRVYAYKEGEGCVTHIEENTDELKFNCEEEVYPTDGTCTNDYTAHQGTAAACN 1138

Qy 1138 SRNAGYEDAYEDVTASVNVKPYEETVTDVRRDNHCEYDRGVNVYPLPAGYMTKELE 1197

Db 1139 SRNAGYEDAYEDVTASVNVKPYEETVTDVRRDNHCEYDRGVNVYPLPAGYMTKELE 1198

Qy 1198 YPETDKWIEIGETEGKFIIVDSVELLMEE 1228

Db 1199 YPETDKWIEIGETEGKFIIVDSVELLMEE 1229

RESULT 15

US-08-176-865-4

Sequence 4, Application US/08176865

Patent No. 5616319

GENERAL INFORMATION:

APPLICANT: Donovan, William P.

APPLICANT: Tan, Yiping

APPLICANT: Jany, Christine S.
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESS: Nadel
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/176,865
APPLICATION NUMBER: US/08/176,865
FILING DATE: 30-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/100,709
FILING DATE: 29-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Egolf, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1229 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-176-865-4

Query Match 80.8%; Score 5237.5; DB 1; Length 1229;
Best Local Similarity 79.9%; Pred. No. 0;
Matches 983; Conservative 94; Mismatches 149; Indels 5; Gaps 3;

QY 1 LTSNRKNEBIIINALSIPAVNSHSTOMDLSFPAEDSLCIAEGNNINPLVASTVQTGI 60
DB 1 LTSNRKNEBIIINALSIPVNSPSTOMNLSFPAEDSLCIAEGNNIDPPVFASTVQTGI 60
QY 61 NIAGRILGLVGPAGQIASFYSLVGLWELPRGDQWEIIFLEHVEQLINQOITENARNTA 120
DB 61 NIAGRILGLVGPAGQIASFYSLVGLWELPRGDQWEIIFLEHVEQLIRQOQVNTNRTA 120
QY 121 LARQLGLGDSFRAYQQSLEDWLENRDARTSRVLYTOYIALELDFNAMPLFAIRNOEVP 180
DB 121 IARLEGLRGYRSYQQALETWLDNRNDARSIIILERYVALELDITTAIPLFRINEEVP 180
QY 181 LLMVYAAQANLHLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSYCVWYNTGLN 240
DB 181 LLMVYAAQANLHLLLRDASLFGSEWGWASSDVNQYQEQIRVTEESYNSHCWQWYNTGLN 240
QY 241 SLRGTHAASVRYNQFRDRLTLGVLDLVALPSPVDTTYPINTSAQLTRREYITDAICATG 300
DB 241 NLRGTHAASVRYNQFRDRLTLGVLDLVALPSPVDTTYPINTSAQLTRREYITDPIGRIN 300
QY 301 V--NMASSMNNYNNAPSFAIETAVIRSPHLLDLEQLTIFSTSSRWASATRHMTYWRGHT 358
DB 301 APSGFATNNFNNAAPSFAIETAAIFRPHLLDPEQLTIYSASRWSSSTQHMYWVGH 360
QY 359 IQSRPIGGLNTSTHGST--NTSINPVRSLFSDRVYVWTSYAGVLLWGIYLEPIHGVPV 417
DB 361 LNFPRIGGLNTSTQGLTNTSINPVTQLFSDRVYVWTSYAGVLLWGIYLEPIHGVPV 418
QY 418 RNFNRNPONTFERGTANYSPYSPGLQDKDSELPETTERPNYESYSHRLSHIGLIS 477

DB 419 RNFNPONTFERGTANYSPYSPGLQDKDSELPETTERPNYESYSHRLSHIGLIS 478
QY 478 QSRVHVVPVSWTHRSADRTNTISSDSITQIPLVKSNLMSGT5VSGPGFTGGDIIRTNV 537
DB 479 GNTLRAPVTSWTHRSADRTNTIGPNRITQIPLVKALNLSHSGVT5VSGPGFTGGDIIRTN 538
QY 538 NGSVLSMGLNFNTSLQRYRVRYAAQTMVLRTVVGSTTDFDQGPSPSTMSANESLTSQ 597
DB 539 TGTGFDIRLNLINPLSQRVRYRIYASTTDLQFFTRINGTTVIGNFSRTMRNGDNLEJR 598
QY 598 SFRFAEPFVPGISASGSGTAGISISNNAGRTQTFHDKIEFIPITATFEAEYDLERAQAVN 657
DB 599 SFRTAGFSTPFLNAQSTFTLGAQSFSNQEVVIDRVEFVPAEVTFEAEYDLERAQAVN 658
QY 658 ALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDSEFCLDEKRELLEKVKYAKRLSDERNLLQ 717
DB 659 ALFTSTNPRRLKTDVTDYHIDQVSNLVACLSDSEFCLDEKRELFEKVKYAKRLSDERNLLQ 718
QY 718 DPNFTSINKQDPFISTNEQSNFTSIHQSEHGWGSENITIQEGNDVFKENYVTLPGTEN 777
DB 719 DPNFTFISGQLSPASIDGOSNFTSINELSHGWGANVTIQEGNDVFKENYVTLPGTEN 778
QY 778 ECRYPTLYQKIGSELKAYTRYQLRGYIEDSQLEIYLIRYNAKHETLDVPGTESVWPLS 837
DB 779 ECPYVLYQKIGSELKAYTRYQLRGYIEDSQLEIYLIRYNAKHETLDVPGTDSLWPLS 838
QY 838 VESPIGRCEPNRCAPHFENWPDLCSCRDGKCAHSHHFSLDIDIGCTDLHENLGVW 897
DB 839 VESPIGRCEPNRCAPHFENWPDLCSCRDGKCAHSHHFTLIDVGCCTDLHENLGVW 898
QY 898 VFKIQTQEGHARLGNLEFTEEEKLLGENLSRVKRAEKKWPKKEKLOLETKRVVYTEAKEA 957
DB 899 VFKIQTQEGYARLGNLEFTEEEKPLIGEALSrvKRAEKKWPKKEKLOLETKRVVYTEAKEA 958
QY 958 VDALLFVDSQVNRLOQADTNIQMIHAADKLVRHIREAYLSLSVPGVNAEIFFEELEGRIT 1017
DB 959 VDALLFVDSQVNRLOQADTNIQMIHAADKLVRHIREAYLSLSVPGVNAEIFFEELEGHIT 1018
QY 1018 AISLYDARNVYKNGDFNNGLACWNVKHVDVQOSHRSVLVPIPEWEAEVSQAVRVCPRG 1077
DB 1019 AMSLYDARNVYKNGDFNNGLTCWNVKHVDVQOSHRSVLVPIPEWEAEVSQAVRVCPRG 1078
QY 1078 YILRVYAYKEGEGCVTTHEIENNTDELKFKNCEEEVYPTDGTGTCNDYTAHQGTAVCN 1137
DB 1079 YILRVYAYKEGEGCVTTHEIENNTDELKFKNCEEEVYPTDGTGTCNDYTAHQGTAAACN 1138
QY 1138 SRNAGYEDAVEVDTTASVNYKPYEETVTVRRDNHCEYDRGVYVNPPLPAGVMTKELE 1197
DB 1139 SRNAGYEDAVEVDTTASVNYKPYEETVTVRRDNHCEYDRGVYVNPPLPAGVMTKELE 1198
QY 1198 YFPETDKVWIEIGETEGKFIVDSVELLMBE 1228
DB 1199 YFPETDKVWIEIGETEGKFIVDSVELLMBE 1229

Search completed: April 21, 2005, 04:18:31
Job time : 63 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 20, 2005, 20:18:09 ; Search time 126 Seconds
(without alignments)
3769.379 Million cell updates/sec

Title: US-10-614-524-2
Perfect score: 6479
Sequence: 1 LTNKRNENIINALSIPAV.....IGTEGKFIVDSVELLMEE 1228

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04.*
1: Geneseqpl980s.*
2: Geneseqpl990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6479	100.0	1228	4 AAB84628	AAB84628 Amino aci
2	6462	99.7	1228	4 AAU02039	AAU02039 B. thurin
3	5926.5	91.5	1227	2 AAW44321	AAW44321 Bacillus
4	5926.5	91.5	1227	4 AAB19950	AAB19950 Bacillus
5	5912.5	91.3	1227	4 AAU02046	AAU02046 B. thurin
6	5740	88.6	1228	2 AAR50955	AAR50955 Bacillus
7	5436.5	83.9	1227	2 AAY31990	AAY31990 Chimeric
8	5237.5	80.8	1229	2 AAR54074	CRYET5. 2
9	5237.5	80.8	1229	2 AAW35259	Bacillus
10	5237.5	80.8	1229	2 AAW17699	CRYET5. 3
11	5237.5	80.8	1229	2 AAW87633	CRYET5 pr
12	5237.5	80.8	1229	2 AAY30923	B. thurin
13	5237.5	80.8	1229	8 ADK98479	B. thurin
14	5233.5	80.8	1230	8 ADK98484	B. thurin
15	5233.5	80.8	1230	8 ADK98489	B. thurin
16	5233.5	80.8	1230	8 ADK98481	B. thurin
17	5233.5	80.8	1230	8 ADK98491	B. thurin
18	5233.5	80.8	1230	8 ADK98487	B. thurin
19	5189.5	80.1	1209	4 AAU02094	Bacillus
20	5183.5	80.0	1221	4 AAU00421	B. thurin
21	5169.5	79.8	1221	4 AAU00420	B. thurin
22	5108	78.8	1186	2 AAY16796	Amino aci
23	4791	73.9	1208	4 AAU02093	Bacillus
24	4303.5	66.4	1217	4 AAU02092	Bacillus
25	3977.5	61.4	1174	2 AAR89494	B.T. toxi

26	3977.5	61.4	1174	2 AAW09043	Bacillus
27	3974.5	61.3	1174	2 AAR25825	Novel tox
28	3969.5	61.3	1174	2 AAR08257	B.thuring
29	3791	58.5	1176	2 AAW46737	Amino aci
30	3791	58.5	1176	2 AAW47035	Bacillus
31	3579	55.2	1170	2 AAR63231	Crystall p
32	3556	54.9	1167	2 AAR54073	CRYET4. 2
33	3556	54.9	1167	2 AAW35258	Bacillus
34	3556	54.9	1167	2 AAW17700	CRYET4. 3
35	3556	54.9	1167	2 AAW87632	CRYET4. 3
36	3556	54.9	1167	2 AAY30922	B. thurin
37	3502.5	54.1	1189	2 AAW61345	a mutated
38	3502.5	54.1	1189	2 AAY17783	EG12111 c
39	3502.5	54.1	1189	3 AAY82431	Bacillus
40	3502.5	54.1	1189	5 AAE26471	Bacillus
41	3502.5	54.1	1189	5 ABG93849	B. thurin
42	3502.5	54.1	1189	7 ABW02350	B. thurin
43	3500.5	54.0	1189	2 AAW61335	A mutated
44	3500.5	54.0	1189	2 AAY17788	B. thurin
45	3500.5	54.0	1189	3 AAY82396	Bacillus

ALIGNMENTS

RESULT 1

AAAB84628
XX AAB84628 standard; protein; 1228 AA.
XX AC AAB84628;
XX 05-SEP-2001 (first entry)
DT
XX
DE Amino acid sequence of a CryIbF insecticidal protein.
XX
XX CryIbF; insecticidal protein; CryIbJd; Cry9Fa; lepidoptera; coleoptera;
KW insect pest; transgenic plant.
XX
XX Bacillus thuringiensis.
XX
XX W0200147952-A2.
XX
PD 05-JUL-2001.
XX
PF 19-DEC-2000; 2000WO-EP013184.
XX
PR 28-DEC-1999; 99US-0173387P.
XX
XX (AVET) AVENTIS CROPS SCIENCE NV.
XX
XX Arnaut G, Boets A, Damme N, Mathieu E, Vanneste S, Van Rie J;
XX
XX WPI; 2001-425619/45.
DR N-PSDB; AAB28240.
XX
PT Novel insecticidal proteins CryIbJd, Cry9Fa and CryIbF, derived from
XX Bacillus thuringiensis, useful for controlling insects in plants.
XX
PS Claim 11; Page 37-41; 65pp; English.
XX
XX The present sequence represents CryIbF, an insecticidal protein derived
XX from Bacillus thuringiensis. The specification also describes CryIbJd and
XX Cry9Fa. The Cry proteins have activity against lepidopteran and
XX coleopteran insect pests. CryIbF, CryIbJd and Cry9Fa polynucleotides and
XX polypeptides are useful for obtaining a plant with resistance to insects.
XX Cry polynucleotides are useful for producing transgenic plants which are
XX resistant to insects
XX
SQ Sequence 1228 AA;
Query Match 100.0%; Score 6479; DB 4; Length 1228;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 LTSNRKNEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVOTGI 60
Db 1 LTSNRKNEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVOTGI 60
QY 61 NIAGRILGVLGVPFAGQIASFYSFLVGLMWRGRDQWEIIFLEHVEQLINQOITENARNTA 120
Db 61 NIAGRILGVLGVPFAGQIASFYSFLVGLMWRGRDQWEIIFLEHVEQLINQOITENARNTA 120
QY 121 LARLOGLGDSFRAYQOQSLDLEWNRDRTARSVLTYQIYIALELDFLNAMPLFAIRNOEVP 180
Db 121 LARLOGLGDSFRAYQOQSLDLEWNRDRTARSVLTYQIYIALELDFLNAMPLFAIRNOEVP 180
QY 181 LLMVYAQAANLHLLLRDASLFGSEFGLTQOEIQRYVEROETRDYSDYCVEMYNITGLN 240
Db 181 LLMVYAQAANLHLLLRDASLFGSEFGLTQOEIQRYVEROETRDYSDYCVEMYNITGLN 240
QY 241 SLRGNTNAASVRVYNQFRDLTLGVLIDLVALFPSTYDTRTPINTSAQLTREVTYDAIGATG 300
Db 241 SLRGNTNAASVRVYNQFRDLTLGVLIDLVALFPSTYDTRTPINTSAQLTREVTYDAIGATG 300
QY 301 VNMAWMNWNAPSPFAIETAVIRSPHLLDFLEQLTIFSTSRWSATRMTYWRGHTIQ 360
Db 301 VNMAWMNWNAPSPFAIETAVIRSPHLLDFLEQLTIFSTSRWSATRMTYWRGHTIQ 360
QY 361 SRPIGGGLNTSTHGSTNTSINPRLSPFSDVYVWTSYAGVLLWGIYLEPIHGVPVTVRFN 420
Db 361 SRPIGGGLNTSTHGSTNTSINPRLSPFSDVYVWTSYAGVLLWGIYLEPIHGVPVTVRFN 420
QY 421 FRNPQNTFERGTANYQSPYSPGLQKXSETLPPTERPNEYSHRSLSHIGLISQSR 480
Db 421 FRNPQNTFERGTANYQSPYSPGLQKXSETLPPTERPNEYSHRSLSHIGLISQSR 480
QY 481 VHPVVISWTHRSADRTNTISDSITQIPLVKSFNLSGTSVWSGPGTGGDIIRTNVNGS 540
Db 481 VHPVVISWTHRSADRTNTISDSITQIPLVKSFNLSGTSVWSGPGTGGDIIRTNVNGS 540
QY 541 VLSMGLNFNTSLQRYVRVRYAASQTMVLRTVVGSTTFDQGPSTMSANESLTSQSPR 600
Db 541 VLSMGLNFNTSLQRYVRVRYAASQTMVLRTVVGSTTFDQGPSTMSANESLTSQSPR 600
QY 601 FAEFPVGISASGQTAGISISNNAGROTTFHDKIEFIPITATFEAEYDLERAQEAVALNF 660
Db 601 FAEFPVGISASGQTAGISISNNAGROTTFHDKIEFIPITATFEAEYDLERAQEAVALNF 660
QY 661 TTNTPRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLKVKYAKRLSDERNLLQDPN 720
Db 661 TTNTPRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLKVKYAKRLSDERNLLQDPN 720
QY 721 FTSINKOPDFISTNEQSNFTSIHQSESHGWMGSENITIQEGNDVFKENYVTLPTFNECY 780
Db 721 FTSINKOPDFISTNEQSNFTSIHQSESHGWMGSENITIQEGNDVFKENYVTLPTFNECY 780
QY 781 PTLYQXIGESSELKAYTRYQLRGYIEDSQDLEIYLIRYNAKHETLDVPGTESVMPLSVES 840
Db 781 PTLYQXIGESSELKAYTRYQLRGYIEDSQDLEIYLIRYNAKHETLDVPGTESVMPLSVES 840
QY 841 PIRCGEPNRCAPHFENWPDLCSCRGEKCAHHSHFSLDIDIGCTDLHENLGVWVFK 900
Db 841 PIRCGEPNRCAPHFENWPDLCSCRGEKCAHHSHFSLDIDIGCTDLHENLGVWVFK 900
QY 901 IKTOEGHARLGNLEFIEEKLPGELSRVRAEKKWDRKLEKQLETKRYVYVTEAKEAVDA 960
Db 901 IKTOEGHARLGNLEFIEEKLPGELSRVRAEKKWDRKLEKQLETKRYVYVTEAKEAVDA 960
QY 961 LFVDSQYRNLQADTNIGMIHAADKLVRHIREAYVLSVLPVGNABEIEFELEGRITAIIS 1020
Db 961 LFVDSQYRNLQADTNIGMIHAADKLVRHIREAYVLSVLPVGNABEIEFELEGRITAIIS 1020
QY 1021 LYDARNVVKNGDFNGLACNVKGVHDVQOQSHRSVLVIPLEWAEVSVQVRVCPGRGIYL 1080
Db 1021 LYDARNVVKNGDFNGLACNVKGVHDVQOQSHRSVLVIPLEWAEVSVQVRVCPGRGIYL 1080
```

```
QY 1081 RVTAYKEGYGEGCVTIHEIENNTDELKFKNCEBEEVYPTDTGTCNDYTAHQGTAVCNRSN 1140
Db 1081 RVTAYKEGYGEGCVTIHEIENNTDELKFKNCEBEEVYPTDTGTCNDYTAHQGTAVCNRSN 1140
QY 1141 AGYEDAYEVDVTTASVNYKPTYBEEYTVDRVDNHCEYDRGYVNYPPPLPAGYMTKELEYFP 1200
Db 1141 AGYEDAYEVDVTTASVNYKPTYBEEYTVDRVDNHCEYDRGYVNYPPPLPAGYMTKELEYFP 1200
QY 1201 ETDKWIETGETGKFIIVDSVELLMEE 1228
Db 1201 ETDKWIETGETGKFIIVDSVELLMEE 1228
RESULT 2
AAU02039 standard; protein; 1228 AA.
XX
XX AAU02039;
XX AC
XX DT
XX 29-AUG-2001 (first entry)
XX DE B. thuringiensis toxic crystal protein, CryE64.
XX Delta endotoxin; Lepidopteran-active; crystal protein; insecticide;
XX transgenic plant; corn; wheat; soybean; oat; cotton; rice; yre; sorghum;
XX sugarcane; tomato; tobacco; kapok; flax; potato; barley; turf grass;
XX pasture grass; berry; fruit; legume; vegetable; ornamental plant; shrub;
XX cactus; tree call; gypsy moth; looper; tobacco budworm; spruce budworm;
XX cotton leaf perforator; CryE64.
XX Bacillus thuringiensis.
XX WO200119859-A2.
XX PD
XX 22-MAR-2001.
XX PF
XX 13-SEP-2000; 2000WO-US025361.
XX PR
XX 15-SEP-1999; 99US-0153995P.
XX PA (MONS ) MONSANTO CO.
XX Baum JA, Chu C, Donovan WP, Gilmer AJ, Rupar MJ;
XX WPI; 2001-281518/29.
XX N-PSDB; AAS02482.
Lepidopteran-active Bacillus thuringiensis delta-endotoxin polypeptides
and the polynucleotides that encode them, useful for increasing the
insect resistance of plant.
Claim 5; Page 139-141; 173pp; English.
The sequence represents a B. thuringiensis Lepidopteran-active delta-
endotoxin, crystal protein CryE64. The Lepidopteran-active B.
thuringiensis delta-endotoxin polypeptides may be used as compositions
that are applied to plant crops to protect them from insect damage. The
polynucleotides may be used in the production of transgenic plants that
express the insecticidal polypeptides and consequently have improved
insect resistance compared to non-transformed plants. Monocotyledonous or
dicotyledonous plants may be protected in this way, for example corn,
wheat, soybean, oat, cotton, rice, yre, sorghum, sugarcane, tomato,
tobacco, kapok, flax, potato, barley, turf grass, pasture grass, berry,
fruit, legume, vegetable, ornamental plant, shrub, cactus and/or tree
cell. A wide range of insects (e.g. gypsy moth, looper, tobacco budworm,
cotton leaf perforator and spruce budworm) may be affected by application
of the insecticidal polypeptides (full details given in specification)
```

SQ Sequence 1228 AA;

Query Match 99.7%; Score 6462; DB 4; Length 1228;
Best Local Similarity 99.6%; Pred. NO. 0;
Matches 1223; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 LTSNRKNEIINALSTPAVNSHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVGTGI 60
 Db :|||||
 QY 1 MTSNRKNEIINALSTPAVNSHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVGTGI 60
 Db :|||||
 QY 61 NIAGRIILGVLPAGPAGIAGFYFLVCELWPRGRDQWEIIFLEHVEQLINOQIITENARNTA 120
 Db :|||||
 QY 61 NIAGRIILGVLPAGPAGIAGFYFLVCELWPRGRDQWEIIFLEHVEQLINOQIITENARNTA 120
 Db :|||||
 QY 121 LARLQGLGDSFRAYQQSLEDWLENRRDARTSRVLYTQYIALELDFLNAMEPLFAIRNOEVP 180
 Db :|||||
 QY 121 LARLQGLGDSFRAYQQSLEDWLENRRDARTSRVLYTQYIALELDFLNAMEPLFAIRNOEVP 180
 Db :|||||
 QY 181 LMVYAQAANLHLLLDASLFGSEFGLTSQETQRYRQVQETRDYSDYCVWEYNTGLN 240
 Db :|||||
 QY 181 LMVYAQAANLHLLLDASLFGSEFGLTSQETQRYRQVQETRDYSDYCVWEYNTGLN 240
 Db :|||||
 QY 241 SLRGTTNAASWVRYNOPFRDITLGLVDLVALFPSPYDTRTYPINTSAQLTRREYVYDAIGATG 300
 Db :|||||
 QY 241 SLRGTTNAASWVRYNOPFRDITLGLVDLVALFPSPYDTRTYPINTSAQLTRREYVYDAIGATG 300
 Db :|||||
 QY 301 VNMAWMYNNNAPSFAIETAVIRSPHLLDFLEQLTIFSTSRWSATRHMTYWRGHTIQ 360
 Db :|||||
 QY 301 VNMAWMYNNNAPSFAIETAVIRSPHLLDFLEQLTIFSTSRWSATRHMTYWRGHTIQ 360
 Db :|||||
 QY 361 SRPIGGGLNTSTHGSTNTSINPRLSPFSDRVYMTESYAGVLLWGIYLEPIHGVPVTRFN 420
 Db :|||||
 QY 361 SRPIGGGLNTSTHGSTNTSINPRLSPFSDRVYMTESYAGVLLWGIYLEPIHGVPVTRFN 420
 Db :|||||
 QY 421 FRNPONTFERGTANYSPYSPGLQKDSLTPETTERPNYESYSHRLSHGLISQSR 480
 Db :|||||
 QY 421 FRNPONTFERGTANYSPYSPGLQKDSLTPETTERPNYESYSHRLSHGLISQSR 480
 Db :|||||
 QY 481 VHPVSVWTHRSADRTNTIISDSTIQPLVKSFNLNSGTSVSGPGFTGDDIIRTNVNGS 540
 Db :|||||
 QY 481 VHPVSVWTHRSADRTNTIISDSTIQPLVKSFNLNSGTSVSGPGFTGDDIIRTNVNGS 540
 Db :|||||
 QY 541 VLSMGLNFNNTSLQRYRVRYRAASQTMVLRLVTVGSGTTFDQGPPTMSANESLTSQSPR 600
 Db :|||||
 QY 541 VLSMGLNFNNTSLQRYRVRYRAASQTMVLRLVTVGSGTTFDQGPPTMSANESLTSQSPR 600
 Db :|||||
 QY 601 FAEPFVGISASGQTAGISINNAAGROTFFDKIEPIPIATFAEYDLERAQEAVALNF 660
 Db :|||||
 QY 601 FAEPFVGISASGQTAGISINNAAGROTFFDKIEPIPIATFAEYDLERAQEAVALNF 660
 Db :|||||
 QY 661 TTNTPRLKTDVTDYHIDQVSNLVACLSDFECLDEKRELEKVKYAKRLSDERNLLQDPN 720
 Db :|||||
 QY 661 TTNTPRLKTDVTDYHIDQVSNLVACLSDFECLDEKRELEKVKYAKRLSDERNLLQDPN 720
 Db :|||||
 QY 721 FTSINKQPDFISTNEQSNFTSIHQSEHGMWGSNITIQEGNDVFKENYVTLPGTFNECY 780
 Db :|||||
 QY 721 FTSINKQPDFISTNEQSNFTSIHQSEHGMWGSNITIQEGNDVFKENYVTLPGTFNECY 780
 Db :|||||
 QY 781 PTYLYQKIGSELKAYTRYQLRGHIEDSQDLEIYLIRYNAKHETLDVPGTESVWPLSVES 840
 Db :|||||
 QY 781 PTYLYQKIGSELKAYTRYQLRGHIEDSQDLEIYLIRYNAKHETLDVPGTESVWPLSVES 840
 Db :|||||
 QY 841 PIGRCGEPNRCAPHFENPDLDSCRCRGEKCAHSHHFSLDIDIGCTDLHENLGVWVFX 900
 Db :|||||
 QY 841 PIGRCGEPNRCAPHFENPDLDSCRCRGEKCAHSHHFSLDIDIGCTDLHENLGVWVFX 900
 Db :|||||
 QY 901 IKTOEGHARLGNLEFIEBKPLLGALSRVKAERKWRDKREKLEKRYVYTAKEAVIDA 960
 Db :|||||
 QY 901 IKTOEGHARLGNLEFIEBKPLLGALSRVKAERKWRDKREKLEKRYVYTAKEAVIDA 960
 Db :|||||
 QY 961 LFVDSQYNRLOADTNIGMIHAADKLVHRIEAYLSLSVPGVNAEIPFEELEGRITTAIS 1020
 Db :|||||
 QY 961 LFVDSQYNRLOADTNIGMIHAADKLVHRIEAYLSLSVPGVNAEIPFEELEGRITTAIS 1020
 Db :|||||
 QY 1021 LYDARNVVKGDGFNGLACNVKGVHDVQOSSHRSVLVIFPEWEAEVQAVRVCPGRCYIL 1080
 Db :|||||
 QY 1021 LYDARNVVKGDGFNGLACNVKGVHDVQOSSHRSVLVIFPEWEAEVQAVRVCPGRCYIL 1080
 Db :|||||

QY 1081 RVTAYKEGYGEGCVTTHEIENNTDELKFKNCBEEVYPTDTGTCNDYTAHQGTAVCNRN 1140
 Db :|||||
 QY 1081 RVTAYKEGYGEGCVTTHEIENNTDELKFKNCBEEVYPTDTGTCNDYTAHQGTAVCNRN 1140
 Db :|||||
 QY 1141 AGYEDAYEVDTTASVNVKPTYEBEETVTDVRRDNHCEYDRGVVNYPPPLPAGYMTKELEYFP 1200
 Db :|||||
 QY 1141 AGYEDAYEVDTTASVNVKPTYEBEETVTDVRRDNHCEYDRGVVNYPPPLPAGYMTKELEYFP 1200
 Db :|||||
 QY 1201 ETDKWIEIGETEGKTFIVDSVELLMBE 1228
 Db :|||||
 QY 1201 ETDKWIEIGETEGKTFIVDSVELLMBE 1228
 Db :|||||
 RESULT 3
 AAW44321
 ID AAW44321 standard; protein; 1227 AA.
 XX
 AC AAW44321;
 XX
 DT 27-MAY-1998 (first entry)
 XX
 DE Bacillus thuringiensis 158C2c toxin.
 XX
 KW Bacillus thuringiensis; 158C2c; toxin; lepidopteran-active; insect;
 KW microbe; transgenic plant; resistant.
 XX
 OS Bacillus thuringiensis.
 XX
 PN US5723758-A.
 XX
 PD 03-MAR-1998.
 XX
 PF 23-MAY-1995; 95US-004448170.
 XX
 PR 13-SEP-1991; 91US-00759247.
 PR 01-JUN-1993; 93US-00069902.
 XX
 PA (MYCO) MYCOGEN CORP.
 XX
 PI Stelman S, Narva KE, Cummings DA, Payne J, Cannon RJ;
 DR WPI; 1998-178600/16.
 DR N-PSDB; AAV15222.
 XX
 PT DNA encoding Bacillus thuringiensis toxin proteins - for producing
 transgenic plants resistant to attack by lepidopteran pests.
 XX
 PS Claim 1; Col 33-40; 25pp; English.
 XX
 CC The present sequence represents a 158C2c toxin from Bacillus
 CC thuringiensis. The present invention describes isolated nucleic acid
 CC sequences encoding toxins active against lepidopteran insects. The
 CC present invention also describes a recombinant host transformed with a
 CC nucleic acid sequence encoding a toxin. The nucleic acid sequence can be
 CC amplified. The product is used for producing transgenic plants resistant
 CC to attack by lepidopteran pests. N.B. The numbers in the sequence listing
 CC do not correspond to the SEQ ID NO.'s mentioned in the specification e.g.
 CC in the specification SEQ ID NO:3, 4, 5 and 6 are said to correspond to
 CC the nucleic acid sequences encoding the toxins, and SEQ ID NO:7, 8, 9 and
 CC 10 are said to correspond to the amino acid sequences of the toxins,
 CC whereas in the sequence listing the amino acid sequence is given after
 CC the nucleic acid sequence encoding it (i.e. SEQ ID NO:3 encodes SEQ ID
 CC NO:4)
 XX
 SQ Sequence 1227 AA;
 : Query Match 91.5%; Score 5926.5; DB 2; Length 1227;
 Best Local Similarity 91.8%; Pred. No. 0;
 Matches 1129; Conservative 36; Mismatches 60; Indels 5; Gaps 3;
 QY 1 LTSNRKNEIINALSTPAVNSHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVGTGI 60
 Db 1 LTSNRKNEIINALSTPAVNSHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVGTGI 60

QY 61 NIAGRIILGVLPVAGIAGSYFLVGLWPRGRDOWEIFLEHVEQLINQOITENARNTA 120
 DB 61 NIAGRIILGVLPVAGIAGSYFLVGLWPRGRDOWEIFLEHVEQLINQOITENARNTA 120
 QY 121 LARLOGLGDSFRAYQOQSLDLEWLNDRDARTSVLYTQYIALEDFLNAFLFAIRNOEVP 180
 DB 121 LARLOGLGDSFRAYQOQSLDLEWLNDRDARTSVLYTQYIALEDFLNAFLFAIRNOEVP 180
 QY 181 LLMYVQAANLHLLLDASLFGSEFGITQEIORYYERQVETQTRDSDYCVIEWYNTGLN 240
 DB 181 LLMYVQAANLHLLLDASLFGSEFGITQEIORYYERQVETQTRDSDYCVIEWYNTGLN 240
 QY 241 SLRGTAASVRYNQFRDRLTLGLVDLVALFPSPYDTRTYPINTSAQLTRVYTDGATG 300
 DB 241 NLRGTAESWLRYNQFRDRLTLGLVDLVALFPSPYDTRTYPINTSAQLTRVYTDGATG 300
 QY 301 V--NMASMMYNNNAPSFAIAETAVIRSPHLLDFLEQLTIFSTSSRWSSATRHMTYWRGHT 358
 DB 301 APSGFATNNFNNAAPSFAIAEAAVIRPPHLLDFPEQLTIFSVLSRWSTQYMYWVGH 360
 QY 359 IQSPICGGLNTSHGTSNTSINPRLSPFRSDYVWYTESVAGULLWGIYLEPHGVPTVR 418
 DB 361 LESRTIRGSLSTHGTSNTSINPRLSPFRSDYVWYTESVAGULLWGIYLEPHGVPTVR 418
 QY 419 FNRPNPONTFERGTANYSQVPSGFLQKDSSETLPETTERPNYESYSHRLSHIGLISQ 478
 DB 419 FNRPNPONTFERGTANYSQVPSGFLQKDSSETLPETTERPNYESYSHRLSHIGLISQ 478
 QY 479 SRVHPVYVWTHRSADRTNTISSDSITQIPLVKSFNLSGTSVVGSGFTGGDIIRTNVN 538
 DB 478 NTLRAPVYVWTHRSADRTNTISSDSITQIPLVKSFNLSGTSVVGSGFTGGDIIRTNVN 537
 QY 539 GSVLSMGLNFNTSLQRYRVRYAASQTMVLRVTVGSGTTFDQGPSTMSANESLTSQS 598
 DB 538 GSVLSMGLNFNTSLQRYRVRYAASQTMVLRVTVGSGTTFDQGPSTMSANESLTSQS 597
 QY 599 FRAEFPPVGISASGQTAGISISNNAQRTFHDKIEFIPITATFAEYDLERAQEAUNA 658
 DB 598 FRAEFPPVGISASGQTAGISISNNAQRTFHDKIEFIPITATFAEYDLERAQEAUNA 657
 QY 659 LFTNTNPRRLKTDVTDHIDOVNVLVACLSDPECLDEKRELLKVKYAKRLSDERNLLQD 718
 DB 658 LFTNTNPRRLKTDVTDHIDOVNVLVACLSDPECLDEKRELLKVKYAKRLSDERNLLQD 717
 QY 719 PNFTSINKQPDFISTNQSNFTSHEQSEHGWSGSENIITIOEGNDVFKENYVTLPGTFNE 778
 DB 718 PNFTSINKQPDFISTNQSNFTSHEQSEHGWSGSENIITIOEGNDVFKENYVTLPGTFNE 777
 QY 779 CYPTLYQKIGESLKAATRYQLRGYTEDSQDLLEIYLIRNAKHETLDVPGTESVWPLSV 838
 DB 778 CYPTLYQKIGESLKAATRYQLRGYTEDSQDLLEIYLIRNAKHETLDVPGTESVWPLSV 837
 QY 839 ESPIGRCGEPRNRCAPHEWNPDLDCSCRDGCKCAHSHHPSLSDIDGCTDLHENLGVVV 898
 DB 838 ESPIGRCGEPRNRCAPHEWNPDLDCSCRDGCKCAHSHHPSLSDIDGCTDLHENLGVVV 897
 QY 899 FKIKTQEGHARLGNLEFIEBKPLLGALSRVKAEEKWRDKREKLOLETXYVTEAKEAV 958
 DB 898 FKIKTQEGHARLGNLEFIEBKPLLGALSRVKAEEKWRDKREKLOLETXYVTEAKEAV 957
 QY 959 DALFVDSQYNRLQADTNIGMHAADKLVRHIREAYLSLSVIFGVNAIEFEELEGRITTA 1018
 DB 958 DALFVDSQYNRLQADTNIGMHAADKLVRHIREAYLSLSVIFGVNAIEFEELEGRITTA 1017
 QY 1019 ISLYDARNVKGDFNNGLAQWNVKGVHDVQOQSHRSVLVPEWEAEVSAQVRCGRGY 1078
 DB 1018 ISLYDARNVKGDFNNGLAQWNVKGVHDVQOQSHRSVLVPEWEAEVSAQVRCGRGY 1077
 QY 1079 ILRVATYKEGVGCGVTHIEIENNTDRLKPKNCEEEVYPTDGTGNDYTAHOGTAVCNS 1138
 DB 1078 ILRVATYKEGVGCGVTHIEIENNTDRLKPKNCEEEVYPTDGTGNDYTAHOGTAVCNS 1137

QY 1139 RNAGYEDAYEDVDTTASVNYKPTVEEETITDVRDHNHCEYDRGVNYPPLPAGYMTKELEY 1198
 DB 1138 RNAGYEDAYEDVDTTASVNYKPTVEEETITDVRDHNHCEYDRGVNYPPLPAGYMTKELEY 1197
 QY 1199 FPETDKVWIEIGTEGKFIVDSVELLMEE 1228
 DB 1198 FPETDKVWIEIGTEGKFIVDSVELLMEE 1227
 RESULT 4
 AAB19950
 ID AAB19950 standard; protein; 1227 AA.
 XX
 AC AAB19950;
 XX
 DT 19-MAR-2001 (first entry)
 XX
 DE Bacillus thuringiensis delta-endotoxin 158C2c.
 XX
 KW Delta-endotoxin; 158C2c; toxin; lepidoptera; crystal protein;
 KW transgenic plant; insect resistance; crop protection; biological control.
 XX
 OS Bacillus thuringiensis.
 XX
 PN US6150589-A.
 XX
 PD 21-NOV-2000.
 XX
 PF 31-OCT-1997; 97US-00961803.
 XX
 PR 23-MAY-1995; 95US-00448170.
 XX
 PA (MYCO) MYCOGEN CORP.
 XX
 PI Narva KE, Stelman S, Payne J, Cummings DA, Cannon RJC;
 XX
 DR WPI; 2001-049107/06.
 DR N-PSDB; AAA89221.
 XX
 PT New genes isolated from Bacillus thuringiensis which encode toxins
 PT against lepidopteran insects and which can be used to transform various
 PT hosts to express the B.t. toxin and confer insect resistance.
 XX
 PS Example 2; Col 35-42; 25pp; English.
 XX
 CC The present sequence is that of the C-terminal region of novel delta-
 CC endotoxin 1582Cc of Bacillus thuringiensis (B.t.) isolate PS158C2 (NRRL B
 CC -18872). The amino acid sequence is predicted from a partial gene
 CC sequence for 1582Cc (see AAA89222) obtained from a PS158C2 gene library.
 CC The invention provides novel B.t. delta-endotoxins 1582Ca-d (see AAB19947
 CC -50), which are active against lepidopteran pests. Expression of the
 CC delta-endotoxins in transformed plants confers resistance to these insect
 CC pests, while transformed microorganisms can be applied to sites where
 CC they will proliferate and be ingested by the pest
 XX
 SQ Sequence 1227 AA;
 Query Match 91.5%; Score 5926.5; DB 4; Length 1227;
 Best Local Similarity 91.8%; Pred. No. 0;
 Matches 1129; Conservative 36; Mismatches 60; Indels 5; Gaps 3;
 QY 1 LTSNRKNEININALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI 60
 DB 1 LTSNRKNEININALSIPAVSNHSAQMNLSLDARIEDSLCIAEGNNIDFVSASTVQTGI 60
 QY 61 NIAGRILGVLPVAGIAGSYFLVGLWPRGRDOWEIFLEHVEQLINQOITENARNTA 120
 DB 61 NIAGRILGVLPVAGIAGSYFLVGLWPRGRDOWEIFLEHVEQLINQOITENARNTA 120
 QY 121 LARLOGLGDSFRAYQOQSLDLEWLNDRDARTSVLYTQYIALEDFLNAFLFAIRNOEVP 180
 DB 121 LARLOGLGDSFRAYQOQSLDLEWLNDRDARTSVLYTQYIALEDFLNAFLFAIRNOEVP 180


```
QY 181 LLVYAAANLHLLLRDASLFGSEGLTQETQRYVERQVETRDYSDYCVENYNTGLN 240
Db 181 LLVYAAANLHLLLRDASLFGSEGLTQETQRYVERQVETRDYSDYCVENYNTGLN 240
QY 241 SLRGTNAASVRYNQFRDRLTLGLVDLVALFPSPDYTRTYPINTSAQLTRVYTDGATG 300
Db 241 NLRGTAESWLRYNQFRDRLTLGLVDLVALFPSPDYTRTYPINTSAQLTRVYTDGATG 300
QY 301 V--NMASMNWNNAPSAFSAETAVIRSPHLLDPLEQLTIFSTSSRWASATRMHYWRGHT 358
Db 301 APGFASTNNFNWNNAPSAFSAEAAVIRPPHLLDPLEQLTIFSVLSRWNSNTQYNNYVWGH 360
QY 359 IQSRPIGGGLNTSHGTSNTSINPVLRSFSDVDYVWTESYAGVLLGYLEPIHGVPTVR 418
Db 361 LERTKIGSLTSHGTSNTSINPVLRSFSDVDYVWTESYAGVLLGYLEPIHGVPTVR 418
QY 419 FNRPNQPTFRGTANYSQPYSPGLQKDSFETLPPETTERPNYESYSHRLSHIGLISQ 478
Db 419 FNRPNQPTFRGTANYSQPYSPGLQKDSFETLPPETTERPNYESYSHRLSHIGLISQ 478
QY 479 SRVHVYVSWTHRSADRTNTISSDITQIPLVKSFNLSGTSVVGPGFTGGDIIRTNVN 538
Db 478 NTLRAPVYVSWTHRSADRTNTISSDITQIPLVKSFNLSGTSVVGPGFTGGDIIRTNVN 537
QY 539 GSVLSMGLNFNNNTSLQRYRVRYAAQOTWLVRYVCGSTTFDQGPSTMSANESLTSQS 598
Db 538 GSVLSMGLNFNNNTSLQRYRVRYAAQOTWLVRYVCGSTTFDQGPSTMSANESLTSQS 597
QY 599 FRAEFPVGISASGSGTAGISINNAGROTFFHDKIEFIPITATFEAEYDLERAQAVNA 658
Db 598 FRAEFPVGISASGSGTAGISINNAGROTFFHDKIEFIPITATFEAEYDLERAQAVNA 657
QY 659 LFTNTPRRLKTDVTDVHIDOVSNLVACLSDFCDEKRELLKVKYAKLSDERNLLQD 718
Db 658 LFTNTPRRLKTDVTDVHIDOVSNLVACLSDFCDEKRELLKVKYAKLSDERNLLQD 717
QY 719 PNFTSINKQPDFSTNEQSFTSIHQSEHGWSGSENIITQEGNDVPKENYVILPGTFNE 778
Db 718 PNFTSINKQPDFSTNEQSFTSIHQSEHGWSGSENIITQEGNDVPKENYVILPGTFNE 777
QY 779 CYPTLYQKIGSELKAYTRQYLRGYEDSDQLEIYLIRNAXHETLDVPGTSVWPLSV 838
Db 778 CYPTLYQKIGSELKAYTRQYLRGYEDSDQLEIYLIRNAXHETLDVPGTSVWPLSV 837
QY 839 ESPIGRCGEPRNRCAPHEWNPDLDCSCRDGKCAHSHHFLSDIDIGCTDLHENLGVVV 898
Db 838 ESPIGRCGEPRNRCAPHEWNPDLDCSCRDGKCAHSHHFLSDIDIGCTDLHENLGVVV 897
QY 899 FKIKTQEGHARLGNLEFIEBKPLIGALSRVRAEKKWRDKREKLQLETGRVYTEAKEAV 958
Db 898 FKIKTQEGHARLGNLEFIEBKPLIGALSRVRAEKKWRDKREKLQLETGRVYTEAKEAV 957
QY 959 DALFVDSQYVNRLOADNTNIGMHAADKLVRIRIAYLSLSVPGVNAIEFEELEGRIT 1018
Db 958 DALFVDSQYVNRLOADNTNIGMHAADKLVRIRIAYLSLSVPGVNAIEFEELEGRIT 1017
QY 1019 ISLYDARNVVKNGDFNNGLAQWNVKGVHDVQSHHRSVLVPEWEAEVSQAVRVCGRGY 1078
Db 1018 ISLYDARNVVKNGDFNNGLAQWNVKGVHDVQSHHRSVLVPEWEAEVSQAVRVCGRGY 1077
QY 1079 ILRVYAYKEGEGCVTIHIEENTDLKFNCEEEBVEYPTDGTGNDYTAHQGTAVCN 1138
Db 1078 ILRVYAYKEGEGCVTIHIEENTDLKFNCEEEBVEYPTDGTGNDYTAHQGTAVCN 1137
QY 1139 RNAGYDAYEVDVTTASVNYKPTPEETTYTDVRDNHCEYDRGVVNPPLPAGVMTKELEY 1198
Db 1138 RNAGYDAYEVDVTTASVNYKPTPEETTYTDVRDNHCEYDRGVVNPPLPAGVMTKELEY 1197
QY 1199 FPETDKWVIEIGETEGKFIIVDSVELLIMEE 1228
Db 1198 FPETDKWVIEIGETEGKFIIVDSVELLIMEE 1227
```

```
RESULT 5
AAU02046
ID AAU02046 standard; protein; 1227 AA.
XX
AC AAU02046;
XX
DT 29-AUG-2001 (first entry)
XX
DE B. thuringiensis toxic crystal protein, CryET54.
XX
KW Delta endotoxin; Lepidopteran-active; crystal protein; insecticide;
KW transgenic plant; corn; wheat; soybean; oat; cotton; rice; sorghum;
KW sugarcane; tomato; tobacco; kapok; flax; potato; barley; turf grass;
KW pasture grass; berry; fruit; legume; vegetable; ornamental plant; shrub;
KW cotton leaf perforator; CryET54.
XX
OS Bacillus thuringiensis.
XX
PN WO200119859-A2.
XX
PD 22-MAR-2001.
XX
PF 13-SEP-2000; 2000WO-US025361.
XX
PR 15-SEP-1999; 99US-0153995P.
XX
PA (MONS ) MONSANTO CO.
XX
PI Baum JA, Chu C, Donovan WP, Gilmer AJ, Rupar MJ;
XX
DR WPI; 2001-281518/29.
XX
DR N-PSDB; AAS02489.
XX
PT Lepidopteran-active Bacillus thuringiensis delta-endotoxin polypeptides
PT and the polynucleotides that encode them, useful for increasing the
PT insect resistance of plant.
XX
PS Claim 17; Page 169-173; 173pp; English.
XX
CC The sequence represents B. thuringiensis Lepidopteran-active delta-
CC endotoxin, crystal protein CryET54. The Lepidopteran-active B.
CC thuringiensis delta-endotoxin polypeptides may be used as compositions
CC that are applied to plant crops to protect them from insect damage. The
CC polynucleotides may be used in the production of transgenic plants that
CC express the insecticidal polypeptides and consequently have improved
CC insect resistance compared to non-transformed plants. Monocotyledonous or
CC dicotyledonous plants may be protected in this way, for example corn,
CC wheat, soybean, oat, cotton, rice, rye, sorghum, sugarcane, tomato,
CC tobacco, kapok, flax, potato, barley, turf grass, pasture grass, berry,
CC fruit, legume, vegetable, ornamental plant, shrub, cactus and/or tree
CC cell. A wide range of insects (e.g. gypsy moth, looper, tobacco budworm,
CC cotton leaf perforator and spruce budworm) may be affected by application
CC of the insecticidal polypeptides (full details given in specification).
CC Note: The present sequence does not have a cryET number assigned.
CC explicitly in the specification, cryET54 (see table 5, page 56) is not
CC assigned to any Seq.ID number, the indexer has matched the spare sequence
CC to the spare cryET number, which may be incorrect
XX
SQ Sequence 1227 AA;
```

```
Query Match 91.3%; Score 5912.5; DB 4; Length 1227;
Best Local Similarity 91.6%; Pred. No. 0;
Matches 1127; Conservative 36; Mismatches 62; Indels 5; Gaps 3;

QY 1 LTSNRKNEIINALSIPAVSNHSTOMDLSPDARIEDSLCIAEGNNINPLVASTVQTGI 60
Db 1 LTSNRKNEIINALSIPAVSNHSAQNLSLSDLSLCLIAEGNNIDPFPVASTVQTGI 60
QY 61 NIAGRILGVLPVFPAGQIASFYSLVGLWPRGDOWEIFLEHVQOLINQIITENARNTA 120
Db 61 NIAGRILGVLPVFPAGQIASFYSLVGLWPRGDOWEIFLEHVQOLINQIITENARNTA 120
```

121 LARLOGLGDSFRAYQOQSLDLEWLNDRDARTSRVLYTQYIALELDFNAMPLFAIRNQVEP 180
 121 LARLOGLGNSFRAYQOQSLDLEWLNDRDARTSRVLYTQYIALELDFNAMPLFAIRNQVEP 180
 181 LLMVYAQAANLHLLLDASLFGSEFGLTQEIQRYYERQVEQTRDYSYCVWYNTGLN 240
 181 LLMVYAQAANLHLLLDASLFGSEFGLTQEIQRYYERQVEQTRDYSYCVWYNTGLN 240
 241 SLRGTAASWVRVYNQFRDLTLGVLDLVALFPSPYDTRTYINTSAQLTRVYTDGAIGATG 300
 241 NLRGTAESWVRVYNQFRDLTLGVLDLVALFPSPYDTRTYINTSAQLTRVYTDGAIGATG 300
 301 V-NMASNNWNNAPSAFSAIETAVIRSPHLLDFLEQLTIFSTSSRSWATRHMTYWRGHT 358
 301 APSGFASNNWNNAPSAFSAIETAVIRSPHLLDFLEQLTIFSTSSRSWATRHMTYWRGHT 358
 359 IQSRPIGGGLTSTHGNTSINPVRSLPFRSDVYWTESYAGVLLWGLIYEPHGVPTVR 418
 361 LESRTIRGSLTHTGNTSINPVRSLPFRSDVYWTESYAGVLLWGLIYEPHGVPTVR 418
 419 FNRPNPONTERRGTANYSQVPSFGLQKDSFELPPTERRPNYSYSHRLSHIGLISQ 478
 419 FNRPNPNSL-RGSLTYIGTGTGLFSEFELPPTERRPNYSYSHRLSNIRLISG 477
 479 SRVHPVYVWTHRSADRTNTISSDITQIPLVKSFNLSGTSVVGSGFTGGDIIRTNVN 538
 478 NTLRAPVYVWTHRSADRTNTISSDITQIPLVKSFNLSGTSVVGSGFTGGDIIRTNVN 537
 539 GSVLSMGLNFNTSLQRYRVRYAASQTMVLRVTVGGSTTFQGGPSTMSANESLTSQS 598
 538 GSVLSMGLNFNTSLQRYRVRYAASQTMVLRVTVGGSTTFQGGPSTMSANESLTSQS 597
 599 FRAEPFVGISASGSGTAGISINNAQRTFHPDKIEFIPITATFAEYDLERAQAVNA 658
 598 FRAEPFVGISASGSGTAGISINNAQRTFHPDKIEFIPITATFAEYDLERAQAVNA 657
 659 LFTNTPRRLKTDVTHIDQVSNLACLSDFCLEKRELLKVKYAKRLSDERNLLQD 718
 658 LFTNTPRRLKTDVTHIDQVSNLACLSDFCLEKRELLKVKYAKRLSDERNLLQD 717
 719 PNFTSINKQPDFSTNEQSFTSHEOSHGWSGSENITIOEGNDVFKENYVTLPGTFNE 778
 718 PNFTSINKQPDFSNNEQSFTSHEOSHGWSGSENITIOEGNDVFKENYVTLPGTFNE 777
 779 CYPTLYQKICESELKATYRQLRGYIEDSQDLEIYLIRYNAKHETLDVPGTESVWPLSV 838
 778 CYPTLYQKICESELKATYRQLRGYIEDSQDLEIYLIRYNAKHETLDVPGTESVWPLSV 837
 839 ESPIGRCGEPRNRCAPHEWNPDLDCSCRDGKCAHSHHPSLDIDGCTDLHENLGVWVV 898
 838 ESPIGRCGEPRNRCAPHEWNPDLDCSCRDGKCAHSHHPSLDIDGCTDLHENLGVWVV 897
 899 FKIKTOGHARLGNLEFIEEKPLLGALSVKAEKKWRDKREKLOLETKRVYTEAKEAV 958
 898 FKIKTOGHARLGNLEFIEEKPLLGALSVKAEKKWRDKREKLOLETKRVYTEAKEAV 957
 959 DALFVDSQYRNLQADTNIGMHAADLVHRIEAYLSVLPVNAEIPFEELEGRIITA 1018
 958 DALFVDSQYRNLQADTNIGMHAADLVHRIEAYLSVLPVNAEIPFEELEGRIITA 1017
 1019 ISLYDARNVVKNGDFNNGLACWNVKGVHDVQOQSHHRSVLVPIPEWAEVQAVRCPGRGY 1078
 1018 ISLYDARNVVKNGDFNNGLACWNVKGVHDVQOQSHHRSVLVPIPEWAEVQAVRCPGRGY 1077
 1079 ILAVTAYKEGCGCVTTHIEENNTDELKPKNCEEEVPTDGTNDYTAHOGTAVCN 1138
 1078 ILAVTAYKEGCGCVTTHIEENNTDELKPKNCEEEVPTDGTNDYTAHOGTAVCN 1137
 1139 RNAGYEDAYEVDITASVNYKPTVEEETITDVRDNHCEYDRGVNYPPLPAGYMTKELEY 1198
 1138 RNAGYEDAYEVDITASVNYKPTVEEETITDVRDNHCEYDRGVNYPPLPAGYMTKELEY 1197
 1199 FPETDKWIEIGETGKFIIVDSVELLMEE 1228

Db 1198 FPETDKWIEIGETGKFIIVDSVELLMEE 1227
 RESULT 6
 AAR50955
 ID AAR50955 standard; protein; 1228 AA.
 XX AAR50955;
 AC AAR50955;
 XX
 DT 16-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 18-OCT-1994 (first entry)
 XX
 DE Bacillus thuringiensis CryIB insecticidal protoxin.
 XX
 KW Insecticidal crystal protein; ICP; cryIB; Ostrinea nubilalis;
 KW European corn borer; Lepidoptera; Pyralidae; toxin.
 XX
 OS Bacillus thuringiensis; (strain entomocidus HD 110).
 XX
 PN EP589110-A1.
 XX
 PD 30-MAR-1994.
 XX
 PF 19-AUG-1992; 92EP-00402307.
 XX
 PR 19-AUG-1992; 92EP-00402307.
 XX
 PA (PLBZ) PLANT GENETIC SYSTEMS NV.
 XX
 PI Peferoen M, Jansens S, Denolf P;
 XX
 DR WPI: 1994-102862/13.
 N-PSDB; AAQ56804.
 XX
 PT Method to control or combat Ostrinia - utilises Bacillus thuringiensis
 cry IB gene/protein for crop prevention.
 XX
 PS Claim 1; Page 11-18; 38pp; English.
 XX
 CC The CryIB toxin gene (disclosed in EP-408403) has been found to be toxic
 to the European corn borer (Ostrinea nubilalis). The use of CryIB
 insecticidal crystal protein for protecting crops against O.nubilalis is
 claimed. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 16-OCT
 -2003 to standardise OS field)
 XX
 SQ Sequence 1228 AA;
 Query Match 88.6%; Score 5740; DB 2; Length 1228;
 Best Local Similarity 89.0%; Pred.No.0;
 Matches 1097; Conservative 36; Mismatches 90; Indels 10; Gaps 3;
 QY 1 LTRNKNENEINALSIPAVSNHSTQDLSPOARIEDSLCIAEGNNINPLVSASTVQTGI 60
 DB 1 MTSNRKNENEIN-----AVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGI 55
 QY 61 NTAGRTILGVLPFAAGIASFYSFLVGLWPRGRDQWEIFLHVEQLINCOITENARNTA 120
 DB 56 NTAGRTILGVLPFAAGIASFYSFLVGLWPRGRDQWEIFLHVEQLINCOITENARNTA 115
 QY 121 LARLOGLGDSFRAYQOQSLDLEWLNDRDARTSRVLYTQYIALELDFNAMPLFAIRNQVEP 180
 DB 116 LARLOGLGDSFRAYQOQSLDLEWLNDRDARTSRVLYTQYIALELDFNAMPLFAIRNQVEP 175
 QY 181 LLMVYAQAANLHLLLDASLFGSEFGLTQEIQRYYERQVEQTRDYSYCVWYNTGLN 240
 DB 176 LLMVYAQAANLHLLLDASLFGSEFGLTQEIQRYYERQVEQTRDYSYCVWYNTGLN 235
 QY 241 SLRGTAASWVRVYNQFRDLTLGVLDLVALFPSPYDTRTYINTSAQLTRVYTDGAIGATG 300
 DB 236 SLRGTAASWVRVYNQFRDLTLGVLDLVALFPSPYDTRTYINTSAQLTRVYTDGAIGATG 295

QY 301 VNMAWMWYNNAPSFSAIETAVIRSPHLLDFLEQLTIFSTSSRWSATRMWYRGHTIQ 360
 DB 296 VNMAWMWYNNAPSFSAIAAAIRSPHLLDFLEQLTIFSSASSRWSATRMWYRGHTIQ 355
 QY 361 SRPIGGGLNTSTGSGTNTSINPRLSPFSDVYWTESYAGVLLWGIYLEPIHGVPTVRFN 420
 DB 356 SRPIGGGLNTSTGAGTNTSINPRLSPASRDVYWTESYAGVLLWGIYLEPIHGVPTVRFN 415
 QY 421 FRNPQNTFERGTANYSPYSPGLQKXSETLPETTERPNYESYSHRLSHIGLISQSR 480
 DB 416 FTNPQNTSDRGTANYSPYSPGLQKXSETLPETTERPNYESYSHRLSHIGLISQSR 475
 QY 481 VHVYVSWTHRSADRTWTISDSITQPLVKSFNLSGTSVVSGPGTGGDIRTNVNGS 540
 DB 476 VNVFVSWTHRSADRTWTIGNRTIQIPMKVKAELPQGTIVVRGPGTGGDIRTNVNGS 535
 QY 541 VLSMLNFNTSLQRYVRVRYAASQTMVLRVTGGSTTPDQGPSTMSANESLTSQSR 600
 DB 536 FGIPTVTVNGPLTQRYIGFYASTVDFPVSRGGTVVNFRLRTNWSGDELKYNFV 595
 QY 601 FAEPFVGISASGSQ-TAGISISNNAQRTQTHFKIEFIPITATPEABYDLERAQEAVAL 659
 DB 596 RRAFTPTFTQIDIIIRTSIQGLSGNGEVYIDKIEIIPVTATPEABYDLERAQEAVAL 655
 QY 660 FTNTNPRRLKTDVTDYHIDQVSNLVACLDEFCLDEKRELLEKVKYAKRLSDERNLLQDP 719
 DB 656 FTNTNPRRLKTDVTDYHIDQVSNLVACLDEFCLDEKRELLEKVKYAKRLSDERNLLQDP 715
 QY 720 NFTSINKQPPFISTNEOSNFTSIHQSEHGWMGSENITIOBGNDVFKENVYVTLPGTNEC 779
 DB 716 NFTSINKQPPFISTNEOSNFTSIHQSEHGWMGSENITIOBGNDVFKENVYVTLPGTNEC 775
 QY 780 YPTLYQKIGSELKAYTRYQLRGYIEDSDLEIYLRYNAGHETLDVPGTESWPLSVE 839
 DB 776 YPTLYQKIGSELKAYTRYQLRGYIEDSDLEIYLRYNAGHETLDVPGTESWPLSVE 835
 QY 840 SPIGRCEPNRCAPHFENWPDLCSDRDEKCAHSHHFLSDIDIGCTDLHENLGVWVWF 899
 DB 836 SPIGRCEPNRCAPHFENWPDLCSDRDEKCAHSHHFLSDIDIGCTDLHENLGVWVWF 895
 QY 900 KIKTOEGHARLGNLEFTEKPLICEALSRVRAEKWRDKREKLOLETKRVYTEAKAVD 959
 DB 896 KIKTOEGHARLGNLEFTEKPLICEALSRVRAEKWRDKREKLOLETKRVYTEAKAVD 955
 QY 960 ALFVDSQYRLQADTNIGMHAADKLVHRIREAYLSLVSIPGVNABIFEELEGRITAI 1019
 DB 956 ALFVDSQYRLQADTNIGMHAADKLVHRIREAYLSLVSIPGVNABIFEELEGRITAI 1015
 QY 1020 SLYDARVWVXGNDPNNGLACWNVKGVHDVQSHRSVLVLPWEAEVVSQAVRVCPRGYI 1079
 DB 1016 SLYDARVWVXGNDPNNGLTCWNVKGVHDVQSHRSVLVLPWEAEVVSQAVRVCPRGYI 1075
 QY 1080 LRVYAYKEGYEGCVTTHIENNTDELKFKNCEEEVYPTDTGTCNDYTAHQGTA---V 1135
 DB 1076 LRVYAYKEGYEGCVTTHIENNTDELKFKNCEEEVYPTDTGTCNDYTAHQGTA---V 1135
 QY 1136 CNSRNAGYDAYEYDVTASVNYKPYEEETVDRDNDHCEYDRGYVNYPPLPAGYMTKE 1195
 DB 1136 CNSRNAGYDAYEYDVTASVNYKPYEEETVDRDNDHCEYDRGYVNYPPLPAGYMTKE 1195
 QY 1196 LEYPPETDKVWIEIGETGKPFIVDSVELLMEE 1228
 DB 1196 LEYPPETDKVWIEIGETGKPFIVDSVELLMEE 1228

RESULT 7

AAY31990

ID AAY31990 standard; protein; 1227 AA.

XX

AC AAY31990;

XX

XX 05-JAN-2000 (first entry)

DT

XX

Chimeric Cry1B insecticide HyFLIB.

XX Insecticide; HyFLIB; crystal protein; delta-endotoxin; toxin; cry1B;
 cry1A(b); maize; transgenic plant; European corn borer;
 Ostrinia nubilalis; entomocide; crop protection; biological control.

Bacillus thuringiensis.

Synthetic.

Key Location/Qualifiers
 Protein 1..845
 Protein /note= "cry1B"
 846..1227
 /note= "cry1A(b)"

W09950293-A1.

07-OCT-1999.

30-MAR-1999; 99WO-EP002175.

01-APR-1998; 98US-00053549.

(NOVS) NOVARTIS AG

(NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

Desai NM;

WPI; 1999-601323/51.

N-PSDB; AAZ20086.

Chimeric insecticidal protein comprising cry1B and cry1A(b) portions.

Claim 12; Page 43-47; 85pp; English.

This sequence represents a chimeric insecticidal protein, termed hyFLIB, that is composed of a cry1B core N-terminal toxin portion of 845 amino acids and a cry1A(b) C-terminal protoxin portion of 382 amino acids. The cry1A(b) and cry1A(b) portions of the synthetic gene (see AAZ20086) encoding HyFLIB were derived from Bacillus thuringiensis with codon usage altered to increase expression in plants, particularly maize. When the chimeric insecticidal protein gene is expressed in transgenic maize from both PEPC and pith promoters, insecticidal activity is observed against European corn borer (*Ostrinia nubilalis*). Recombinant microbial strains transformed with the hyFLIB gene can be used in endotomocidal formulations for the biological control of Lepidopteran pests

Sequence 1227 AA;

Query Match 83.9%; Score 5436.5; DB 2; Length 1227;

Best Local Similarity 84.3%; Pred. No. 0;

Matches 1040; Conservative 63; Mismatches 118; Indels 13; Gaps 5;

QY 1 LTSNRKNEEIIINALSTPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVOTGI 60

DB 1 MTSNRKNEEIIIN-----AVSNHSAQMDLLPDARIEDSLCIAEGNNIDPPFVSASTVOTGI 55

QY 61 NIAGRILGVLPVFPAGQIASFYSLVGLWPRGRDQWEI FLEHVEQLINQOITENARNTA 120

DB 56 NIAGRILGVLPVFPAGQIASFYSLVGLWPRGRDQWEI FLEHVEQLINQOITENARNTA 115

QY 121 LARLQGLGDSFRAYQQSLEDWLENRDDARTSRVLYTQYIALELDPLNAMPFAIRNQEVP 180

DB 116 LARLQGLGDSFRAYQQSLEDWLENRDDARTSRVLYTQYIALELDPLNAMPFAIRNQEVP 175

QY 181 LLMVYQAANLHLLLRDASLFGSEFGLTSQETQRYRYERQVETRDYSDYCVHYNTGLN 240

DB 176 LLMVYQAANLHLLLRDASLFGSEFGLTSQETQRYRYERQVETRDYSDYCVHYNTGLN 235

QY 241 SLRGTNAASWVRYNQFRDITLGLVDLVALPPSYDTRTYPINTSAQLTREVYTDAGTG 300

DB 236 SLRGTNAASWVRYNQFRDITLGLVDLVALPPSYDTRTYPINTSAQLTREVYTDAGTG 295

Db 479 GNTLRAPVSWTHRSADRTNIGPNRITQIPLVKALNLSGVTVVGGFTGCDILRRTN 538
 Qy 538 NGSVLSMGLNPNNTSLQRYRVRYAASQTMVLRTVVGSTTFDQGPSTMSANESLTSQ 597
 Db 539 TGTFGDIRLNLNPLSQRYRVRYASTTDLQFFTRINGTIVNIGNFSRTWNRGDNLEYR 598
 Qy 598 SFRFAEPVGVISAGSQTAGISISNAGROTFFDKIEFIPITATFAEYDLERAQAVN 657
 Db 599 SFRTAGSTFPNFLNAOSTTTLGAQSFNSQEVYIDRVEFPAEVTFAEYDLERAQAVN 658
 Qy 658 ALFTNTNPRLKTDTVTDYHIDQVSNLVACLSDEFCLDEKRELEKVKYAKRLSDERNLLQ 717
 Db 659 ALFTSTNPRLKTDTVTDYHIDQVSNLVACLSDEFCLDEKRELEKVKYAKRLSDERNLLQ 718
 Qy 718 DPNFTSINKQPDFSTNEQSNFTSIHQSHGHWGNSNITIOEGNDVFNKENVYTLPTFN 777
 Db 719 DPNFTSINKQPDFSTNEQSNFTSIHQSHGHWGNSNITIOEGNDVFNKENVYTLPTFN 778
 Qy 778 ECPYLYQKIGESLAKAYTRYQLRGYEDSQDLEIYLIRYNAKHETLDVPGTESVWPLS 837
 Db 779 ECPYLYQKIGESLAKAYTRYQLRGYEDSQDLEIYLIRYNAKHETLDVPGTESVWPLS 838
 Qy 838 VESPIGRGEPNRCAPHFENWPDLDSCRDGCKCAHSHHFSLDIDIGCTDLHENLGVW 897
 Db 839 VESPIGRGEPNRCAPHFENWPDLDSCRDGCKCAHSHHFSLDIDIGCTDLHENLGVW 898
 Qy 898 VFKIQTQEGHARLGNLFEBEKLPLGALSRVKAERKWRDKREKLOLETQRYVYTEAKEA 957
 Db 899 VFKIQTQEGHARLGNLFEBEKLPLGALSRVKAERKWRDKREKLOLETQRYVYTEAKEA 958
 Qy 958 VDALFVDSQYRNLQADNIGMHAADKLVHRIEAYLSLSVPGVNAEIFELEGGHII 1017
 Db 959 VDALFVDSQYRNLQADNIGMHAADKLVHRIEAYLSLSVPGVNAEIFELEGGHII 1018
 Qy 1018 AISLYDARNVVKNGDFNGLACWNVKGHDVQOSHRSVLVPEWEAEVSQAVRVCPCRG 1077
 Db 1019 AMSLYDARNVVKNGDFNGLTCNVKGHDVQOSHRSVLVPEWEAEVSQAVRVCPCRG 1078
 Qy 1078 YILRVTAAYKEGYGEGCVTHIEINNTDELKFKNCEEEVYPTDGTGNDYTAHQGTAVCN 1137
 Db 1079 YILRVTAAYKEGYGEGCVTHIEINNTDELKFKNCEEEVYPTDGTGNDYTAHQGTAVCN 1138
 Qy 1138 SRNAGVEDAYEDVTASVNTKPYEETVYDVRDNHCEYDRGVNYPPLPAGVMTKELE 1197
 Db 1139 SRNAGVEDAYEDVTASVNTKPYEETVYDVRDNHCEYDRGVNYPPLPAGVMTKELE 1198
 Qy 1198 YFPETDKVTEIGETEGKFIVDSVELLMEE 1228
 Db 1199 YFPETDKVTEIGETEGKFIVDSVELLMEE 1229

RESULT 9
 AAW35259
 ID AAW35259 standard; protein; 1229 AA.
 AC AAW35259;
 XX
 XX
 XX 17-FEB-1998 (first entry)
 DE Bacillus thuringiensis crystal toxin CryET5.
 XX
 XX EG7283; crystal toxin; CryET5; lepidopteran pest; Lymantria dispar;
 KW Ostrinia nubilalis; Pseudoplusia includens; Plutella xylostella;
 KW Spodoptera exigua; Spodoptera frugiperda; Trichoplusia ni.
 XX
 XX Bacillus thuringiensis.
 XX
 XX US5679343-A.
 XX
 XX 21-OCT-1997.
 XX
 XX 07-JUN-1995; 95US-00474038.
 XX

PR 29-JUL-1993; 93US-00100709.
 PR 30-DEC-1993; 93US-00176865.
 PA (MONS) MONSANTO CO.
 XX
 XX Jany CS, Gonzalez JM, Donovan WP, Tan Y;
 XX WPI; 1997-525682/48.
 DR N-PSDB; AAT95051.
 XX
 XX Lepidopteran toxic Bacillus thuringiensis crystal protein - useful to
 control Lepidopteran pests.
 PT
 XX
 XX Claim 2; Fig 2; 50pp; English.
 XX
 XX The present sequence is the Bacillus thuringiensis EG7283 crystal toxin
 CC CryET5, which, optionally in association with B. thuringiensis EG7283,
 CC can be used against lepidopteran pests. CryET5 is especially useful for
 CC controlling Lymantria dispar, Ostrinia nubilalis, Pseudoplusia includens,
 CC Plutella xylostella, Spodoptera exigua, Spodoptera frugiperda and
 CC Trichoplusia ni
 XX
 XX Sequence 1229 AA;
 Qy Match 80.8%; Score 5237.5; DB 2; Length 1229;
 Best Local Similarity 79.9%; Pred. No. 0;
 Matches 983; Conservative 94; Mismatches 149; Indels 5; Gaps 3;
 Qy 1 LTSNRKNEIINALSIPAVSNHSTOMDLPDARIEDSLCIAEINNINPLVSASTVOTGI 60
 Db 1 LTSNRKNEIINALSIPVSNSTQNNLSPDARIEDSLCIAEINNINPLVSASTVOTGI 60
 Qy 61 NIAGRILGVLPAGQIASFYSLVGLMWRGRDQWEIFLEHVEQLINQOITENARNTA 120
 Db 61 NIAGRILGVLPAGQIASFYSLVGLMWRGRDQWEIFLEHVEQLIRQOVTENTRNTA 120
 Qy 121 LARLOGISFRAYQOSLEDWLNRRDARTRSVLYTQYIALELDLFNAMPLFAIRNOEVP 180
 Db 121 IARLEGGRGYRQOALETWLNRDARSIRILERYVALELDITTAIFLRINEEVP 180
 Qy 181 LLMVYAAANLHLLLRDASLFGSEFGLTSQETQRYRVEROVEDYSDYCVVNTGLN 240
 Db 181 LLMVYAAANLHLLLRDASLFGSEMGMASSDYNQYQOIRYTEESNHCVMYNTGLN 240
 Qy 241 SLRGTNAASVRYNQFRRLDTLGLDLVALFPSTYDRTYPTINTSAQLTREYVYDAIGATG 300
 Db 241 NLRGTAESWLRYNQFRRLDTLGLDLVALFPSTYDRTYPTINTSAQLTREYVYDAIGATG 300
 Qy 301 V--NMASMWYNNNAPSPSAIETAVIRSHLLDFLEQLTIFSTSSRSWATRHMTYWRGHT 358
 Db 301 APSGFASITMFWNNNAPSPSAIAEAI FRPPHLLDFPEQLTIYSASSRSSTQHMMYVYVGR 360
 Qy 359 IQSRPIGGGLNTSTHGST--NTSINPVRLSPFSRDVYVWTSYAGVLLMGVILEPIHGVPTV 417
 Db 361 INFRPIGGTLNTSTQGLTNTSINPVLTQTSRDVYRTESNAGTNI--LFTTPVGVVPA 418
 Qy 418 RFNFRNPQNTFERGTANYSQYSPGLQKDSLTPPETTERPNYESYSHRLSHIGLIS 477
 Db 419 RFNFINQNIYERGATTYSQYQGVGLQDFDSELPETTERPNYESYSHRLSHIGLII 478
 Qy 478 QSRVHVTVSWTHRSADRTNITSSDSITQIPLVKSFNLSGTSVWVGPGTGGDIIRTNV 537
 Db 479 GNTLRAPVSWTHRSADRTNITGPNRITQIPLVKALNLSGVTVVGGFTGCDILRRTN 538
 Qy 538 NGSVLSMGLNPNNTSLQRYRVRYAASQTMVLRTVVGSTTFDQGPSTMSANESLTSQ 597
 Db 539 TGTFGDIRLNLNPLSQRYRVRYASTTDLQFFTRINGTIVNIGNFSRTWNRGDNLEYR 598
 Qy 598 SFRFAEPVGVISAGSQTAGISISNAGROTFFDKIEFIPITATFAEYDLERAQAVN 657
 Db 599 SFRTAGSTFPNFLNAOSTTTLGAQSFNSQEVYIDRVEFPAEVTFAEYDLERAQAVN 658
 Qy 658 ALFTNTNPRLKTDTVTDYHIDQVSNLVACLSDEFCLDEKRELEKVKYAKRLSDERNLLQ 717

Db 659 ALFTSTNPRRLKTDVTDYHIDQVSNMVACLSDPECLDEKRELFKVKYAKRLSDERNLQ 718
 Qy 718 DPNFTSINKOPDETSTNEQSNFTSIHQSHGWSNITIQENDVFKENYVTLPGTFN 777
 Db 719 DPNFTFISGQUSFASIDQSNFSPINELSHGWSANVTIQENDVFKENYVTLPGTFN 778
 Qy 778 ECPYLYLQKIGESLKYATRYQLRGVIEDSDLEIYLIRYNAKHETLDVPGTVESVWPLS 837
 Db 779 ECPYLYLQKIGESLKYATRYQLRGVIEDSDLEIYLIRYNAKHETLDVPGTVESVWPLS 838
 Qy 838 VESPIGRGCBPNRCAPHFENWPDLDSCRDGEKCAHSHHFSLDIDIGCTDLHENLGVV 897
 Db 839 VESPIGRGCBPNRCAPHFENWPDLDSCRDGERCAHSHHFTLIDVGCCTDLHENLGVV 898
 Qy 898 VFKIKTOEGHARLGNLFIEBKPLGALSRVKRAEKKWRDKREKLOLETKRVYTEAKEA 957
 Db 899 VFKIKTOEGHARLGNLFIEBKPLGALSRVKRAEKKWRDKREKLOLETKRVYTEAKEA 958
 Qy 958 VDALFVDSQYNRLQADTNIGMIHAADKLVHRIEAYLSLSVIPGVNAEIFEELGRIT 1017
 Db 959 VDALFVDSQYDQLQADTNIGMIHAADKLVHRIEAYLSLSVIPGVNAEIFEELGHIT 1018
 Qy 1018 AISLYDARNVVKGDFFNGLACMNVKGVVDVQSSHRSVLVPIPEWAEVSAQVRVCPGRG 1077
 Db 1019 AMSLYDARNVVKGDFFNGLTCNVKGVVDVQSSHRSDLVPIPEWAEVSAQVRVCPGRG 1078
 Qy 1078 YILRVTAKEGEGCVYTHIENNTDELKFKCEEEVYPTDTGTCTNDYTAHQGTAVCN 1137
 Db 1079 YILRVTAKEGEGCVYTHIENNTDELKFKCEEEVYPTDTGTCTNDYTAHQGTAAACN 1138
 Qy 1138 SRNAGYEDAYEDVTASVNYKPTVEEYTYDVRDNHCEYDRGVNYPPLPAGVMTKELE 1197
 Db 1139 SRNAGYEDAYEDVTASVNYKPTVEEYTYDVRDNHCEYDRGVNYPPLPAGVMTKELE 1198
 Qy 1198 YFPETDKVWIEIGETGKFIQVDSVELLMEE 1228
 Db 1199 YFPETDKVWIEIGETGKFIQVDSVELLMEE 1229

RESULT 10

AAW17699
 ID AAW17699 standard; protein; 1229 AA.
 XX
 AC AAW17699;
 XX
 DT 25-MAR-2003 (revised)
 DT 07-JUL-1997 (first entry)
 XX
 DE CryET5.
 XX
 KW CryET5; cryET4; Bacillus thuringiensis; insecticidal crystal protein;
 KW ICP; toxin; CryI protein; lepidopteran insect; insecticide.
 XX
 OS Bacillus thuringiensis.
 XX
 PN US5616319-A.
 XX
 PD 01-APR-1997.
 XX
 PF 30-DEC-1993; 93US-00176965.
 XX
 PR 29-JUL-1993; 93US-00100709.
 XX
 PA (MONS) MONSANTO CO.
 XX
 PI Gonzalez JM, Donovan WP, Tan Y, Jany CS;
 XX
 DR WPI; 1997-212077/19.
 DR N-PSDB; AAT68434.
 XX
 PT Bacillus thuringiensis cryET5 gene encoding insecticidal protein - useful
 PT for control of lepidopteran pests.

xx
 PS
 xx
 CC This sequence represents the cryET5 protein of Bacillus thuringiensis
 CC (B.t.) isolate EG847. B.t. produces inclusions during sporulation which
 CC include insecticidal crystal proteins (ICP). ICP toxins are active in
 CC insects only after ingestion. Once ingested, the toxic components disrupt
 CC the midgut cells, resulting in cessation of feeding, and eventually
 CC death. The CryI proteins produced by B.t. are active against lepidopteran
 CC insects. This protein, and the CryET4 protein (see AAW17700) belong to
 CC the CryI family of ICPs. The DNA encoding this sequence can be used to
 CC transform bacteria, which are useful as insecticides against a wide range
 CC of lepidopteran pests, and can be applied to crops, soil and seeds. This
 CC protein, or especially its toxic N terminal region, can be expressed in
 CC plants, to provide protection against lepidopteran pests. The gene
 CC encoding this sequence, or its fragments, can also be used to isolate
 CC other similar genes. (Updated on 25-MAR-2003 to correct PF field.)
 xx
 SQ Sequence 1229 AA;
 Query Match 80.8%; Score 5237.5; DB 2; Length 1229;
 Best Local Similarity 79.9%; Pred. NO. 0;
 Matches 983; Conservative 94; Mismatches 149; Indels 5; Gaps 3;
 Qy 1 LTSNRKNEEINALSIPAVSNHSTQWDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI 60
 Db 1 LTSNRKNEEINALSIPVSNPSTQWDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI 60
 Qy 61 NIAGRILGVLPVFPAGQIASFYSLVGLWPGRDQWEIFLEHVEQLINQOITENARNTA 120
 Db 61 NIAGRILGVLPVFPAGQIASFYSLVGLWPGRDQWEIFLEHVEQLINQOITENARNTA 120
 Qy 121 LARLQGLGSPRAYQSLDLEWLRDADTRSVLYTQYIALELDLNAMEPLFAIRNOEVP 180
 Db 121 IARLEGLGRISYQALETWLDNRDARSRIILERYVALELDITAITPLFIRNEEVP 180
 Qy 181 LLMVYAAANLHLLLRDASLFGSEFGLTSQETQYRYERQVEQTRDYSYCVWYNTGLN 240
 Db 181 LLMVYAAANLHLLLRDASLFGSEGMASDDVNYQYQYQYRYEYSNHCWQYNTGLN 240
 Qy 241 SLRGTAAASWVRYNQPRRLDTLGLDLVALFPSTYTRTPINTSAQLTREIVYDAIGATG 300
 Db 241 NLRGTTNAESWLRYNQPRRLDTLGLDLVALFPSTYTRTPINTSAQLTREIVYDTPGRTN 300
 Qy 301 V--NMASMMWNNNAPSFAIETAVIRSPHLLDFLEQLTIFSTSSRWSATRHMYWRGHT 358
 Db 301 APGCFASTWNNNAPSFAIETAAIFRPHLLDFPEQLTIYSSASSWSSTQHNNYVWVGR 360
 Qy 359 IQSRPIGGGLNTSTHGST-NTSINPVRSLFFSRDVTYVWTSYAGVLLWGLYLEPIHGVPV 417
 Db 361 LNFPRPIGGTLNTSTQGLTNNTSINPVTLOFTSRDVTYVWTSNAGTNI--LFTTTPVNGVPA 418
 Qy 418 RNFNRPQNTFPGTANYQPYSPGLQKDETELPPETTERPNYESHRLSHLGLIS 477
 Db 419 RNFNRPQNTFPGTANYQPYSPGLQKDETELPPETTERPNYESHRLSHLGLII 478
 Qy 478 QSRVHPVYVSWTHRSADRTNTSSDSITQIPLVKSPNLNSGTSVWSGPGFTGGDIIRTNV 537
 Db 479 GNTLRAPVYVSWTHRSADRTNTIGPNRITQIPLVKALNLSGTVVCGPGFTGGDIIRRTN 538
 Qy 538 NGSVLSMGLNFNNNTSLQRYRVRYAAQTMVLRVTVGGSTTDFDQGFPTSMANESLTSQ 597
 Db 539 TGTFGDIRLNINPLSORYVRVIRYASTTDLQFTFRINGTIVNIGNFSRTMRGNLEVR 598
 Qy 598 SRFAPFPVGISAGSGOTAGISINNAGROTDFDKIEPIPTATFEAEVDLERAQAVN 657
 Db 599 SFTAGFTFPFNLAQSTFTLGAOSFSNQEVYIDRFVFPVAEVTFEAEVDLERAQAVN 658
 Qy 658 ALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDPECLDEKRELFKVKYAKRLSDERNLQ 717
 Db 659 ALFTNTNPRRLKTDVTDYHIDQVSNMVACLSDPECLDEKRELFKVKYAKRLSDERNLQ 718
 Qy 718 DPNFTSINKOPDETSTNEQSNFTSIHQSHGWSNITIQENDVFKENYVTLPGTFN 777

Claim 1; Fig 2; 50pp; English.

```

Db 719 DPNTFISGQLSFASIDCGNQFNSINLSHGWSANVTIQGNDVFKENYVTLPGTFN 778
Qy 778 ECPYTYLYQKIGESLKYTRYQLRGYIEDSQBLEIYLIRYNAKHETLDVPGTESVWPLS 837
Db 779 ECPYTYLYQKIGESLKYTRYQLRGYIEDSQBLEIYLIRYNAKHETLDVPGTDSLWPLS 838
Qy 838 VESPIGRGCPNRCAPHFENPDLDCSCROGCKCAHSHHSFSLDIDIGCTDLHENLGVWV 897
Db 839 VESPIGRGCPNRCAPHFENPDLDCSCROGCKCAHSHHSFSLDIDIGCTDLHENLGVWV 898
Qy 898 VFPIKTOEGHARLGNLEFIEBEKPLIGALSRRVRAEKWRDKREKQLQLETKRVVYTRAKEA 957
Db 899 VFPIKTOEGHARLGNLEFIEBEKPLIGALSRRVRAEKWRDKREKQLQLETKRVYTRAKEA 958
Qy 958 VDALFVDSQYNRLQADTNIGMIHAADKLVHRIREAYLSLSESVIPGVNAEIFELEGRIT 1017
Db 959 VDALFVDSQYDQLQADTNIGMIHAADKLVHRIREAYLSLSESVIPGVNAEIFELEGHIT 1018
Qy 1018 AISLYDARNVVKNGDFNGLACWNKGVHDVQSHHRSVLVIVPEWAEVSAQVRVCPGRG 1077
Db 1019 AMSLYDARNVVKNGDFNGLTCWNKGVHDVQSHHRSVLVIVPEWAEVSAQVRVCPGRG 1078
Qy 1078 YILRVYAYKEGYGEGCVTTHIEINNTDELKFKNCEEEVYPTDTGTCNDYTAHOGTAVCN 1137
Db 1079 YILRVYAYKEGYGEGCVTTHIEINNTDELKFKNCEEEVYPTDTGTCNDYTAHOGTAACN 1138
Qy 1138 SRNAGVEDAYEVDTTASVNYKPYEETTYDVRDNHCEYDRGVNYPPLPAGVMTKELE 1197
Db 1139 SRNAGVEDAYEVDTTASVNYKPYEETTYDVRDNHCEYDRGVNYPPLPAGVMTKELE 1198
Qy 1198 YFPETDKVWIEIGETEGKFIVDSVELLLMEE 1228
Db 1199 YFPETDKVWIEIGETEGKFIVDSVELLLMEE 1229

```

RESULT 11

```

AAW87633
ID AAW87633 standard; protein; 1229 AA.
AC AAW87633;
XX 03-MAR-1999 (first entry)
DT CryET5 protein sequence.
DE CryET4; Bacillus thuringiensis strain EG5847; crystal toxin; CryET5;
KW Lepidoptera; Helicoverpa zea; resistant strain; Plutella xylostella;
KW Spodoptera exigua; S. frugiperda; S. frugiperda; Trichoplusia ni.
XX Bacillus thuringiensis.
XX US5854053-A.
XX 29-DEC-1998.
XX 06-JAN-1997; 97US-00779046.
XX 29-JUL-1993; 93US-00100709.
XX 30-DEC-1993; 93US-00176865.
XX 07-JUN-1995; 95US-00474038.
XX (ECOG-) ECOGEN INC.
XX Donovan WP, Gonzalez JM;
XX WPI; 1999-094915/08.
XX DR N-PSDB; AAW83927.
XX New strains EG5847 and EG10368 of Bacillus thuringiensis - producing
XX crystal toxins active against Lepidoptera, particularly Helicoverpa zea,
XX Plutella xylostella and spodoptera species.
XX

```

```

PS Example 2; Fig 2A-J; 49pp; English.
XX The present sequence represents a CryET5 protein. The protein is isolated
CC from a new strain of Bacillus thuringiensis (B.t.), strain EG5847 (NRRL B
CC -21110). EG5847 contains two new crystal toxin genes (cryET4 and cryET5)
CC that produce proteins active against Lepidoptera. CryET4 is more active
CC than CryIA(a) against Helicoverpa zea resistant-strains of Plutella
CC xylostella, Spodoptera exigua and S. frugiperda, while CryET5 is more
CC active than CryIB against S. frugiperda and Trichoplusia ni (and both are
CC active against additional insect species)
XX
SQ Sequence 1229 AA;
Query Match 80.8%; Score 5237.5; DB 2; Length 1229;
Best Local Similarity 79.9%; Pred. No. 0;
Matches 983; Conservative 94; Mismatches 149; Indels 5; Gaps 3;
Qy 1 LTSNRKNEININALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVOTGI 60
Db 1 LTSNRKNEININALSIPVSNSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVOTGI 60
Qy 61 NIAGRILGVLPFAQGIASFYSLVGLMWRGRDQWEIFLEHVEQLIRQVTTENTTA 120
Db 61 NIAGRILGVLPFAQGIASFYSLVGLMWRGRDQWEIFLEHVEQLIRQVTTENTTA 120
Qy 121 LARQLGLGDSFRAYQOSLEDWLENRDDARTSRVLYTQYIALELDFLNMPFLAIRNOEVP 180
Db 121 LARQLGLGDSFRAYQOSLEDWLENRDDARTSRVLYTQYIALELDFLNMPFLAIRNOEVP 180
Qy 181 LLMVYAAQANLHLLLDASLFGSEGLTSQETQRYVYEROVEOTRSDYCVCEWYNTGLN 240
Db 181 LLMVYAAQANLHLLLDASLFGSEGLTSQETQRYVYEROVEOTRSDYCVCEWYNTGLN 240
Qy 241 SLRGTTNAASVRYNQFRDITLGLVDLVALFPSTYDTRTYPIINTSAQLTREYVYDAIGATG 300
Db 241 SLRGTTNAASVRYNQFRDITLGLVDLVALFPSTYDTRTYPIINTSAQLTREYVYDAIGATG 300
Qy 301 V--NMASMWYNNAPSFSAIETAVIRSPHLLDFLEQLTIFSTSSRWASATRHMTYWRGT 358
Db 301 APSGFASTNMFNNAPSFSAIETAVIRSPHLLDFLEQLTIFSTSSRWASATRHMTYWRGT 360
Qy 359 IQSRPIGGGLTSTHGST-NTSINPVRLSPFSRDVYMTESYAGVLLMGVILEPHGVPTV 417
Db 361 LNFRPIGGTLTSTQGLTNTSINPVRLSPFSRDVYMTESYAGVLLMGVILEPHGVPTV 418
Qy 418 RNFNRPNQTFERTGANYSQYSPGLQKDSLETLPETTERPNYVESYSHRLSHIGLIS 477
Db 419 RNFNRPNQTFERTGANYSQYSPGLQKDSLETLPETTERPNYVESYSHRLSHIGLIS 478
Qy 478 QSRVHVYVSWTHRSADRTNTISSDSITQIPLVKSFNLSNGTSGVSGPGTGGDIIRTNV 537
Db 479 GNTLRAPVYVSWTHRSADRTNTIGPNRITQIPLVKSFNLSNGTSGVSGPGTGGDIIRTNV 538
Qy 538 NGSVLSMGLNFNTSLQRYRVRYAASQTMVLRVTVGSGSTTFDQGPSPMSANESLTSQ 597
Db 539 TGTFGDIRLNLINPLSQRYRVRYAASQTMVLRVTVGSGSTTFDQGPSPMSANESLTSQ 598
Qy 598 SFRFAEPFVPGISASGQTAGISISNNAGROTTFHDKIEFIPITATFEAYDLERAQAVN 657
Db 599 SFRFAEPFVPGISASGQTAGISISNNAGROTTFHDKIEFIPITATFEAYDLERAQAVN 658
Qy 658 ALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDFCLDEKRELKVKYAKRLSDERNLLQ 717
Db 659 ALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDFCLDEKRELKVKYAKRLSDERNLLQ 718
Qy 718 DPNFTSINKQPDFISTNEQSNFTSIHQSEHGWGSENITIQEGNDVFKENYVTLPGTFN 777
Db 719 DPNFTSINKQPDFISTNEQSNFTSIHQSEHGWGSENITIQEGNDVFKENYVTLPGTFN 778
Qy 778 ECPYTYLYQKIGESLKYTRYQLRGYIEDSQBLEIYLIRYNAKHETLDVPGTESVWPLS 837
Db 779 ECPYTYLYQKIGESLKYTRYQLRGYIEDSQBLEIYLIRYNAKHETLDVPGTDSLWPLS 838

```

QY 838 VESPIGRCEPNRCAPHEWNPDLDCSCDGECAHSHHFLSLDIDIGCTDLHENLGVWV 897
 DB 839 VESPIGRCEPNRCAPHEWNPDLDCSCDGERCAHSHHFLDIDVGTDLHENLGVWV 898
 QY 898 VFKIQTQGHARLGNLEFIEBKPLGEALSRYKRAEKKWRDKREKLOLETKRVYTEAKEA 957
 DB 899 VFKIQTQGHARLGNLEFIEBKPLGEALSRYKRAEKKWRDKREKLOLETKRVYTEAKEA 958
 QY 958 VDALFVDSQYVNLQADTNIGMIHADKLVRIRAYLSELVIFGVNAIEFEELEGRIT 1017
 DB 959 VDALFVDSQYVNLQADTNIGMIHADKLVRIRAYLSELVIFGVNAIEFEELEGRIT 1018
 QY 1018 AISLYDARNVKNQGFNNGLACMNVKGVHDVQOQSHRSVLVPEWEAEVSQAVRVCPRG 1077
 DB 1019 AMSLYDARNVKNQGFNNGLTCMNVKGVHDVQOQSHRSVLVPEWEAEVSQAVRVCPRG 1078
 QY 1078 YILRVYAYKEGCGCVTIHIEINNTDELKPKNCEEEVYPTDGTQNDYTAHQTAVCN 1137
 DB 1079 YILRVYAYKEGCGCVTIHIEINNTDELKPKNCEEEVYPTDGTQNDYTAHQTAACN 1138
 QY 1138 SRNAGYEDAYEVDVTASVNYKPTVEEETDVRDNDHCEYDRGVYVPPPLPAGVYTKELE 1197
 DB 1139 SRNAGYEDAYEVDVTASVNYKPTVEEETDVRDNDHCEYDRGVYVPPPLPAGVYTKELE 1198
 QY 1198 YFPETDKWIEIGTEGKFIIVDSVELLMEE 1228
 DB 1199 YFPETDKWIEIGTEGKFIIVDSVELLMEE 1229

RESULT 12

AA30923

ID AAY30923 standard; protein; 1229 AA.

XX AC AAY30923;

XX DT 18-OCT-1999 (first entry)

XX DE B. thuringiensis cryET5 partial protein.

XX KW Toxin; cryET4; cryET5; insecticidal; Lepidoptera; transformed plant;

XX OS Bacillus thuringiensis.

XX FH Key Location/Qualifiers

FT Protein 1. 1229

FT /note= "partial protein sequence. No ATG start codon

XX given"

XX US5942658-A.

XX 24-AUG-1999.

XX 24-JUN-1997; 97US-00881340.

XX 29-JUL-1993; 93US-00100709.

XX 30-DEC-1993; 93US-00176865.

XX 07-JUN-1995; 95US-00474038.

XX (MONS) MONSANTO CO.

XX Gonzalez JM, Jany CS, Tan Y, Donovan WP;

XX WPI; 1999-493544/41.

XX N-PSDB; AAZ09160.

XX Transformed plant comprising insecticidal crystal proteins.

XX Claim 3; Fig 2A-J; 50pp; English.

XX This invention describes novel transformed plants containing Bacillus

XX thuringiensis strain EG5847 insecticidal crystal protein genes cryET4 or

XX cryET5. cryET4 and cryET5 are novel toxin genes which produce

CC insecticidal proteins with activity against a broad spectrum of insects
 CC of the order Lepidoptera. This sequence represents the cryET5 protein
 CC described in the method of the invention

XX SQ Sequence 1229 AA;

Query Match 80.88; Score 5237.5; DB 2; Length 1229;
 Best Local Similarity 79.94; Pred. No. 0;
 Matches 983; Conservative 94; Mismatches 149; Indels 5; Gaps 3;

QY 1 LTSNRKNEIINALSIPAVSNHSTOMDLPDARIEDSLCIAEINNINPLVSASTVOTGI 60
 DB 1 LTSNRKNEIINALSIPVSNHSTOMDLPDARIEDSLCIAEINNINPLVSASTVOTGI 60
 QY 61 NIAGRILGVLPVGPAGIASFYSLVGLMWRGRDOMEIFLEHVEQLINOQITENARNTA 120
 DB 61 NIAGRILGVLPVGPAGIASFYSLVGLMWRGRDOMEIFLEHVEQLINOQITENARNTA 120
 QY 121 LARLQGLGDSFRAYQOSLEDWLENRDDARTSRVLYTQYIALELDLFLNAPLFAIRNOEVP 180
 DB 121 LARLQGLGDSFRAYQOSLEDWLENRDDARTSRVLYTQYIALELDLFLNAPLFAIRNOEVP 180
 QY 181 LLMVYAQAANLHLLLRDASLFGSEFGSLTSQEIQRYYRQVEQTRDYSYCVWEYNTGLN 240
 DB 181 LLMVYAQAANLHLLLRDASLFGSEFGSLTSQEIQRYYRQVEQTRDYSYCVWEYNTGLN 240
 QY 241 SLRGTAASWVRYNQFRDLTIGVLDLVALFPSYDTRTPINTSAQLTREYVYDAIGATG 300
 DB 241 SLRGTAASWVRYNQFRDLTIGVLDLVALFPSYDTRTPINTSAQLTREYVYDAIGATG 300
 QY 301 V--NMASMMWYNNNAPSFAIETAVIRPHLLDLEQLATFSTSSRSWSATRHMYTWRGHT 358
 DB 301 V--NMASMMWYNNNAPSFAIETAVIRPHLLDLEQLATFSTSSRSWSATRHMYTWRGHT 358
 QY 359 IQSRPIGGGLNTSTHGST-NTSINPVLRSFFSRDVTYTESYAGVLLMWLYLEPIHGVTYV 417
 DB 359 IQSRPIGGGLNTSTHGST-NTSINPVLRSFFSRDVTYTESYAGVLLMWLYLEPIHGVTYV 417
 QY 418 RNFNPQNTFERGTANYQPYESPGQLKDETELPPETTERPNYSESYSRSLSHGLIS 477
 DB 418 RNFNPQNTFERGTANYQPYESPGQLKDETELPPETTERPNYSESYSRSLSHGLIS 477
 QY 478 QSRVHVYVSWTHRSADRTNTISSDSITQIPVKSFNLSNGTSVVSQPGFTGGDIIRTNV 537
 DB 478 QSRVHVYVSWTHRSADRTNTISSDSITQIPVKSFNLSNGTSVVSQPGFTGGDIIRTNV 537
 QY 479 GNTLRAPVYVSWTHRSADRTNTIGPNRIQTQIPVKAALNLSHGVTVVGGPGFTGDIILRRN 538
 DB 479 GNTLRAPVYVSWTHRSADRTNTIGPNRIQTQIPVKAALNLSHGVTVVGGPGFTGDIILRRN 538
 QY 538 NGSVLSMGLNFNTSLQRYRVRYAASOTMVLRTVVGSTFTDQGPSTMGANESLTSQ 597
 DB 538 NGSVLSMGLNFNTSLQRYRVRYAASOTMVLRTVVGSTFTDQGPSTMGANESLTSQ 597
 QY 598 SPFRABFPVVGISAGSOTAGISINNAGQTFHDKIEFIPITATPEAEVDLERAEAVN 657
 DB 598 SPFRABFPVVGISAGSOTAGISINNAGQTFHDKIEFIPITATPEAEVDLERAEAVN 657
 QY 658 ALFTNTNPRRLKTDVTDYHIDQVSNLVACLSEDFCLDEKRELEKVKYAKRLSDERNLQ 717
 DB 658 ALFTNTNPRRLKTDVTDYHIDQVSNLVACLSEDFCLDEKRELEKVKYAKRLSDERNLQ 717
 QY 718 DPNFTSINKQDPFISTNEQSNFTSHEQSEHGWGSENITIQENDVFENYVTLPGTGN 777
 DB 718 DPNFTSINKQDPFISTNEQSNFTSHEQSEHGWGSENITIQENDVFENYVTLPGTGN 777
 QY 778 ECVPTYLYQKIGESSELKAYTRYQLRGYIEDSDQLEIYLIRYNAKHETLDVPGTESVWPLS 837
 DB 778 ECVPTYLYQKIGESSELKAYTRYQLRGYIEDSDQLEIYLIRYNAKHETLDVPGTESVWPLS 837
 QY 838 VESPIGRCEPNRCAPHEWNPDLDCSCDGBKCAHSHHFLSDIDIGCTDLHENLGVWV 897
 DB 838 VESPIGRCEPNRCAPHEWNPDLDCSCDGBKCAHSHHFLSDIDIGCTDLHENLGVWV 897
 QY 898 VFKIQTQGHARLGNLEFIEBKPLGEALSRYKRAEKKWRDKREKLOLETKRVYTEAKEA 957
 DB 898 VFKIQTQGHARLGNLEFIEBKPLGEALSRYKRAEKKWRDKREKLOLETKRVYTEAKEA 957

Qy 958 VDALFVDSQVNRLOADTNIGMHAADKLVHRIIRAYLSLSVPGVNAEIPFEELEGRIT 1017
 Db 959 VDALFVDSQVDQADTNIGMHAADKLVHRIIRAYLSLSVPGVNAEIPFEELEGRIT 1018
 Qy 1018 AISLYDARNVVKNGDFNGLACNVKGVHDVQOSSHRSVLVPEWEAEVSQAVRVCPRG 1077
 Db 1019 AMSLYDARNVVKNGDFNGLACNVKGVHDVQOSSHRSVLVPEWEAEVSQAVRVCPRG 1078
 Qy 1078 YILRVTAKEGEGGCVTIHEIENNTDELKFKNCEEEVPTDTGTCDNYTAHQGTAVCN 1137
 Db 1079 YILRVTAKEGEGGCVTIHEIENNTDELKFKNCEEEVPTDTGTCDNYTAHQGTAAACN 1138
 Qy 1138 SRNAGYEDAYEDVTASVNVKPYEETTYDVRDNCHEVDGRGVNTPPLPAGVMTKELE 1197
 Db 1139 SRNAGYEDAYEDVTASVNVKPYEETTYDVRDNCHEVDGRGVNTPPVAGVVTKELE 1198
 Qy 1198 YFPETDKVWIEIGTEGKFIVDSVELLMEE 1228
 Db 1199 YFPETDKVWIEIGTEGKFIVDSVELLMEE 1229

RESULT 13

ADK98479
 ID ADK98479 standard; protein; 1229 AA.

AC ADK98479;

DT 03-JUN-2004 (first entry)

DE B thuringiensis cry1Bb partial protein sequence SeqID2.

KW insecticidal protein; plant; pesticide; gene therapy;

KW lepidopteran insect pest; transgenic plant;

KW insect infestation resistance; monocot; dicot; cry1Bb.

OS Bacillus thuringiensis.

XX WO2004020636-A1.

XX 11-MAR-2004.

XX 26-AUG-2003; 2003WO-US026510.

XX 29-AUG-2002; 2002US-0407428P.

XX (MONS) MONSANTO TECHNOLOGY LLC.

XX (BOGD/) BOGDANOVA N N.

XX (ROMA/) ROMANO C P.

XX Bogdanova NN, Romano CP;

XX WPI: 2004-269221/25.

XX N-PSDB; ADK98478.

XX New polynucleotide sequence optimized for expression of an insecticidal protein in a plant, useful in the control of lepidoptera insect pests, and for producing transgenic plants with the ability to resist insect infestations.

XX Claim 7; SEQ ID NO 2; 138pp; English.

XX This invention relates to a novel polynucleotide sequence optimised for expression of an insecticidal protein in a plant. The invention may be useful for the production of pesticides whilst the disclosed sequences may be used for gene therapy. The polynucleotide sequence and methods are useful in the control of lepidopteran insect pests, and for producing transgenic plants with the ability to resist insect infestations. The invention provides polynucleotide sequences with enhanced, improved and optimised expression in monocot and dicot plant species. The present sequence is that of the (partial) B thuringiensis cry1Bb protein which is related to the invention.

XX

SQ Sequence 1229 AA;

Query Match 80.8%; Score 5237.5; DB 8; Length 1229;
 Best Local Similarity 79.9%; Pred. No. 0;
 Matches 983; Conservative 94; Mismatches 149; Indels 5; Gaps 3;

Qy 1 LTSNRKNEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVASTVGTGI 60
 Db 1 LTSNRKNEIINALSIPVSNSTQMDLSPDARIEDSLCIAEGNNINPLVASTVGTGI 60
 Qy 61 NIAGRILGVGVFAGFAGFAGFAGFAGFAGFAGFAGFAGFAGFAGFAGFAGFAGFAG 120
 Db 61 NIAGRILGVGVFAGFAGFAGFAGFAGFAGFAGFAGFAGFAGFAGFAGFAGFAGFAG 120
 Qy 121 LARLOGLGDSFRAYQOQSLDWNLRDNDARTSRVLYTOYIALELDLFNAMPLFAIRNOEVP 180
 Db 121 IARLEGLGRGYSYQQALETWLDNRNDARSIIERYVALELDITTAIPLFIRNEEVP 180
 Qy 181 LLMVYQAANLHLLLRDASLFGSEFGLTSQETQRYRQVVEQTRDYSDYCVHYNTGLN 240
 Db 181 LLMVYQAANLHLLLRDASLFGSEWMASSDVNQYQEQIRYTEESNHCVOYNTGLN 240
 Qy 241 SLRGTNAASWVRVYNQFRRLTLGVLDLVALFPSPYDTRTYPINTSAQLTRVYTDAGATG 300
 Db 241 NLRGTAESWLRVYNQFRRLTLGVLDLVALFPSPYDTRTYPINTSAQLTRVYTDPIGRTN 300
 Qy 301 V--NMASMMYNNNAPSFAIETAVIRSPHLLDPLEQLTIFSTSSRSWASRTHMYTWRGHT 358
 Db 301 APSGFASTNWFNNAPSFAIAEAIAPRPHLLDPLEQLTIFSTSSRSWASRTHMYTWVGH 360
 Qy 359 IQSRPIGGGLNTSTHGST-NTSINPVRLSFFSDVWVWTESYAGVLLGWILEPHIGVPTV 417
 Db 361 LNFRPIGGTLNTSTQGLTNNTSINPVTLQFTSDVWVWTESNAGTNI--LFTTPVNGVPWA 418
 Qy 418 RFNRPNQNTFERGTANYOPYESPGLOKXDSLELPPETTERPNYESYSHRLSHIGLIS 477
 Db 419 RFNFIPQNIYERGATYSQYQGVGLQFDSLELPPETTERPNYESYSHRLSHIGLII 478
 Qy 478 QSRVHVSVSWTHRSADRTNTISSDSITQIPLVKSFNLSNGTSVSGPFGTGGDIIRTNV 537
 Db 479 GNTLRAPVSVSWTHRSADRTNTIGPNRITQIPLVKAALNLSGVTVVGGPGTGGDILARTN 538
 Qy 538 NGSVLGMFLNFTSLQRYRVRYAASQTMVLRVTVGGSTTDFDQGPSTMSANESLTSQ 597
 Db 539 TGTFGDIRLNLNINPLSQRYRVRYASTTDLQFTFRINGTVAIGNFSRTMRGDNLEYR 598
 Qy 598 SFRFAEPFVGISASGSGTAGISISNNAGROTFFDKIEFIPITATPEAEYDLERAQAVN 657
 Db 599 SFRTAGFPTPFNFNAQSTFTLGAQSFNSQEVYIDRVFPAEVTFAEYDLERAQAVN 658
 Qy 658 ALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDBFCLDEKRELEKVKYAKRLSDERNLLQ 717
 Db 659 ALFTSINPRRLKTDVTDYHIDQVSNMVACLSDBFCLDEKRELEKVKYAKRLSDERNLLQ 718
 Qy 718 DPNFTSINKQDPFISNTEQSNFTSIHQSHGWGSENITIQGNDVFKENYVTLPGTFN 777
 Db 719 DPNFTFISQLSFASIDGOSNFTSINELSHGWGSGANVTIQGNDVFKENYVTLPGTFN 778
 Qy 778 ECPYTVLYOKIGESSELKAYTRYOLRGVIEDSQLEIYLIIRYNAKHETLDVPGTESVPLS 837
 Db 779 ECPYNYLYOKIGESSELKAYTRYOLRGVIEDSQLEIYLIIRYNAKHETLDVPGTDSLPLS 838
 Qy 838 VESPIGRCEPNRCAPHFENWPDLCSCRDGECACAHSHHFSLDIDIGCTDLHENLGWV 897
 Db 839 VESPIGRCEPNRCAPHFENWPDLCSCRDGECACAHSHHFTLIDVGCCTDLHENLGWV 898
 Qy 898 VFVKIQEGHARLGNLEFIEEKPLGELASRVKRAEKKMRDKREKLOLETFRVYTEAKEA 957
 Db 899 VFVKIQEGHARLGNLEFIEEKPLGELASRVKRAEKKMRDKREKLOLETFRVYTEAKEA 958
 Qy 958 VDALFVDSQVNRLOADTNIGMHAADKLVHRIIRAYLSLSVPGVNAEIPFEELEGRIT 1017
 Db 959 VDALFVDSQVDQADTNIGMHAADKLVHRIIRAYLSLSVPGVNAEIPFEELEGRIT 1018

QY 1018 AISLYDARNVVKNGDFNNGLACMNKGVHVDVQOQSHRSVLVPEWEAEVSQAVRVCPRG 1077
 DB 1019 AMSLYDARNVVKNGDFNNGLTCNWKGVHVDVQOQSHRSVLVPEWEAEVSQAVRVCPRG 1078
 QY 1078 YILRVATYKEGYGCGCVTHIEIENNTDELKPKNCEEEVYPTDGTCTNDYTAHQGTAVCN 1137
 DB 1079 YILRVATYKEGYGCGCVTHIEIENNTDELKPKNCEEEVYPTDGTCTNDYTAHQGTAAACN 1138
 QY 1138 SRNAGYEDAVEVDITASVNYKPTVEEETDVRDNEHCEVDRGVNYPPLPAGVMTKELE 1197
 DB 1139 SRNAGYEDAVEVDITASVNYKPTVEEETDVRDNEHCEVDRGVNYPVPAGVYTKELE 1198
 QY 1198 YFPETDKVWIEIGTEGKFIIVDSVELLIMEE 1228
 DB 1199 YFPETDVWIEIGTEGKFIIVDSVELLIMEE 1229

RESULT 14
 ADK98484
 ID ADK98484 standard; protein; 1230 AA.
 XX AC ADK98484;
 XX 03-JUN-2004 (first entry)
 XX DE B thuringiensis cry1Bb-related expression cassette protein SeqID7.
 XX KW insecticidal protein; plant; pesticide; gene therapy;
 XX KW lepidopteran insect pest; transgenic plant;
 XX KW insect infestation resistance; monocot; dicot; cry1Bb.
 XX OS Bacillus thuringiensis.
 XX OS Synthetic.
 XX PN W02004020636-A1.
 XX PD 11-MAR-2004.
 XX PF 26-AUG-2003; 2003WO-US026510.
 XX PR 29-AUG-2002; 2002US-0407428P.
 XX PA (MONS) MONGANTO TECHNOLOGY LLC.
 XX PA (BOGD/) BOGDANOVA N N.
 XX PA (ROMA/) ROMANO C P.
 XX PI Bogdanova NN, Romano CP;
 XX DR WPI; 2004-269221/25.
 XX DR N-PSDB; ADK98482.

XX New polynucleotide sequence optimized for expression of an insecticidal
 PT protein in a plant, useful in the control of Lepidoptera insect pests,
 PT and for producing transgenic plants with the ability to resist insect
 PT infestations.
 XX Claim 7; SEQ ID NO 7; 138pp; English.

XX This invention relates to a novel polynucleotide sequence optimised for
 CC expression of an insecticidal protein in a plant. The invention may be
 CC useful for the production of pesticides whilst the disclosed sequences
 CC may be used for gene therapy. The polynucleotide sequence and methods are
 CC useful in the control of lepidopteran insect pests, and for producing
 CC transgenic plants with the ability to resist insect infestations. The
 CC invention provides polynucleotide sequences with enhanced, improved and
 CC optimised expression in monocot and dicot plant species. The present
 CC sequence is that of a B thuringiensis cry1Bb expression cassette protein
 CC which is related to the invention.

XX SQ Sequence 1230 AA;
 Query Match 80.8%; Score 5233.5; DB 8; Length 1230;

Best Local Similarity 79.8%; Pred. No. 0;
 Matches 982; Conservative 94; Mismatches 149; Indels 5; Gaps 3;
 QY 2 TSNRKNENEIINALSPAVSNHSTOMDLPDARIEDSLCTAEGNNINPLVASTVQTGIN 61
 DB 3 TSNRKNENEIINALSPAVSNHSTOMDLPDARIEDSLCTAEGNNINPLVASTVQTGIN 62
 QY 62 IACRIILGVLPAGQIASFYSPLVGLMPPRGDOWEIFLEHVEQLINQOITENARTAL 121
 DB 63 IACRIILGVLPAGQIASFYSPLVGLMPPRGDOWEIFLEHVEQLINQOITENARTAL 122
 QY 122 ARLOGLGDSFRAYQOQSLDNLNRRDARTSRVLYTQYIALLELDFLNMPLFAIRNOEVL 181
 DB 123 ARLEGLGRGYSQQALETLWLDNRNDARSRIILERYVALELDITTAIPLFRIRNEEVL 182
 QY 182 LMVYQAANLHLLLRDASLFGSEFGLTQOEIORYYERQVEQTRDYSDYCEVWYNTGLNS 241
 DB 183 LMVYQAANLHLLLRDASLFGSEMGWASDVNQYQEQIRYTEYSNHCVOYNTGLNN 242
 QY 242 LRGITNAASWVRVNOFRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREYVTDIGATGV 301
 DB 243 LRGITNAESWLRVNOFRDLTLGVLDLVALFPSYDTRTYPINTSAQLTREYVTDIGATGV 302
 QY 302 --NMASMNWYNNNAPSFAIETAVIRSPHLLDFLEQLTIFSTSSRWSATRHMTYWRGHTI 359
 DB 303 PSGFATNFWNNAPSFALEAAIPRPHLLDFPEQLTIYSASSRWSSTQHMYNVVGHRL 362
 QY 360 QSRPIGGLTSTHGST-NYSINPVLSFRSDRVYWTESYAGVLLWGIYLEPHGVPTVR 418
 DB 363 NFRPIGGLTSTHGST-NYSINPVLSFRSDRVYWTESYAGVLLWGIYLEPHGVPTVR 420
 QY 419 FNFPRNPQTFERTANYSQPYSPGLQKDSLETLPETTERPNVYESYSHRSLHIGLISQ 478
 DB 421 FNFPRNPQTFERTANYSQPYSPGLQKDSLETLPETTERPNVYESYSHRSLHIGLISQ 480
 QY 479 SRVHPVYSWTHRSADRTNTISSDSITQIPLVKSFNLSGTSVVGPGTGGDIIRTNVN 538
 DB 481 NTLRAPVYSWTHRSADRTNTIGPNRITQIPLVKSFNLSGTSVVGPGTGGDIIRTNVN 540
 QY 539 GSVLSMGLNPNNTSLORVYRVRYAASOTMVLRTVVGSTTDDGPPSPMSANESITQS 598
 DB 541 GTFGDIRLNVPLSQRVRYRYASTTDLQPFTRINGTIVNIGNFSRTNMGDNLEYS 600
 QY 599 FRFAEPFVGISASGSGTAGISISNNAGROTFFDKIEFIPITATFEAEYDLERAQAVNA 658
 DB 601 FRFAEPFVGISASGSGTAGISISNNAGROTFFDKIEFIPITATFEAEYDLERAQAVNA 660
 QY 659 LFTNTNPRRLKTDVTDYHIDQVSNLVACLSDFCLDEKRELEKVKYAKRLSDERNLLQD 718
 DB 661 LFTNTNPRRLKTDVTDYHIDQVSNLVACLSDFCLDEKRELEKVKYAKRLSDERNLLQD 720
 QY 719 PNFTSINKOPDFTSTNEQSNFTSIHQSEHGWGSENITIQEGNDVFKENYVTLPGTFNE 778
 DB 721 PNFTSINKOPDFTSTNEQSNFTSIHQSEHGWGSENITIQEGNDVFKENYVTLPGTFNE 780
 QY 779 CYPTVLYQKIGSELKAYTRYQYRGYIEDSQDLEIYLRINAKHETLDVPGTESVWPLSV 838
 DB 781 CYPTVLYQKIGSELKAYTRYQYRGYIEDSQDLEIYLRINAKHETLDVPGTESVWPLSV 840
 QY 839 ESPIGRCGPNRCAPHFENWPDLCSCRDGECAGHSHHFSLDIDIGCTDLHENLGVWV 898
 DB 841 ESPIGRCGPNRCAPHFENWPDLCSCRDGECAGHSHHFSLDIDIGCTDLHENLGVWV 900
 QY 899 FKIKQEGHARLGNLEFIEEKPLGHALSRVRAEKKWRDREKLEQLKRVVTEAKEAV 958
 DB 901 FKIKQEGHARLGNLEFIEEKPLGHALSRVRAEKKWRDREKLEQLKRVVTEAKEAV 960
 QY 959 DALFVDSQYNRLQADNTNIGMHAADKLVRHIREAYLSLSVPGVNAEIFELEGRIITA 1018
 DB 961 DALFVDSQYNRLQADNTNIGMHAADKLVRHIREAYLSLSVPGVNAEIFELEGRIITA 1020
 QY 1019 ISLYDARNVVKNGDFNNGLACMNKGVHVDVQOQSHRSVLVPEWEAEVSQAVRVCPRG 1078

Db 1021 MSLYDARNVVKNGDFNGLTCMNKGVHDVQQSHHRSDLVIPWEAEVSQAVRVCGRGY 1080
 Qy 1079 ILRVATYKEGYGEGCVTHIEIENNTDELKFKNCBEEVYPDTGTCNDYTAHQGTAVCNS 1138
 Db 1081 ILRVATYKEGYGEGCVTHIEIENNTDELKFKNCBEEVYPDTGTCNDYTAHQGTAAACNS 1140
 Qy 1139 RNAGYEDAYEDVTASVNYKPTVEEYTYDVRDNHCEYDGVYNYPLPAGVMTKELEY 1198
 Db 1141 RNAGYEDAYEDVTASVNYKPTVEEYTYDVRDNHCEYDGVYNYPPVAGVYTKLEY 1200
 Qy 1199 FPETDKWIEIGETEGKFIIVDSVELLMEE 1228
 Db 1201 FPETDTWIEIGETEGKFIIVDSVELLMEE 1230

RESULT 15
 ADK98489
 ID ADK98489 standard; protein; 1230 AA.
 XX
 AC ADK98489;
 DT 03-JUN-2004 (first entry)
 XX B thuringiensis cry1Bb-related expression cassette protein SeqID12.
 DE insecticidal protein; plant; pesticide; gene therapy;
 XX lepidopteran insect pest; transgenic plant;
 KW insect infestation resistance; monocot; dicot; cry1Bb.
 KW
 XX Bacillus thuringiensis.
 OS Synthetic.
 OS
 XX WO2004020636-A1.
 PN
 XX 11-MAR-2004.
 PD
 XX 26-AUG-2003; 2003WO-US026510.
 PF
 XX 29-AUG-2002; 2002US-0407428P.
 PR
 XX (MONS) MONSANTO TECHNOLOGY LLC.
 PA (BOGD/) BOGDANOVA N N.
 PA (ROMA/) ROMANO C P.
 XX
 PI Bogdanova NN, Romano CP;
 XX WPI; 2004-269221/25.
 DR N-PSDB; ADK98488.
 DR
 XX New polynucleotide sequence optimized for expression of an insecticidal
 PT protein in a plant, useful in the control of lepidoptera insect pests,
 PT and for producing transgenic plants with the ability to resist insect
 PT infestations.
 PT
 XX Claim 7; SEQ ID NO 12; 138pp; English.
 PS
 XX This invention relates to a novel polynucleotide sequence optimised for
 CC expression of an insecticidal protein in a plant. The invention may be
 CC useful for the production of pesticides whilst the disclosed sequences
 CC may be used for gene therapy. The polynucleotide sequence and methods are
 CC useful in the control of lepidopteran insect pests, and for producing
 CC transgenic plants with the ability to resist insect infestations. The
 CC invention provides polynucleotide sequences with enhanced, improved and
 CC optimised expression in monocot and dicot plant species. The present
 CC sequence is that of a B thuringiensis cry1Bb expression cassette protein
 CC which is related to the invention.
 XX
 SQ Sequence 1230 AA;

Query Match 80.8%; Score 5233.5; DB 8; Length 1230;
 Best Local Similarity 79.8%; Pred. No. 0;
 Matches 982; Conservative 94; Mismatches 149; Indels 5; Gaps 3;

Qy 2 TSNRKNENELINALSTPAVSNHSTOMDLSDPARIEDSLCIAEGNNINPLYSASTVQTGIN 61
 Db 3 TSNRKNENELINALSTPTVSNPSTOMNLSPARIEDSLCVAEANNIDPFVSASTVQTGIN 62
 Qy 62 IAGRIILGVLPAGQIASFYSLVGBELWPRGRDOMEIFLEHVHQLINQQTENARNTAL 121
 Db 63 IAGRIILGVLPAGQLASFYSLVGBELWPSGRDPWEIFLEHVHQLIRQVVTENTRTAI 122
 Qy 122 ARIOGLGDSFRAYQOQSLEDWLENRDDARTSVLYTYQVIALELDFLNAMPFAIRNQEVPL 181
 Db 123 ARLEGLGRGYSYQOALETWLDNRNDARSISILERYVALELDTTATPLPRIREEVPL 182
 Qy 182 LMVYAQAANLHLLLRDASLPGSEFGLTSQEIQRYYEROVEQTRDYSDYCWEVNTGLNS 241
 Db 183 LMVYAQAANLHLLLRDASLPGSEWGMASDVNQYQOEIRYTEESYHNCHVQWNTGLNN 242
 Qy 242 LRGTNAAASVRYNQFRDLTLGVLDLVALFPSTRTYPTINTSAQLTREVVTDAIGATGV 301
 Db 243 LRGTNAAESWLRYNQFRDLTLGVLDLVALFPSTRTYPTINTSAQLTREIYTDPIGRNA 302
 Qy 302 --NMASMNWYNNNAPSASIAETAVIRSPHLLDFLEQLTIFSTSRWSATRHMTYWRGHTI 359
 Db 303 PSGFASNTWNNNAPSASIAEAAIFRPPHLLDPPEQLTIYSASSRWSSTQHMTYVWGHRL 362
 Qy 360 QSRPIGGLNTSTHGST-NTSINPRLSPFSRDVYWTSTESYAGVLLWGIYLEPIHGVTVR 418
 Db 363 NFRPIGGLNTSTQGLTNTSINPVTQLQTSRDVYRTESNAGTNI--LFTTPVNGVPWAR 420
 Qy 419 FNFRNPQNTFERGTANYSPQSPGLQKDSSETLPETTERPNYESYSHRLSHIGLISQ 478
 Db 421 FNFINPQNIYERGATYSPQYQGVQLFDSSETLPETTERPNYESYSHRLSHIGLII 480
 Qy 479 SRVHPVYVSWTHRSADRTNTISSDITQIPLVKSFNLSGTSVVGPGFTGGDIIRTNVN 538
 Db 481 NTLRAPVYVSWTHRSADRTNTIGPNRITQIPLVKALNLHSGVTVVGGPGFTGGDLIRRTNT 540
 Qy 539 GSVLSMGLNFNTSLQRYRVRYAASQTMVLRVTVGSGSTTFDQGFSTTSANESLSQS 598
 Db 541 GTFGDILRLNINPLSQRYRVIRYASTDQLQFTRINGTNTVINGFSTWNRGNLBYRS 600
 Qy 599 FRFAEPVVGISASGSGOTAGISISNAGROTFFHPKIEFIPITATFEAEYDLERAQEAUNA 658
 Db 601 FRTAGFSTPNFLNAQSTFTLGAQSPSNQEVYIDRVFVFAEVTFEAEYDLERAQKAVNA 660
 Qy 659 LFTNTPRRLKTDVTDVHIDQVSNLVACLSDDEFCLDEKRELLEKVKYAKLSDBRNLLQD 718
 Db 661 LFTSTNPRRLKTDVTDVHIDQVSNMVACLSDDEFCLDEKRELFEKVKYAKLSDBRNLLQD 720
 Qy 719 PNFTSINKQDPFISTNEQSNFTSIHEQSEHGWSGSENITIQEGNDVFKENYVTLPGTFNE 778
 Db 721 PNFTFISGQLSFASIDQGSNFPISINELSEHGWSGANVTIQEGNDVFKENYVTLPGTFNE 780
 Qy 779 CYPYLYQKIGESSELKAYTRYQLRGYIEDSQDLEIYLIRYNAXHETLDVPGTESWPLSV 838
 Db 781 CYPNLYQKIGESSELKAYTRYQLRGYIEDSQDLEIYLIRYNAXHETLDVPGTDSLWPLSV 840
 Qy 839 ESPIGRCGEPRNCAPHEWNPDLDCSCRDGKCAHSHHFLSDIDICTDLHENLGVWV 898
 Db 841 ESPIGRCGEPRNCAPHEWNPDLDCSCRDGKCAHSHHFTLDDVCGCTDLHENLGVWV 900
 Qy 899 FKIKTQEGHARLGNLFIEBKPLLGEALSRVKAERKWKREKJQLETXRVYTEAKEAV 958
 Db 901 FKIKTQEGHARLGNLFIEBKPLLGEALSRVKAERKWKREKJQLETXRVYTEAKEAV 960
 Qy 959 DALFVDSQYNRLQADTNIGMIHAADKLVRIRRAYLSLSVIPCVAEIPFEELEGRITTA 1018
 Db 961 DALFVDSQYDQLQADTNIGMIHAADKLVRIRRAYLSSELVPIPGVNAIPEELEGHIIITA 1020
 Qy 1019 ISLYDARNVVKNGDFNGLTCMNKGVHDVQQSHHRSVLVIPWEAEVSQAVRVCGRGY 1078
 Db 1021 MSLYDARNVVKNGDFNGLTCMNKGVHDVQQSHHRSDLVIPWEAEVSQAVRVCGRGY 1080
 Qy 1079 ILRVATYKEGYGEGCVTHIEIENNTDELKFKNCBEEVYPDTGTCNDYTAHQGTAVCNS 1138

Db	1081	ILRVTAKEGYGEGCVTHIEIENNTDELKFNCEEEVYPTDGTGTCNDYTAHQGTAAONS	1140
Qy	1139	RNAGYEDAYEVDTTASVNYKPTYEEETTDVRRDNHCEYDRGYVNYPLPAGYVTKLEY	1198
Db	1141	RNAGYEDAYEVDTTASVNYKPTYEEETTDVRRDNHCEYDRGYVNYPPVAGYVTKLEY	1200
Qy	1199	FPETDKWIEIGETEGKFIVDSVELLLMEE	1228
Db	1201	FPETDTWIEIGETEGKFIVDSVELLLMEE	1230

Search completed: April 21, 2005, 04:12:16
Job time : 133 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 21, 2005, 00:32:39 ; Search time 134 Seconds
(without alignments)
4692.785 Million cell updates/sec

Title: US-10-614-524-2
Perfect score: 6479
Sequence: 1 LTSNRKNEIINALSIPAV.....IGTEGKFIVDSVELLMEE 1228

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5924.5	91.4	1227	1 C1BE_BACTU	O95805 bacillus th
2	5745	88.7	1228	1 C1BA_BACTK	P05517 bacillus th
3	5740	88.6	1228	2 O93T75	O93T75 bacillus th
4	5737	88.5	1228	2 O93NM5	O93NM5 bacillus th
5	5235.5	80.8	1229	1 C1BB_BACTU	O45739 bacillus th
6	5214.5	80.5	1231	1 C1BD_BACTZ	O93az25 bacillus th
7	5188.5	80.1	1231	2 Q8KN72	Q8KN72 bacillus th
8	4959.5	76.5	1233	1 C1BC_BACTM	O45774 bacillus th
9	4284.5	66.1	1215	1 C1KA_BACTM	O45715 bacillus th
10	3977.5	61.4	1174	1 C1EB_BACTA	O03745 bacillus th
11	3901.5	60.2	849	2 O6PVW8	O6PVW8 bacillus th
12	3791	58.5	1176	1 C1CB_BACTG	P56953 bacillus th
13	3579	55.2	1170	1 C1JB_BACTU	O45716 bacillus th
14	3556	54.9	1167	1 C1JA_BACTU	O45738 bacillus th
15	3495.5	54.0	1189	1 C1CA_BACTE	P05518 bacillus th
16	3495.5	54.0	1189	2 O6YNB8	O6YNB8 bacillus th
17	3485.5	53.8	1189	2 Q9LSV8	Q9LSV8 bacillus th
18	3455.5	53.3	1180	2 Q9S5V8	Q9S5V8 bacillus th
19	3433.5	53.0	1165	1 C1DA_BACTA	PI9415 bacillus th
20	3433	53.0	1166	1 C1GA_BACTU	O45746 bacillus th
21	3428	52.9	1179	1 C1AD_BACTA	Q03744 bacillus th
22	3426.5	52.9	1181	1 C1AE_BACTL	O03748 bacillus th
23	3426	52.9	1171	2 O06894	O06894 bacillus th
24	3426	52.9	1171	2 Q71TW6	Q71TW6 bacillus th
25	3425	52.9	1177	2 Q6EIX3	Q6EIX3 bacillus th
26	3421	52.8	1171	1 C1EA_BACTX	O57458 bacillus th
27	3413.5	52.7	1174	2 Q45749	O45749 bacillus th
28	3413.5	52.7	1176	2 Q7WZT9	O7WZT9 bacillus th
29	3412.5	52.7	1174	1 C1FA_BACTA	O03746 bacillus th
30	3411	52.6	1160	1 C1DB_BACTU	O45747 bacillus th
31	3405.5	52.6	1176	2 Q45736	O45736 bacillus th

32	3401	52.5	1160	2 Q93TF9	Q93TF9 bacillus th
33	3400.5	52.5	1176	1 C1AA_BACTK	P02965 bacillus th
34	3399.5	52.5	1178	1 C1AC_BACTK	P05068 bacillus th
35	3399.5	52.5	1178	2 O6XLN7	O6XLN7 bacillus th
36	3398	52.4	1177	2 O8GLY5	O8GLY5 bacillus th
37	3393.5	52.4	1178	2 O45768	O45768 bacillus th
38	3392	52.4	1177	2 Q03743	Q03743 bacillus th
39	3391.5	52.3	1178	2 Q9R826	Q9R826 bacillus th
40	3388.5	52.3	1176	2 Q9RC30	Q9RC30 bacillus th
41	3387	52.3	1177	2 Q45735	O45735 bacillus th
42	3384	52.2	1169	1 C1FB_BACTM	O66377 bacillus th
43	3364	51.9	1177	2 Q71JF1	Q71JF1 bacillus th
44	3356	51.8	1169	2 O8GHE8	O8GHE8 bacillus th
45	3355	51.8	1169	1 C1GB_BACTZ	Q93az26 bacillus th

ALIGNMENTS

RESULT 1
C1BE_BACTU ID C1BE_BACTU STANDARD; PRT; 1227 AA.
AC O85805;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Pesticidal crystal protein cryIbe (Insecticidal delta-endotoxin
DE CryIB(e)) (Crystalline entomocidal protoxin) (139 kDa crystal protein).
GN Name=cryIbe; Synonyms=158C2B, cryIB(e);
OS Bacillus thuringiensis.
OC Plasmid pMYC2383.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=NRRL B-18872 / PS158C2;
RA Payne J.M., Cummings D.A., Cannon R.J.C., Narva K.E., Stelman S.;
RT "Bacillus thuringiensis genes encoding lepidopteran-active toxins.";
RL Patent number US5723758, 03-MAR-1998.
CC -!- FUNCTION: Promotes colloidotomic lysis by binding to the midgut
epithelial cells of many lepidopteran larvae.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
sporulation and is accumulated both as an inclusion and as part of
the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF077326; AAC32850.1; -
CC HSPSP; P07130; 1DLC.
CC InterPro; IPR001178; Endotoxin.
CC InterPro; IPR005638; endotoxin_N.
CC InterPro; IPR005639; endotoxin_N.
CC InterPro; IPR008979; Gal_bind_like.
CC Pfam; PF03944; Endotoxin_C; 1.
CC Pfam; PF00555; Endotoxin_M; 1.
CC Pfam; PF03945; Endotoxin_N; 1.
CC Plasmid; Sporulation; Toxin.
SQ SEQUENCE 1227 AA; 139084 MW; CBA847BEA0B34CD3 CRC64;

Query Match 91.4%; Score 5924.5; DB 1; Length 1227;
Best Local Similarity 91.7%; Pred. No. 0;
Matches 1128; Conservative 37; Mismatches 60; Indels 5; Gaps 3;

QY 1 LTSNRKNEIINALSIPAVNSHTQMDLSFPDARIEDSLCIAEGNINPLVSTVQTGI 60

1 MTSNRKNEIINALSIPAVSNHSAQNLSTDAIEDSLCIAEGNNIDPFVASTVGTGI 60
61 NIAGRIILGVLPAGQIAGFYSLVGLWPRGRDQWEI FLEHVEQLINQOITENARNTA 120
61 NIAGRIILGVLPAGQIAGFYSLVGLWPRGRDQWEI FLEHVEQLINQOITENARNTA 120
121 LARLOGLGDSFRAYQOISLEWLNDRDARTSRVLYTOYIALELDPLNAPLFAIRNOEVP 180
121 LARLOGLGDSFRAYQOISLEWLNDRDARTSRVLYTOYIALELDPLNAPLFAIRNOEVP 180
181 LMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSDYCVWEYNTGLN 240
181 LMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSDYCVWEYNTGLN 240
241 SLRGNTAASVRVYNQFRDITLGLVDLVALPSPYDTRTYINTSAQLTRVYTDATGATG 300
241 NLRGNTAASVRVYNQFRDITLGLVDLVALPSPYDTRTYINTSAQLTRVYTDATGATG 300
301 V--NMASMNWYNNAPSFSALETAIVRSPLHLPLEOLTIFPSTSSRSWATRHMTYNRGHT 358
301 APSGFATNNFNNAPSFSALETAIVRSPLHLPLEOLTIFPSTSSRSWATRHMTYNRGHT 358
359 IQSRPIGGGLNTSTHGTNTSINPVLRSFFSRDYWTESYAGVLLWGIYLEPIHGVPVTR 418
361 LESRTIRGSLSTHGTNTSINPVLRSFFSRDYWTESYAGVLLWGIYLEPIHGVPVTR 418
419 FNRFPNONTERTGANYSQYSPGLQKQSETLPPETTERNYRSYSHRLSHIGLISQ 478
419 FNRFPNONTERTGANYSQYSPGLQKQSETLPPETTERNYRSYSHRLSHIGLISQ 478
419 FNRFPNONTERTGANYSQYSPGLQKQSETLPPETTERNYRSYSHRLSHIGLISQ 478
479 SRVHPVYVSWTHRSADRTNISDSITQIPLVKSFNLSGTSVVGPGFTGGDIIRTNVN 538
479 SRVHPVYVSWTHRSADRTNISDSITQIPLVKSFNLSGTSVVGPGFTGGDIIRTNVN 538
478 NTRAPVYVSWTHRSADRTNISDSITQIPLVKSFNLSGTSVVGPGFTGGDIIRTNVN 537
539 GSVLSMGLNFNNTSLQRYRVRYAASQTMVLRVTVGGSTTFQGGPSTMSANESLTSQS 598
538 GSVLSMGLNFNNTSLQRYRVRYAASQTMVLRVTVGGSTTFQGGPSTMSANESLTSQS 597
599 FRAEFPVGLSASQTAGISINAGROTHFDFKIEFIPITATFAEYDLERAQAVNA 658
598 FRAEFPVGLSASQTAGISINAGROTHFDFKIEFIPITATFAEYDLERAQAVNA 657
659 LFTNTNPRRLKTVDTHIDQVSNLVAFLSDFCLDEKRELLKVKYAKLSDERNLLQD 718
658 LFTNTNPRRLKTVDTHIDQVSNLVAFLSDFCLDEKRELLKVKYAKLSDERNLLQD 717
719 PNFTSINKQPDFISTNQSNFTSIHQSEHGWSGSENIITQEGNDVFKENYVTLPGTFNE 778
718 PNFTSINKQPDFISTNQSNFTSIHQSEHGWSGSENIITQEGNDVFKENYVTLPGTFNE 777
779 CYPTLYQKIGSELKAYTRYQIRGYIEDSDQLEIYLIRYNAKHETLDVPGTSEVWPLSV 838
778 CYPTLYQKIGSELKAYTRYQIRGYIEDSDQLEIYLIRYNAKHETLDVPGTSEVWPLSV 837
839 ESPIGRCGEPRNRCAPFENWPDLDCCRCDEKCAHSHHPSFLDIDGCTDLHENLGVWV 898
838 ESPIGRCGEPRNRCAPFENWPDLDCCRCDEKCAHSHHPSFLDIDGCTDLHENLGVWV 897
899 FKIKTOEGHARLGNLFEIEBKPLLGALSRVKAERKWRDKREKLOLETKRVYTEAKEAV 958
898 FKIKTOEGHARLGNLFEIEBKPLLGALSRVKAERKWRDKREKLOLETKRVYTEAKEAV 957
959 DALFVDSQYNRLOADNTNIGMHAADKLVRIRAYLSLSVIPGVNAEIPFEELEGRITTA 1018
958 DALFVDSQYNRLOADNTNIGMHAADKLVRIRAYLSLSVIPGVNAEIPFEELEGRITTA 1017
1019 ISLYDARNVVKNGDFNNGLACWNVKGVVDVQOSSHRSVLVPIPEWAEVSAQVRCFGRGY 1078
1018 ISLYDARNVVKNGDFNNGLACWNVKGVVDVQOSSHRSVLVPIPEWAEVSAQVRCFGRGY 1077
1079 ILRVATYKEGYGCGCVTIHEIENNTDELKPKNCEEEVYPTDGTGNDYTAHQGTAVCNS 1138

1078 ILRVATYKEGYGCGCVTIHEIENNTDELKPKNCEEEVYPTDGTGNDYTAHQGTAVCNS 1137
1139 RNAGYEDAEVDVTTASVNYKPTVEETTYDVRDNDHCEYDRGVVNPPLPAGVMTKELEY 1198
1138 RNAGYEDAEVDVTTASVNYKPTVEETTYDVRDNDHCEYDRGVVNPPLPAGVMTKELEY 1197
1199 FPETDKVWIEIGETEGKFIIVDSVELLMEER 1228
1198 FPETDKVWIEIGETEGKFIIVDSVELLMEER 1227
RESULT 2
C1BA_BACTK STANDARD; PRT: 1228 AA.
ID C1BA_BACTK STANDARD; PRT: 1228 AA.
AC P05517; Q45731;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIIa (Insecticidal delta-endotoxin
DE CryIIa(a)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
DE Name-cryIIa; Synonyms-cryA4, cryIIa(a);
GN Bacillus thuringiensis (subsp. kurstaki), and
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OC NCBI_TaxID=29339, 1436;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.kurstaki; STRAIN=HD-2;
RA MEDLINE=88203216; PubMed=3362680;
RX Brizzard B.L., Whiteley H.R.;
RT "Nucleotide sequence of an additional crystal protein gene cloned from
RT Bacillus thuringiensis subsp. thuringiensis";
RL Nucleic Acids Res. 16:2723-2723 (1988).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.entomocidus; STRAIN=HD-110;
RA Soetaert P.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Promotes colloidomotic lysis by binding to the midgut
CC epithelial cells of insects.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X06711; CAA29898.1; -
CC EMBL; X95704; CAA55003.1; -
CC FIR; S00873; S00873.
CC HSP; P07130; IDLC.
CC InterPro; IPR001178; Endotoxin.
CC InterPro; IPR005638; endotoxin_C.
CC InterPro; IPR005639; endotoxin_N.
CC InterPro; IPR008979; Gal_bind_like.
CC Pfam; PF03944; Endotoxin_C; 1.
CC Pfam; PF00555; Endotoxin_M; 1.
CC Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
FT VARIANT 150 150 Y -> H (in strain HD-110).
SQ SEQUENCE 1228 AA; 139647 MW; C8E3A19B5D98575 CRC64;
Query Match 88.7%; Score 5745; DB 1; Length 1228;
Best Local Similarity 89.1%; Pred. No. 0;
Matches 1098; Conservative 35; Mismatches 90; Indels 10; Gaps 3;

```
Qy 1 LTSNRKNEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MTSNRKNEIIN-----AVSNHSAQMDLLPDARIEDSLCIAEGNNIDPPFVSASTVQTGI 55

Qy 61 NIAGRIILGVLPAGPAGIASFYSFLVGLWPRGRDQWEIPLFHEVQELINQOITENARNTA 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
56 NIAGRIILGVLPAGPAGIASFYSFLVGLWPRGRDQWEIPLFHEVQELINQOITENARNTA 115

Qy 121 LARLOGLGDSFRAYQQSLEDWLENRDARTSRVLYTQYIALFELDFLAMPFLAIRNQSEVP 180
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
116 LARLOGLGDSFRAYQQSLEDWLENRDARTSRVLYTQYIALFELDFLAMPFLAIRNQSEVP 175

Qy 181 LLMYAQAANLHLLLDASLFGSEFGLTSGEIQRYRQYERQVQTRDYSYCVWYNTGLN 240
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
176 LLMYAQAANLHLLLDASLFGSEFGLTSGEIQRYRQYERQVQTRDYSYCVWYNTGLN 235

Qy 241 SLRGTAASWVRVYNQFRDRLTLGLVDLVALFPSPDYTRTPINTSAQLTREYITDAIGATG 300
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
236 SLRGTAASWVRVYNQFRDRLTLGLVDLVALFPSPDYTRTPINTSAQLTREYITDAIGATG 295

Qy 301 VNMAWMYNNNAPSFAIETAVIRSPHLLDFLEQLTIFSTSSRSWSTRHMYWRGHTIQ 360
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
296 VNMAWMYNNNAPSFAIETAVIRSPHLLDFLEQLTIFSTSSRSWSTRHMYWRGHTIQ 355

Qy 361 SRPIGGGLNTSTHGSTNTSINPVLRSFSDRVYWTESYAGVLLMGIIYLEPIHGVTFRFN 420
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
356 SRPIGGGLNTSTHGATNTSINPVLRFASRDVYWTESYAGVLLMGIIYLEPIHGVTFRFN 415

Qy 421 FRNPONTFECTANYSPYSPGLOKDSFELPPTETTERPNYESYSHRLSHGILISQSR 480
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
416 FTNPQNTSDRGATANYSPYSPGLOKDSFELPPTETTERPNYESYSHRLSHGILISQSR 475

Qy 481 VHVPEVSWTHRSADRTNTISDSITQPLVKFSFNLNGSTSVSGPFGTGGDIIRTNVNGS 540
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
476 VNVPEVSWTHRSADRTNTIGNRITQIPMKVASELPQGTTVVRGPGTGGDILARTWGG 535

Qy 541 VLSMGLNFNTSLQRYRVRYAASQTVLRVTVGGSTTFDQGPSPMSANESITSQSR 600
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
536 FGPIRVTVNGPLTKRYRIGFRYASTVDFDFVSRGGTAVNFRFLRTWNSGDELKYGNFV 595

Qy 601 FAEFPVGISASGSO-TAGISISNAGQTFHFDKIEIPITATFEASYDLERAQEVNAL 659
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
596 RRAEFTTFTTQIQDIIRTSIQGLSGNGEVYIDKIEIIPVATFEASYDLERAQEVNAL 655

Qy 660 FTNTPNRLKTDVTDYHIDQVSNLVACLSDFCLEKRELLKVKYAKRLSDERNLLQDP 719
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
656 FTNTPNRLKTDVTDYHIDQVSNLVACLSDFCLEKRELLKVKYAKRLSDERNLLQDP 715

Qy 720 NFTSINKOPDFISTNEQSNFTSIHQSEHGWWGSENITIQEGNDVFKENYVTLPGTFNEC 779
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
716 NFTSINKOPDFISTNEQSNFTSIHQSEHGWWGSENITIQEGNDVFKENYVTLPGTFNEC 775

Qy 780 YPTLYOKIGESLKAATRYQLRGYIEDSQDLEIYLIRYNKAKHETLDPGTSWVPLSVE 839
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
776 YPTLYOKIGESLKAATRYQLRGYIEDSQDLEIYLIRYNKAKHETLDPGTSWVPLSVE 835

Qy 840 SPIGRCEPNRCAPHFENWPDLCSCRDGEKCAHSHHFLSDIDIGCTDLHENLGVWVVF 899
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
836 SPIGRCEPNRCAPHFENWPDLCSCRDGEKCAHSHHFLSDIDIGCTDLHENLGVWVVF 895

Qy 900 KIKTOEGHARLGNLEFIEEKPPLGALSVRKRAEKKWRDKREKLQLETKRYYTEAKBAVD 959
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
896 KIKTOEGHARLGNLEFIEEKPPLGALSVRKRAEKKWRDKREKLQLETKRYYTEAKBAVD 955

Qy 960 ALFVDSQVNRLOADNTGIMHAADKLVRHIREAYLSELVTPGVNAEIPFEELEGRITAI 1019
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
956 ALFVDSQVNRLOADNTGIMHAADKLVRHIREAYLSELVTPGVNAEIPFEELEGRITAI 1015

Qy 1020 SLYDARNVKNKGFNGLACNNVKGHVDVQOSHRSVLVPEWEAEYSQAVRVCPCGGYI 1079
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1016 SLYDARNVKNKGFNGLTCNNVKGHVDVQOSHRSVLVPEWEAEYSQAVRVCPCGGYI 1075
```

```
Qy 1080 LRTAYKEGEGCVTHIEIENNTDELKFNKCEEEVYPTDTGTCNDYTAHQSTA-----V 1135
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1076 LRTAYKEGEGCVTHIEIENNTDELKFNKCEEEVYPTDTGTCNDYTAHQSTA-----V 1135

Qy 1136 CNSNAGYDAYEVDTTASVNYKPTYEEETVTVRRDNHCEYDRGVNYPPLPAGYMTKE 1195
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1136 CNSNAGYDAYEVDTTASVNYKPTYEEETVTVRRDNHCEYDRGVNYPPLPAGYMTKE 1195

Qy 1196 LEYPPETDKWIEIGETEGKPIVDSEVLLMEE 1228
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1196 LEYPPETDKWIEIGETEGKPIVDSEVLLMEE 1228

RESULT 3
Q93T75 PRELIMINARY; PRT; 1228 AA.
ID Q93T75 AC Q93T75, 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Delta-endotoxin CryIa2.
GN Name=CryIa2;
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD-9;
RA Mat Isa M.N., Abdullah M.A.F., Mahadi N.M.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF363025; AAK51084.1; -.
DR HSP; P07130; IDLC.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin_C.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 1228 AA; 139620 MW; 3DA2A4DBF59C95C3 CRC64;

Query Match 88.6%; Score 5740; DB 2; Length 1228;
Best Local Similarity 89.0%; Pred. No. 0;
Matches 1097; Conservative 36; Mismatches 90; Indels 10; Gaps 3;

Qy 1 LTSNRKNEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MTSNRKNEIIN-----AVSNHSAQMDLLPDARIEDSLCIAEGNNIDPPFVSASTVQTGI 55

Qy 61 NIAGRIILGVLPAGPAGIASFYSFLVGLWPRGRDQWEIPLFHEVQELINQOITENARNTA 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
56 NIAGRIILGVLPAGPAGIASFYSFLVGLWPRGRDQWEIPLFHEVQELINQOITENARNTA 115

Qy 121 LARLOGLGDSFRAYQQSLEDWLENRDARTSRVLYTQYIALFELDFLAMPFLAIRNQSEVP 180
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
116 LARLOGLGDSFRAYQQSLEDWLENRDARTSRVLYTQYIALFELDFLAMPFLAIRNQSEVP 175

Qy 181 LLMYAQAANLHLLLDASLFGSEFGLTSGEIQRYRQYERQVQTRDYSYCVWYNTGLN 240
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
176 LLMYAQAANLHLLLDASLFGSEFGLTSGEIQRYRQYERQVQTRDYSYCVWYNTGLN 235

Qy 241 SLRGTAASWVRVYNQFRDRLTLGLVDLVALFPSPDYTRTPINTSAQLTREYITDAIGATG 300
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
236 SLRGTAASWVRVYNQFRDRLTLGLVDLVALFPSPDYTRTPINTSAQLTREYITDAIGATG 295

Qy 301 VNMAWMYNNNAPSFAIETAVIRSPHLLDFLEQLTIFSTSSRSWSTRHMYWRGHTIQ 360
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
296 VNMAWMYNNNAPSFAIETAVIRSPHLLDFLEQLTIFSTSSRSWSTRHMYWRGHTIQ 355

Qy 361 SRPIGGGLNTSTHGSTNTSINPVLRSFSDRVYWTESYAGVLLMGIIYLEPIHGVTFRFN 420
```

```
Db 356 SRPIGGGLNTSTHGATNTSINPVTLRFASRDVYRTESYAGVLLAGVILPEIHGVPVTFN 415
Qy 421 FRNPQNTFERGTANYSQPYESPGQLKDSFETLPPETTERPNYESYSHRSLSHIGLIQSQR 480
Db 416 FTNPQNTSDRTANYSQPYESPGQLKDSFETLPPETTERPNYESYSHRSLSHIGLIQSQR 475
Qy 481 VHVVPYSWTHRSADRTNTISSDITQIPLVKSNLNGTSVVGPGFTGGDIIRTNVNGS 540
Db 476 VNVVPYSWTHRSADRTNTIGPNRITQIPWKASLPGQTTVVRGPGFTGGDILRTWGG 535
Qy 541 VLSMGLNFNTSLQRYRVRYAASQTMVLRTVVGSGFTPDQGPSTMSANESLTSQSF 600
Db 536 FGPIRVTVNGPLTQRYRIGFRYASTVDFDFVSRGGTTVNNFRFLRTMWSGDELYKGNFV 595
Qy 601 FAEPFVGISASGSO-TAGISISNNAQRTFHFDKIEPIPTATFEAYDYLERAEAVNAL 659
Db 596 RRAFTTPTFTQIQTIDIRTSIQGLSGNGEVYDKIEIIPVTATFEAYDYLERAEAVNAL 655
Qy 660 FTNTNPRRLKTDVTDYHIDQVSNLVACLDFCLDEKRELLEKVKYAKRLSDERNLLQDP 719
Db 656 FTNTNPRRLKTDVTDYHIDQVSNLVACLDFCLDEKRELLEKVKYAKRLSDERNLLQDP 715
Qy 720 NFTSINKQPDFISTNEQSNFTSIHQSEHGWMGSENITIQEGNDVFKENYVTLPGTFNEC 779
Db 716 NFTSINKQPDFISTNEQSNFTSIHQSEHGWMGSENITIQEGNDVFKENYVTLPGTFNEC 775
Qy 780 YPTLYYKIGESLKAATRYQLRGYIEDSQLEIYLRYNAKHETLDPGTSWPLSV 839
Db 776 YPTLYYKIGESLKAATRYQLRGYIEDSQLEIYLRYNAKHETLDPGTSWPLSV 835
Qy 840 SPIGRCEPNRCAPHFENPDLDCSCRDGEKCAHSHHFLSDIDIGCTDLHENLGVWV 899
Db 836 SPIGRCEPNRCAPHFENPDLDCSCRDGEKCAHSHHFLSDIDIGCTDLHENLGVWV 895
Qy 900 KIKTOEGHARLGNLEFIEEKPPLGEALSRVKRAEKKWRDKREKLQLETKRYVTEAKEAVD 959
Db 896 KIKTOEGHARLGNLEFIEEKPPLGEALSRVKRAEKKWRDKREKLQLETKRYVTEAKEAVD 955
Qy 960 ALFVDSQYNRLQADTNGIMHAADKLVRHIREAYLSLSELVPGVNAEIPFELEGRITAI 1019
Db 956 ALFVDSQYNRLQADTNGIMHAADKLVRHIREAYLSLSELVPGVNAEIPFELEGRITAI 1015
Qy 1020 SLVDARNVKNGDPNNGLACVNVKGVHDVQOSSHRSVLVPEAEVSAQVRCVPCRGYI 1079
Db 1016 SLVDARNVKNGDPNNGLACVNVKGVHDVQOSSHRSVLVPEAEVSAQVRCVPCRGYI 1075
Qy 1080 LRVYAYKEGYGEGCVTTHIEENNTDELKFNKCBEEVYPTDGTGNDYTAHQGTA---V 1135
Db 1076 LRVYAYKEGYGEGCVTTHIEENNTDELKFNKCBEEVYPTDGTGNDYTAHQGTA 1135
Qy 1136 CNSRNAGYDAYEVDTTASVNYKPTYEEYTVDRDNDHCEYDRGYNYNPLPAGYMTKE 1195
Db 1136 CNSRNAGYDAYEVDTTASVNYKPTYEEYTVDRDNDHCEYDRGYNYNPPVAGYVTK 1195
Qy 1196 LEYFPETDKVWIEIGETEGKFIVDSVLELLMEE 1228
Db 1196 LEYFPETDKVWIEIGETEGKFIVDSVLELLMEE 1228
```

RESULT 4

```
Q93NM5 ID Q93NM5 PRELIMINARY; PRT; 1228 AA.
AC Q93NM5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cyl1Ba.
GN Name=Cyl1Ba;
OS Bacillus thuringiensis;
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
```

```
RP SEQUENCE FROM N.A.
RA Zhang J., Song F., Huang D.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF368257; AAK63251.1; -
DR HSP; P07130; IDLC.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 1228 AA; 139665 MW; E86D9842341FB439 CRC64;
```

Query Match 88.5%; Score 5737; DB 2; Length 1228;
Best Local Similarity 89.0%; Pred. No. 0;
Matches 1097; Conservative 35; Mismatches 91; Indels 10; Gaps 3;

```
Qy 1 LTSNRKNENIINALSIPAVSNHSTOMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI 60
Db 1 MTSNRKNENIIN-----AVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGI 55
Qy 61 NIAGRILGVLPFAGQIASFYSLGELWPRGDQWEIFLEHVEQLINQOITENARNTA 120
Db 56 NIAGRILGVLPFAGQIASFYSLGELWPRGDQWEIFLEHVEQLINQOITENARNTA 115
Qy 121 LARLOGLGDSFRAYQOSLEDWLENRDDARTSRVLYTYQYIALELDFLNAMPLFAIRNQEVP 180
Db 116 LARLOGLGDSFRAYQOSLEDWLENRDDARTSRVLYTYQYIALELDFLNAMPLFAIRNQEVP 175
Qy 181 LMVYAQAANLHLLLRDASLFGSEFGLTSQETQRYRQVQVETRDYSDYCVEWYNTGLN 240
Db 176 LMVYAQAANLHLLLRDASLFGSEFGLTSQETQRYRQVQVETRDYSDYCVEWYNTGLN 235
Qy 241 SLRGTTNAASWVRYNQFRRLTLGLVLDLVALFPSYDTRTPINTSAQLTREVVYTDALGATG 300
Db 236 SLRGTTNAASWVRYNQFRRLTLGLVLDLVALFPSYDTRTPINTSAQLTREVVYTDALGATG 295
Qy 301 VNMAWMNWNNAAPSFSAIETAVIRSPHLLDFLEQLTIFSTSSRWASATRMHTYWRGHTIQ 360
Db 296 VNMAWMNWNNAAPSFSAIETAVIRSPHLLDFLEQLTIFSTSSRWASATRMHTYWRGHTIQ 355
Qy 361 SRPIGGGLNTSTHGATNTSINPVTLRFASRDVYRTESYAGVLLAGVILPEIHGVPVTFN 420
Db 356 SRPIGGGLNTSTHGATNTSINPVTLRFASRDVYRTESYAGVLLAGVILPEIHGVPVTFN 415
Qy 421 FRNPQNTFERGTANYSQPYESPGQLKDSFETLPPETTERPNYESYSHRSLSHIGLIQSQR 480
Db 416 FTNPQNTSDRTANYSQPYESPGQLKDSFETLPPETTERPNYESYSHRSLSHIGLIQSQR 475
Qy 481 VHVVPYSWTHRSADRTNTISSDITQIPLVKSNLNGTSVVGPGFTGGDIIRTNVNGS 540
Db 476 VNVVPYSWTHRSADRTNTIGPNRITQIPWKASLPGQTTVVRGPGFTGGDILRTWGG 535
Qy 541 VLSMGLNFNTSLQRYRVRYAASQTMVLRTVVGSGFTPDQGPSTMSANESLTSQSF 600
Db 536 FGPIRVTVNGPLTQRYRIGFRYASTVDFDFVSRGGTTVNNFRFLRTMWSGDELYKGNFV 595
Qy 601 FAEPFVGISASGSO-TAGISISNNAQRTFHFDKIEPIPTATFEAYDYLERAEAVNAL 659
Db 596 RRAFTTPTFTQIQTIDIRTSIQGLSGNGEVYDKIEIIPVTATFEAYDYLERAEAVNAL 655
Qy 660 FTNTNPRRLKTDVTDYHIDQVSNLVACLDFCLDEKRELLEKVKYAKRLSDERNLLQDP 719
Db 656 FTNTNPRRLKTDVTDYHIDQVSNLVACLDFCLDEKRELLEKVKYAKRLSDERNLLQDP 715
Qy 720 NFTSINKQPDFISTNEQSNFTSIHQSEHGWMGSENITIQEGNDVFKENYVTLPGTFNEC 779
Db 716 NFTSINKQPDFISTNEQSNFTSIHQSEHGWMGSENITIQEGNDVFKENYVTLPGTFNEC 775
```


QY 898 VFILKTQEGHARLGNLEFIEKPLLGALSRVKAERKWRDKREKLOLETKRVVTEAKEA 957
 Db 899 VFILKTQEGYARLGNLEFIEKPLIGALSRVKAERKWRDKREKLOLETKRVVTEAKEA 958
 QY 958 VDALFVDSQYNRLQADTNIGMIHAADKLVRHREAYLSLSVPGVNAEIPFEELEGRIT 1017
 Db 959 VDALFVDSQYDQLQADTNIGMIHAADKLVRHREAYLSLSVPGVNAEIPFEELEGRIT 1018
 QY 1018 AISLYDARNVKNQGFNGLACWVKGHVQVQSHHRSVLVLPWEAEVQAVRVCPRG 1077
 Db 1019 AMSLYDARNVKNQGFNGLTCWVKGHVQVQSHHRSVLVLPWEAEVQAVRVCPRG 1078
 QY 1078 YILRVATYKEGYGCGCVTHIEINNTDELKPKNCEEEVPTDGTGNDYTAHOGTAVCN 1137
 Db 1079 YILRVATYKEGYGCGCVTHIEINNTDELKPKNCEEEVPTDGTGNDYTAHOGTAACN 1138
 QY 1138 SRNAGYEDAVEVDTTASVNYKPTVEEYTTDVRDNCHEYDRGVYVPPVAGVYTKELE 1197
 Db 1139 SRNAGYEDAVEVDTTASVNYKPTVEEYTTDVRDNCHEYDRGVYVPPVAGVYTKELE 1198
 QY 1198 YFPETDVTWIEIGETGKFIVDSEVLLMEE 1228
 Db 1199 YFPETDVTWIEIGETGKFIVDSEVLLMEE 1229

RESULT 6
 C1BD_BACTZ STANDARD; PRT: 1231 AA.
 ID C1BD_BACTZ
 AC Q9AZS;
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE Peptidic crystal protein cryIbD (Insecticidal delta-endotoxin
 DE CryIbD) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
 GN Name: cryIbD; Synonyms: cryEI, cryIb(d), cryIaI;
 OS Bacillus thuringiensis (subsp. wuhanensis).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=52024;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HD-525;
 RX MEDLINE=20153386; PubMed=10688690;
 RA Kuo W.-S., Lin J.-H., Tzeng C.-C., Kao S.-S., Chak K.-F.;
 RT "Cloning of two new cry genes from *Bacillus thuringiensis* subsp.
 RL *wuhanensis* strain";
 RL Curr. Microbiol. 40:227-232 (2000).
 CC -1- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut
 CC epithelial cells of lepidopteran larvae. Toxic to plutella
 CC xylostella.
 CC -1- DEVELOPMENTAL STAGE: The crystal protein is produced during
 CC sporulation and is accumulated both as an inclusion and as part of
 CC the spore coat.
 CC -1- MISCELLANEOUS: Toxic segment of the protein is located in the N-
 CC terminus.
 CC -1- SIMILARITY: Belongs to the delta endotoxin family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U70726; AAD10292.1; --
 CC HSP; P02965; 1C1Y.
 DR InterPro; IPR001178; Endotoxin.
 DR InterPro; IPR005638; Endotoxin C.
 DR InterPro; IPR005639; Endotoxin N.
 DR InterPro; IPR008979; Gal bind like.
 DR Pfam; PF03944; Endotoxin_C_1.
 DR Pfam; PF00555; Endotoxin_M; 1.
 DR Pfam; PF03945; Endotoxin_N; 1.

KW Sporulation; Toxin.
 SQ SEQUENCE 1231 AA; 139654 MW; 129A0371CDDBE52 CRC64;
 Query Match 80.5%; Score 5214.5; DB 1; Length 1231;
 Best Local Similarity 79.7%; Pred. No. 0;
 Matches 987; Conservative 94; Mismatches 140; Indels 17; Gaps 9;
 QY 1 L TSNRKNENIINALSIPAVSNHSTOMDLSPPDARIEDSLCIAEGNNINPLVSASTVGTGI 60
 Db 1 MTSNRKNENIINALSIPAVSNHSAQMDLSLDARIEDSLCIAEGNNINPLVSASTVGTGI 60
 QY 61 NIAGRILGVGVFPAGQASFYFLGELWPRGDOWEIEFLEHVEQLINOITENARNTA 120
 Db 61 NIAGRILGVGVFPAGQASFYFLGELWPRGDOWEIEFLEHVEQLINOITENARNTA 120
 QY 121 LARLOGLGDSFRAYQOQSLDLEWNRDARTSRVLYTYQYIALELDFLNAMFLFAIRNQEVP 180
 Db 121 IARLEGLGRGYSYQALETWLDNRNDARSRIILERYVALELDITTAIPLFRIRNEEVP 180
 QY 181 LLMVYAAQANLHLLILDASLFGSEFGLTSGEQLTQSOETQRYRQVEQTRDYSYCVWEYNTGLN 240
 Db 181 LLMVYAAQANLHLLILDASLFGSEWMASSDVNQYQEQIRYTEESYNSHCVQMYNTGLN 240
 QY 241 SLRGITNAASWRYNQFRRLTLGLVDLVALFPSYDTRTYPINTSAQLTRVYTDALGATG 300
 Db 241 NLRGITNAESWLRYNQFRRLTLGLVDLVALFPSYDTRTYPINTSAQLTRVYTDALGATG 300
 QY 301 V--NMASMNWYNNNAPSFSAIETAVIRSHLLDFLEQLTIFSTSSRWASRTHMYWRGHT 358
 Db 301 APSGFASNTWNNNAPSFSAIEAAIIRPRLHLLDFPEQLTISASSRWSSQTHMYVWGH 360
 QY 359 IQSRPIGGGLNTHSGST-NTSINPVRLSFFSDVWVTSYAGVLLWGLYLEIHHGVPTV 417
 Db 361 LNRFPFGITLNTSTQGLTNTSINPVLTQTSKDVYRTESNAGTNI--LFTTPVNGVPM 418
 QY 418 RFNFRNPQNTFERGTANYSQYESPGQLQKDSSTELPPTETTERPNYESYSHRLSHGLIS 477
 Db 419 RFNFINPQNIYERGATTSYQYGVGVLQKDSSTELPPTETTERPNYESYSHRLSHGLII 478
 QY 478 QSRVHVPTVSWTHRSADRTNTISSDSITQIPLVKSFNLSGTSVVGSGPFTGGDIIRTN- 536
 Db 479 GNTLRAPVYVSWTHRSADRTNTIGPNRITQIPAVKGRFLFNG-SVIGSGPFTGGDVVLNR 537
 QY 537 VNGSVLSMG-----LNFNNTSLQRVVRVRYAASQTMVLRTVVGSTTDDQGPSPMSAN 591
 Db 538 NNGNIQNRGVIIEVPIQFTSTS-TRYRVRVRYASVTSIELNVNLGNSIITNTLPAFASL 596
 QY 592 ESITSQSPFAFPFVGI-SASGSQTAGISISNAGRQTFHFQKIEFIPITATPEAEYDLE 650
 Db 597 DNLQSGDFGVVEINNAFTSATGNIVGARNFSANA---EVIDRFEFIPVATPEAEYDLE 653
 QY 651 RQAEAVNALFTWNPRLKTDVTHIDQVSNLVACLSEDFCLDEKRELLKVKYAKRLS 710
 Db 654 RQAKAVNALFTSTNPRRLKTDVTHIDQVSNLVACLSEDFCLDEKRELLKVKYAKRLS 713
 QY 711 DERNLLODNFTSINKOPPFISTNEOSNFTSIHQSEHGWGSENIIOEGNDVFKENVY 770
 Db 714 DERNLLODNFTFISQLSFASIDGOSNFTSINELSEHGWGSENIIOEGNDVFKENVY 773
 QY 771 TLPGTNECYPTLYKIGESLKYATRYOLRGYIEDSQDLIYLIRYNAKHETLDPVGT 830
 Db 774 TLPGTNECYPNVLYKIGESLKYATRYOLRGYIEDSQDLIYLIRYNAKHETLDPVGT 833
 QY 831 ESWPVLVSFPIGRCEPNRCAPHPEWNPDLDCSDGCEKAHSHHFLSDIDIGCTDLH 890
 Db 834 DSLVPLSVKSPIGRCGEPNRCAPHPEWNPDLDCSDGCEKAHSHHFLSDIDIGCTDLH 893
 QY 891 ENLGVWVVEFKITQEGHARLGNLEFIEKPLLGALSRVKAERKWRDKREKLOLETKRV 950
 Db 894 ENLGVWVVEFKITQEGYARLGNLEFIEKPLIGALSRVKAERKWRDKREKLOLETKRV 953
 QY 951 YTEAKEAVDALFVDSQYNRLQADTNIGMIHAADKLVRHREAYLSLSVPGVNAEIPFEE 1010

```

Db 954 YTEAKETVDALFVDSHYNRLQADTNIGMHAADRLVHRIHEAYLPELPPFGINAVIFEE 1013
Qy 1011 LEGRIITAIISLYDARNVVKNGDFNGLACWNVKGHDVQOSHRSVLVLPWEAEVSQAV 1070
Db 1014 LENRISTAFSLYDARNVVKNGDFNGLSCWNVKGHDVQOSHRSDLVLPWEAEVSQAV 1073
Qy 1071 RVCPRGYILLRVTAKEYGEGCVTHIEINNTDELAFKNCBEEVYPTDGTGNDYTAH 1130
Db 1074 RVCPRGYILLRVTAKEYGEGCVTHIEINNTDELAFKNCBEEVYPTDGTGNDYTAH 1133
Qy 1131 QGTAVCNRSNAGYEDAYEVDVTTASVNYKPYEBEETDVRDNDHCEYDRGVVNPPLPAG 1190
Db 1134 QGTAAACNSRNAGYEDAYEVDVTTASVNYKPYEBEETDVRDNDHCEYDRGVVNPVPAG 1193
Qy 1191 YMTKELEYFPETDKWIEIGETGKFIIVDSVLELLMBE 1228
Db 1194 YVTKLEYFPETDVTWIEIGETGKFIIVDSVLELLMBE 1231

RESULT 7
Q8KNY2 PRELIMINARY; PRT; 1231 AA.
AC Q8KNY2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CryiBII.
GN Name=CryiBII;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
SEQUENCE FROM N.A.
RA Iakova I.A., Ieakov Y.B., Rymar' S.E., Yarovoi S.V.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
EMBL: AY138457; AM933496.1;
DR HSP; P02965; ICIY.
DR GO: 0005102; F:receptor binding; IEA.
DR GO: 0006952; P:defense response; IEA.
DR GO: 0009405; P:pathogenesis; IEA.
DR InterPro: IPR001178; Endotoxin.
DR InterPro: IPR005638; endotoxin_C.
DR InterPro: IPR005639; endotoxin_N.
DR InterPro: IPR008979; Gal bind like.
DR Pfam: PF03944; Endotoxin_C; 1.
DR Pfam: PF00555; Endotoxin_M; 1.
DR Pfam: PF03945; Endotoxin_N; 1.
SQ SEQUENCE 1231 AA; 139764 Mw; C9F2848A9297EA00 CRC64;

Query Match 80.1%; Score 5188.5; DB 2; Length 1231;
Best Local Similarity 79.3%; Pred. No. 2.4e-317;
Matches 982; Conservative 97; Mismatches 142; Indels 17; Gaps 9;

Qy 1 LTSNRKNEIINALSTPAVNSHSTQMDLSPDARIEDSLCIAEGNNINPLVASTVGTGI 60
Db 1 MTSNRKNEIINALSTPAVNSHSTQMDLSPDARIEDSLCIAEGNNINPLVASTVGTGI 60
Qy 61 NIAGRLGLGVPPAGQAGFYSLVGLWLPGRGDOWEIEFLHVEQLINQOITENARNTA 120
Db 61 NIAGRLGLGVPPAGQAGFYSLVGLWLPGRGDOWEIEFLHVEQLINQOITENARNTA 120
Qy 121 LARLQGLGDSFRAYQQSLEDWLENRDARTSRVLYTOYIALELDPLNAMPLFAIRNOEVP 180
Db 121 IARLEGLGRVRSYQQALETWLDNRNDARSIIILRYVALELDITTAIPLFIRNEEVP 180
Qy 181 LMVYQAANLHLLLRDASLFGSEFGLTSQETQRYRQEQTRDYSYCVIEWYNTGLN 240
Db 181 LMVYQAANLHLLLRDASLFGSEWGWASSNQYQEQIRYEEYSNHCVQWYNTGLN 240
Qy 241 SLRGTAASVRYNQFRDRLTLGLVDLVALFPSPYDTETYPINTSAQLTRVYTDALCATG 300
Db 241 NLRGTAASVRYNQFRDRLTLGLVDLVALFPSPYDTETYPINTSAQLTRVYTDPIGRTN 300

```

```

Qy 301 V--NMASMYNNAPSFAIETAVIRSPHLLDFLEOLTIFSTSSRSATRHMTYWRGHT 358
Db 301 APGFASTNNFNANNAPSFAIEAIAIRPPHLLDFPEQLTIYSASSRSSTQHMMYWGHR 360
Qy 359 IQSRPIGGGLNTSTHGST-NTSINPVRLSFPFSDRVYMTESVAGVLLMGVILEPIHGVPV 417
Db 361 LNFPRPGTGLNTSTOGLTNTSINPVTLOFTSRDYVTESNAGTNI--LFTTPGVNVPWD 418
Qy 418 RFNFRPONTFERGTANYSPYSPGLQKDSFTELPEPETERPNYESYSHRLSHIGLIS 477
Db 419 RFNFINPQNIYERGATTYSPYQGVGLQFDSFTELPEPETERPNYESYSHRLSHIGLII 478
Qy 478 QSRVHVYVSWTHRSADRTNTISSDSITQIPLVKSFNLSGTSVVGSGPTGGDIIRTN- 536
Db 479 GNTLRAPVYVSWTHRSADRTNTIGFNRIQTQIPAVKGRFLFNG-SVISGPGFTGGVVRNLR 537
Qy 537 VNGSVLSMG-----LNFNNTSLQRYRVRYAASQTMVLRVTVGGSTTFDQGFPTMSAN 591
Db 538 NNGNIQNRGYIEVPIQFTSTS-TRYRVRYASVTSIELNVNLGNSISFINTLPATAASL 596
Qy 592 ESITSOSFRFAEPFVGI-SASGSQTAGISINNAGROTFFHDKIEFTIPITATPEAEVDLE 650
Db 597 DNLQSGDFGYVEINNAFTSATGNIVGARFNSANA---EVIIDRPEFIPVTATPEAEVDLE 653
Qy 651 RAQEAVALFTNTPRLKTDVTDYHIDQVNLVACLSDFCLDEKELKEKVKYAKRLS 710
Db 654 RAQKAVNALFTNTPRLKTDVTDYHIDQVSNMVACLSDFCLDEKELKEKVKYAKRLS 713
Qy 711 DERNLLQDPNFTSINKOPDFISTNEQSNFTSIHQSEHGWMGSENITIQGNDVFKENYV 770
Db 714 DERNLLQDPNFTSISQGLSPASIDGQSNFTSINELSEHGWMGSENITIQGNDVFKENYV 773
Qy 771 TLPCTNECYPTLYQKIGSELKAYTRYQLRGYIEDSQDLEIYLIRYNAKHETLDVPGT 830
Db 774 TLPCTNECPVLYQKIGSELKAYTRYQLRGYIEDSQDLEIYLIRYNAKHETLDVPGT 833
Qy 831 ESVPILSVESPIGRCEPNRCAPHFENWPDLCSCRDGECACAHSHHPSLDDIDGCTDLH 890
Db 834 DSLWPLSVKSPIGRCGPNRCAPHFENWPDLCSCRDGECACAHSHHFTLDDIDVGCDDLH 893
Qy 891 ENLGVWVVKIKTOEGHARLGNLEFTEKPLLGALSRVKRAEKWRDKREKLQLETKRV 950
Db 894 ENLGVWVVKIKTOEGHARLGNLEFTEKPLLGALSRVKRAEKWRDKREKLQLETKRV 953
Qy 951 YTEAKEAVDALFVDSQVNRLOADTNIGMHAADRLVHRIHEAYLPELPPFGINAVIFEE 1010
Db 954 YTEAKETVDALFVDSHYNRLQADTNIGMHAADRLVHRIHEAYLPELPPFGINAVIFEE 1013
Qy 1011 LEGRIITAIISLYDARNVVKNGDFNGLACWNVKGHDVQOSHRSVLVLPWEAEVSQAV 1070
Db 1014 LENRISTAFSLYDARNVVKNGDFNGLSCWNVKGHDVQOSHRSDLVLPWEAEVSQAV 1073
Qy 1071 RVCPRGYILLRVTAKEYGEGCVTHIEINNTDELAFKNCBEEVYPTDGTGNDYTAH 1130
Db 1074 RVCPRGYILLRVTAKEYGEGCVTHIEINNTDELAFKNCBEEVYPTDGTGNDYTAH 1133
Qy 1131 QGTAVCNRSNAGYEDAYEVDVTTASVNYKPYEBEETDVRDNDHCEYDRGVVNPPLPAG 1190
Db 1134 QGTAAACNSRNAGYEDAYEVDVTTASVNYKPYEBEETDVRDNDHCEYDRGVVNPVPAG 1193
Qy 1191 YMTKELEYFPETDKWIEIGETGKFIIVDSVLELLMBE 1228
Db 1194 YVTKLEYFPETDVTWIEIGETGKFIIVDSVLELLMBE 1231

RESULT 8
C1BC BACTM
ID C1BC BACTM STANDARD; PRT; 1233 AA.
AC Q45774;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidial crystal protein cryIbC (Insecticidal delta-endotoxin)

```

DE CryIB(c) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
GN Name=cryIb; Synonyms=cryIB(c), cryIbC;
OS Bacillus thuringiensis (subsp. morrisoni).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1441;
RN [1]
RP SEQUENCE FROM N.A.
RA Bishop A.H., Bone E.J., Ellar D.J.;
RT "Cloning of novel Bacillus thuringiensis delta-endotoxin.";
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut
epithelial cells of insects.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
sporulation and is accumulated both as an inclusion and as part of
the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see <http://www.ebi.ac.uk/announcements/>
or send an email to license@sib.ch).
CC -----
DR EMBL; Z46442; CAA86568.1; --
DR HSP; P02965; ICIY.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin C.
DR InterPro; IPR005639; endotoxin N.
DR InterPro; IPR008979; Gal bind Like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
SQ SEQUENCE 1233 AA; 140451 MW; 7318382413529F21 CRC64;

Query Match 76.58; Score 4959.5; DB 1; Length 1233;
Best Local Similarity 75.18; Pred. No. 5.7e-303;
Matches 928; Conservative 118; Mismatches 180; Indels 9; Gaps 4;

QY 1 LTSNRKNEINLALSIPAVNSHSTQMDLSPDARIEDSLCTAEGNNINPLVSASTVQTGI 60
DB 1 MTSNRKNEINLALSIPVSNPSTQNLSPDARIEDSLCAEVNNDPFSASTVQTGI 60
QY 61 NIAGRILGVLPAGQIAGFYSPLVGLWPRGRDQWEIFLEHVEQLINQOITENARNTA 120
DB 61 NIAGRILGVLPAGQIAGFYSPLVGLWPRGRDQWEIFLEHVEQLIRQVNTENTNTA 120
QY 121 LARLQGLGDSFRAYQOQSLQEDWLENDRDARTSVLYTOYIALELDFLNAMPFAIRNOEVP 180
DB 121 IARLEGUGRYSYQQALQETWLDNRDARSILERYALELDTITAIPLFRIRNEVP 180
QY 181 LLMVYAQAANLHLLLDASLFGSEFGLTSGEIQRYRVERQVETRDYSYCVENYNTGLN 240
DB 181 LLMVYAQAANLHLLLDASLFGSEWGWASDQVYQEQIRYTEEYSHCVQWYNTGLN 240
QY 241 SLRGTNAASWVRYNQFRDRLTLGVLDLVALFPSPYDTRTYINTSAQLTRREYVTAIGATG 300
DB 241 NLRGTNAESWLRVYNQFRDRLTLGVLDLVALFPSPYDTRTYINTSAQLTRREYVTDPIGRTN 300
QY 301 V-NWASMNWYNNAAPSFAETAVIESPHLLDPLEQLTIFSTSSRSWATRHWTYWGHT 358
DB 301 APGFGASTNFWNNAPFSFAIEAIFRPHLLDPPEQLTISYSSRSSTQHWNWVGHR 360
QY 359 IQRSPICGLNTSTHGST-NTSINPVRSPFSRDVYVWYTESYAGVLLWGIYLEPHIGVPTV 417
DB 361 LNRFPICGLNTSTQGLTNTSINPVLQTSRDVYVWYTESNAGTNI--LFTTPVNGVPA 418
QY 418 RPNFRNPONTFERGTANYSPQESFGLQKDSKSETLPPETTERPNYESYSHRSLHIGLS 477

DB 419 RPNFRNPONTFERGTANYSPQESFGLQKDSKSETLPPETTERPNYESYSHRSLHIGLSII 478
QY 478 QSRVHVPPVYSWTHRSADRTNTTSSDSTOPLVKFSNLSGTSVSVSGPFTGGDIIITNV 537
DB 479 GNTLRAPVYVSWTHRSADRTNTTGNRITQPLVKNLHSGVTVVGPGFTGGDIIIRTN 538
QY 538 NSGLVSMGLNFNNTSLQRYRVRVRYAASQTMVLRTVVGSGSTTFDQGPSPPTANESITSQ 597
DB 539 TGTFGDIRLNLNPLSQRYRVRIRYASTTDLQFFTRINGTIVNIGNFSRTMRGNDLNEYR 598
QY 598 SFRPAFPVGISASGQTAGISISNNAGRTQTFHDKIEFIPITATFAEYDLERAQAVN 657
DB 599 SFTAGFSTPFNLQAQSTFLQAQSFNSQEVYIDRVFPAEYVTFPAEYDLERAQAVN 658
QY 658 ALFTNTNPRKLTVDYDHYDQVSNVACLSDFCLDEKRELLKVKYAKRLSDERNLQ 717
DB 659 ALFTNTNPRKLTVDYDHYDQVSNVACLSDFCLDEKRELLKVKYAKRLSDERNLQ 718
QY 718 DPNFTSINKQPDFISTNEQSNFTSIHQSESHGWGSENITIQEGNDVFKENYVTLPGTFN 777
DB 719 DPNFTSISGQLSPASIDGQSNFSSINELSHGWGSAVNTIQEGNDVFKENYVTLPGTFN 778
QY 778 ECPYLYQKIGESSELKAYTRYQIRGYIEDSQDLEIYLIRYNAKHETLDVPGTESVWPLS 837
DB 779 ECPYLYQKIGESSELKAYTRYQIRGYIEDSQDLEIYLIRYNAKHETLDVPGTESVWPLS 838
QY 838 VESPIRGCGPNRCAPEFWNPDLDCSDRGEKCAHSHHFDLIDIGCTDLHENLGVV 897
DB 839 AESTIGKCTEPNRCAPHYWNPDLCSDRGEKCAHSHHSTLIDVGCCTDLHENLGVV 898
QY 898 VPKIKTQEGHARLGNLEFTEKPLLGALSRVRAEKKWRDKREKLOLETKRVVYTEAKEA 957
DB 899 IFPKIKTQEGHARLGNLEFTEKPLLGALSRVRAEKKWRDKREKLOLETKRVVYTEAKEA 958
QY 958 VDALFVDSQVNRLOADNTNIGMHAADKLVRIRIERYSELSESVIPGVNAEIFELEGRIT 1017
DB 959 VDALFVDSQVNRLOADNTNIGMHAADKLVRIRIERYSELSESVIPGVNAEIFELEGRIT 1018
QY 1018 AISLYDARNVKNKGNFNGGLACVNVKGVHDVQOQSHRSVLVPIPEWAEVSOAVRVCPRG 1077
DB 1019 AFSLYDARNVKNKGNFNGGLACVNVKGVHDVQOQSHRSVLVPIPEWAEVSOAVRVCPRG 1078
QY 1078 YILRVTAAYKEGYGEGCVTTHIEINNTDELKFKNCEEEVYPTDGTGNTYAHQGTAV-- 1135
DB 1079 YILRVTAAYKEGYGEGCVTTHIEINNTDELKFKNCEEEVYPTDGTGNTYAHQGTAV-- 1138
QY 1136 --CNSRNAGYEDAYEDVTTASVNVKPYTEETVYDRDNHCEYDRGVNYPPLPAGYMT 1193
DB 1139 NECGRNEDYDINAYEINAKSSLEYRPTTEETVYDRDNHCEYDRGVNYPPLPAGYMT 1198
QY 1194 KELEYPTDQVWIEIGETEGKFIIVDSVELLMEE 1228
DB 1199 KELEYPTDQVWIEIGETEGKFIIVDSVELLMEE 1233

RESULT 9
C1KA BACTM STANDARD; PRT; 1215 AA.
ID C1KA BACTM
AC Q45715;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIb (insecticidal delta-endotoxin
DE CryIb(a)) (crystalline entomocidal protoxin) (137 kDa crystal protein).
GN Names=cryIb; Synonyms=cryIb, cryIb(a);
OS Bacillus thuringiensis (subsp. morrisoni).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1441;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=F190;
RA MEDLINE=96102856; PubMed=8586263; DOI=10.1016/0378-1097(95)00397-1;
Koo B.T., Park S.-K., Choi S.-K., Shin B.S., Kim J.I., Yu J.H.;

Qy	1	LT	NR	KNE	NEI	I	N	A	L	S	I	P	A	V	N	H	S	T	Q	M	D	L	S	P	A	R	I	E	D	S	L	C	I	A	E	G	N	N	I	N	P	L	S	A	S	T	V	Q	T	I	60						
Db	1	MT	SR	KNE	NEI	I	N	A	L	S	I	P	A	V	N	H	S	A	Q	M	N	L	S	D	A	R	I	E	D	S	L	C	I	A	E	G	N	N	I	D	P	F	S	A	S	T	V	Q	T	I	60						
Qy	61	NI	AG	R	I	I	L	G	V	L	G	P	P	A	G	O	I	A	S	F	V	L	G	E	L	W	P	R	G	D	O	W	E	I	F	L	E	H	V	B	O	L	I	N	Q	O	I	T	E	N	A	R	N	T	A	120	
Db	61	NI	AG	R	I	I	L	G	V	P	P	A	G	O	I	A	S	F	V	L	G	E	L	W	P	R	G	D	P	W	E	I	F	L	E	H	V	B	O	L	I	Q	O	V	T	E	N	T	R	D	A	120					
Qy	121	L	A	R	L	Q	L	G	D	S	P	R	A	Y	Q	O	S	L	E	D	W	L	E	N	R	D	A	R	T	S	V	L	T	Q	I	A	L	E	D	F	I	N	A	M	P	L	F	A	I	R	N	O	E	V	P	180	
Db	121	L	A	R	L	Q	L	G	N	S	P	R	A	Y	Q	O	S	L	E	D	W	L	E	N	R	D	A	R	T	S	V	L	T	Q	I	A	L	E	D	F	L	N	A	M	P	L	F	A	I	R	N	O	E	V	P	180	
Qy	181	L	L	M	Y	A	A	N	L	H	L	L	L	R	D	A	S	I	F	C	S	E	F	G	L	T	S	O	E	I	Q	R	Y	E	R	O	V	E	O	T	R	D	Y	S	D	C	V	E	W	T	N	T	G	L	N	240	
Db	181	L	L	M	Y	A	A	N	L	H	L	L	R	D	A	S	I	F	C	S	E	F	G	L	T	S	O	E	I	Q	R	Y	E	R	O	V	E	K	T	R	E	Y	S	D	C	A	R	W	T	N	T	G	L	N	240		
Qy	241	S	L	R	G	T	N	A	S	W	Y	R	N	Q	F	R	D	L	T	G	V	L	D	L	V	A	L	P	S	Y	D	T	R	V	P	I	N	T	S	A	Q	L	R	E	V	T	D	A	I	G	T	300					
Db	241	N	L	R	G	T	N	A	E	S	W	L	Y	N	Q	F	R	D	L	T	G	V	L	D	L	V	A	L	P	S	Y	D	T	R	V	P	P	M	N	T	S	A	Q	L	R	E	I	Y	D	T	D	I	G	R	T	N	300
Qy	301	V	-	N	M	A	S	M	N	W	N	N	N	A	P	S	A	I	E	T	A	V	I	R	S	P	H	L	D	F	L	E	Q	L	T	I	F	S	T	S	R	S	G	A	T	R	H	M	T	Y	R	G	H	T	358		
Db	301	A	P	S	G	F	A	S	T	N	N	N	N	A	P	S	A	I	E	A	V	I	R	P	H	L	D	F	E	Q	L	T	I	F	S	V	L	S	R	G	S	N	T	Q	Y	M	N	W	V	G	H	R	360				
Qy	359	I	Q	S	R	P	I	G	G	L	T	S	T	H	G	S	T	N	I	N	P	V	R	L	S	F	F	R	D	V	Y	T	W	T	E	S	Y	A	G	V	L	L	W	G	I	Y	L	E	I	H	G	V	P	T	V	R	418
Db	361	L	E	S	R	T	I	R	G	S	L	T	S	T	H	G	S	T	N	I	N	P	V	T	L	O	F	T	S	R	D	V	Y	T	E	S	P	A	G	I	N	-	L	T	T	P	V	N	G	V	P	W	A	R			

RESULT 12

C1CB_BACTG	STANDARD;	PRT; 1176 AA.
ID	C1CB_BACTG	
AC	P56953;	
DT	30-MAY-2000 (Rel. 39, Created)	
DT	30-MAY-2000 (Rel. 39, Last sequence update)	
DT	05-JUL-2004 (Rel. 44, Last annotation update)	
DE	Pesticidal crystal protein cryICb (Insecticidal delta-endotoxin	
DE	DE cryIC(b)) (crystalline entomocidal protoxin) (133 kDa crystal protein).	
GN	Name=cryICb; Synonyms=cryIC(b);	
OS	Bacillus thuringiensis (subsp. galleriae).	

```

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
CN NCBI_TaxID=29338;
RN [1]
RX SEQUENCE FROM N.A.
RC STRAIN=HD-29;
RX MEDLINE=93236401; PubMed=8476286;
KA Kalman S.S.;
RT "Cloning a novel cryIC-type gene from a strain of Bacillus
RT thuringiensis galleriae.";
RL Appl. Environ. Microbiol. 59:1131-1137(1993).
CC -/- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of insects. Toxic to Spodoptera exigua and
CC Trichoplusia ni.
CC -/- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -/- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -/- SIMILARITY: Belongs to the delta endotoxin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M97880; -; NOT_ANNOTATED_CDS.
DR PIR; A48970; A48970.
DR HSP; P02965; 1C1Y.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF031944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
SQ SEQUENCE 1176 AA; 132867 MW; 108233494C2AC018 CRC64;
Query Match 58.5%; Score 3791; DB 1; Length 1176;
Best Local Similarity 62.3%; Pred. No. 1.9e-229;
Matches 762; Conservative 125; Mismatches 241; Indels 96; Gaps 16;
Qy 40 CIAEGNNINPLSVASTVQTG---INTAGRILGVL---GVFFAGQIAFYSLFVGLMWRG 93
Db 14 CLSNPEEI---LLDGERISTGSSIDISLSVLQVLSNFPVGGFLVGLLDFVWVGIVGP-- 69
Qy 94 RDWEIFLEHVHVEQLINQOITENARNTALAEGLGDSFRAYQOSLEDWLENRDDARTSV 153
Db 70 -SPWDAPLVQIEGLINERIAAYARSAISNLEGLGNFNIFYEAFKEWEADDPNVTRTR 128
Qy 154 LYTQYTALELDLFNANPLFAIRNQEPVLLMVYAQAANLHLLLRDASLFGSEFGLTSQEI 213
Db 129 VVDFRPLDGLLERRDIPSPFIAGFEVPLLSVYAQAANLHLALRRDSSIFGARWGLTTINV 188
Qy 214 QRYYERQVEQTRDYSYCVENYNTGLNSLRGTNAASWVRVYQPFRRDLTLGVLDLVALFPPS 273
Db 189 NENYNLRIRHIDEYANHCDATYNRGLNPLPKSTYQDWITYNLRRLDRLTLVLDAIAFFPS 248
Qy 274 YDRTFYPINTSAQLTREVTYDADGATGVNMAWMNWNNAAPSAITAIVRSPHLDEL 333
Db 249 YDNRNPVIOVGQTRHEIYVDLITFNPOQSV-----AQLPTFNVMESNAIRTPHLEFDVL 304
Qy 334 EQLTIFSTSRWSATRHMTYWRGHTIQSRPIGGGLANTSTHGSTNTSINPVLRSFFSRDVI 393
Db 305 NNLTIFD---WFSVGENFWGGRHVISNPIGCGNITSPYIGREANQEPSPRSTFNGPVF 361
Qy 394 WTESYAGVLWGLYLPBIGHGVPTVR-----FN-----FRNPQNTFE---RGT 432
Db 362 RTLSN-----PFRPLQOQWPAPPFNLRGVGEVFTSLNSFTYRGRT 405

```

Query Match	58.5%;	Score 3791;	DB 1;	Length 1176;
Best Local Similarity	62.3%;	Pred. No. 1.9e-229;		
Matches 762;	Conservative 125;	Mismatches 241;	Indels 96;	Gaps 16;
Qy	40	CIAGEGNNINPLVGASTVQTC--	INTAGRIILGVL---	GVPFAGQIASFYSFVLGELWPRG 93
Db	14	CLSNPEI--LLDGERISTGSSSIDISLSIVQLVSNFVPGGFLVCLLDFVWGI	VP--	69
Qy	94	RDQWEIFLEHVQOLINQITENARTALARLOGIGDSFRAYQOSLELDWLNRRDARTRSV	153	
Db	70	-SPWDAFLVQIEQLINERIAAYARSAAISNLEGIGNNFNIYVEAFKEWADDPNPVTR	128	
Qy	154	LYTQYIALELDFLNAMPLFAIRNQVEPLLMVYAAQANLHLLLDASLFGSEFGLTSQEI	213	
Db	129	VDFRIFLDGLLERDIPFRIAGFEVPLLSVYAAQANLHLLAIIRDSSIFGARWGLTTINV	188	
Qy	214	QRYERQVEQTRDYSYDCEVYNTGLNSLGTNAASWRYNQFRDLTLGLVLDLVALFPPS	273	
Db	189	NENYNLRIRHIDEVANHCAITYNRGLNNLPKSTVQDWITYNRLRRDLTLVLDAIAAFPS	248	
Qy	274	YDRFTPTINTSAQITREYVYTDALGATGVNWMASMMWYNNAPSPAETAVIRSPHLDDL	333	
Db	249	YDNRNRYPIQSGVLTREIVYDPLITTFNPQLQSV----	AQLPTFNVMESNAIRTPHLFDVL 304	
Qy	334	EQLTIFSTSRWSATRHMTYWRGHTTQSRPIGGGLNTSTHGSTNTSINPVLGFFSFSDVY	393	
Db	305	NNLITIFTD---WFSVGENFWGGRHVISNPIGGGNITSPITYGREANQEPSPSTTFNGP	361	
Qy	394	WTESYAGVLWGIYLBEIHGVPTVR-----FN-----	FNPNQTFE----	RGT 432
Db	362	RTLNSN-----	PTFRPLQOQWPAPPENLRGVGEVGFSTPLNSFTYRGRGT	405

Qy	433	ANYSQPYESPCLQJLKDSETELPPTTERTPNVYESYSHRLSHGLILSQSRVH----	PYVSW	488
Db	406	V-----D\$LTELPDPEDNSVPPREGYSHRLCHATFVQ\$R\$STPLATTGPVFSW	451	
Qy	489	THRSADRTNTISSDIITQJPLVKFNLNSGTSVVSQFGTGGDIIRTNVNGSVLSMGLNF	548	
Db	452	THRSATDRNIYPDVINQJPLVKAFNLTSGTSVVRGFGTGGDIIRTNVNGSVLSM\$LN	511	
Qy	549	NNTSLQRYRVRVRYAASQTWVLRYVTVG\$STTFDQGFPT\$MSAN\$SLTSQS\$RFA\$FPVGI	608	
Db	512	SNITLQRYRVRVRYAASQTWMSVTVG\$STTGNQGFPT\$MSANGALTSQS\$RFA\$FPVGI	571	
Qy	609	SAG\$SOTAGISISNNA\$GROTFHPDKIF\$PI\$TATFEAYEDLERAQ\$A\$VNALFTWNTN\$PRL	668	
Db	572	SAG\$Q\$ASISISNNVGRQMPHLDRIEFLPVT\$TFE\$EYDLERAQ\$A\$VNALFT\$TNQJL	631	
Qy	669	KTDVTDYHIDQVSNLVA\$CLDEFCLDEKRELLEKVKYAK\$LSDBRNLLQDPNFT\$INKQP	728	
Db	632	KTDVTDYHIDQVSNLVE\$CLDEFCLDEKRELSEKVKHAK\$LSDBRNLLQDRNFR\$INGQL	691	
Qy	729	DFISTNEQ\$NFTS\$IH\$E\$SEHGWG\$ENITIQ\$E\$NDVFKENYVTLPGTFN\$ECPYLYOKI	788	
Db	692	D-----R\$WRGSTDTITQGGDDV\$FENYVTLPGTFN\$ECPYLYOKI	733	
Qy	789	GE\$ELKATRYQJRGYTED\$QDL\$EYLIRYNNAKHETLDV\$CTESVWPL\$SVESPIGR\$CEP	848	
Db	734	DE\$KLK\$SYTRYELURGYTED\$QDL\$EYLIRYNNAKH\$EIVNVP\$TGS\$LWPL\$S\$EN\$IGPC\$EP	793	
Qy	849	NRCAPH\$E\$WNP\$D\$C\$SRD\$E\$KCAH\$H\$H\$F\$SLDIDIGCTDLHENL\$G\$VWV\$FKITQ\$GHA	908	
Db	794	NRCAPHLEWNP\$NLD\$C\$SRD\$E\$KCAH\$H\$H\$F\$SLDIDV\$GCTDLNEDL\$G\$VWV\$FKITQD\$GHA	853	
Qy	909	RLGNLEPI\$E\$KPLLGEAL\$SRV\$R\$A\$E\$K\$W\$D\$K\$REKJQL\$ET\$R\$V\$Y\$T\$E\$A\$E\$V\$D\$ALF\$V\$D\$S\$QYN	968	
Db	854	RLGNLEFLE\$E\$KPLLGEAL\$R\$V\$R\$A\$E\$K\$W\$D\$K\$REKLEWETNIVY\$K\$E\$A\$E\$S\$V\$D\$ALF\$V\$N\$S\$QYD	913	
Qy	969	RLQADTNIGM\$H\$A\$D\$KLVHRI\$R\$E\$A\$Y\$L\$S\$E\$L\$SVIPGVNA\$E\$I\$F\$E\$E\$LE\$G\$R\$IITAI\$S\$LYD\$ARNV	1028	
Db	914	RLQADTNIM\$H\$A\$D\$KRVHRI\$R\$E\$A\$Y\$L\$P\$E\$L\$SVIPGVNAGI\$F\$E\$E\$LE\$G\$R\$FTAY\$S\$LYD\$ARNVI	973	
Qy	1029	KNGDFNGLLACWNVK\$H\$VDV--Q\$SHH\$R\$S\$V\$LVI\$PEW\$E\$A\$E\$S\$Q\$A\$VRV\$C\$P\$G\$R\$YILLR\$V\$TAYKE	1087	
Db	974	KNGDFNGLLLCNLKG\$H\$VDV\$E\$E\$Q\$N\$H\$R\$S\$V\$LVP\$E\$W\$E\$A\$E\$S\$Q\$E\$VRV\$C\$P\$G\$R\$YILLR\$V\$TAYKE	1033	
Qy	1088	GYGEGCVTHIEINNTDEL\$K\$F\$C\$E\$E\$E\$V\$V\$P\$D\$T\$G\$T\$C\$N\$D\$Y\$T\$A\$H\$Q--C\$TAV\$C\$R\$N\$NAGYE	1144	
Db	1034	GYGEGCVTHIEINNTDEL\$K\$F\$N\$C\$E\$E\$E\$V\$V\$P\$N\$T\$V\$T\$C\$N\$D\$Y\$T\$A\$T\$Q\$E\$Y\$G\$G\$AY--T\$R\$N\$H\$G\$Y	1092	
Qy	1145	DAY\$E\$V\$D\$T\$TAS\$N\$Y\$K\$P\$T\$E\$E\$E\$Y\$T\$D\$V\$R\$D\$N\$H\$C\$E\$Y\$D\$R\$G\$V\$V\$N\$P\$P\$I\$PAG\$Y\$M\$T\$K\$E\$Y\$F\$P\$E\$T\$D\$K	1204	
Db	1093	K\$V\$E\$N\$S\$S\$V\$Q\$A\$D\$Y\$A\$V\$Y\$E\$K\$A\$D\$T\$G\$R\$D\$N\$H\$C\$E\$N\$R\$G\$Y\$D\$T\$P\$P\$AG\$Y\$V\$T\$K\$E\$Y\$F\$P\$E\$T\$D\$K	1152	
Qy	1205	VWIEIGTEGKFIVDSV\$E\$LLMEE	1228	
Db	1153	VWVEIGTEGTFIVDSV\$E\$LLMEE	1176	

RESULT 13

NCBI_TaxID=1428;	OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1428;	OX	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
[1]	RN	
SEQUENCE FROM N.A.	RP	
STRAIN=NRRL B-18973 / EG5092;	RC	

[illegible]

Db 160 YAOANLHLATLRDSVIFGERWGLTTINNVNENYRLIRHIDEYADHCANTYNRGLNNLPK 219
Qy 245 TNAASWRYNQFRDLTLGVLDLVALPSPYDTRYPIINTSAQLTREYVYTAIGATGVNMA 304
Db 220 STYQDMITYNRLRRDLTLVLDIAAFPFPYDNRRYPQPVGQLTREYVYDPL-----INFN 275
Qy 305 SMWYNNNAPSFAIETAVIRSPLLDFLEOLTIFSTSSRWSATRHMTYMRGHTIQSRPI 364
Db 276 PQLOSVALPPTFNWESSAIRNPHLFDLLNNLTIFTD---WFSVGRNPFYMGGRHVSSLI 332
Qy 365 GGGTLTSTHGSTNTSINPRLSPFSRDVYMTESYAGVLL-----WGIYLEPIHGVPTVRFN 420
Db 333 GGGNITSPIYCREANQPPRSFTENGPFVRLSNPTLRLLQQPWPAPPFNLRGVGVGEFS 392
Qy 421 FRNPQTFE---RGTANYQPYSPGLQDKDSELPETTERPNYESYSHRLSHIGLIS 477
Db 393 --TPTNSFTYRGCTV-----DSLTELPEONSVPREGYSHRLCHATFVQ 436
Qy 478 QSRVHV---PVYSWTHRSADRTNTISSDSITQIPLVKSNNLSNGTSVVSQPGTGGDII 533
Db 437 RSGTFFLTGTVFSWTHRSATLTNTIDPERINQIPLVKGRVWGGTSVITGPGTGGDIL 496
Qy 534 RTNVNGSVLSMGLNFNNTSLQRYVRVRYAASQ-----TMVLRTVTVGGSTTFDQGFPS 586
Db 497 RRNTFGDFSVLQVNNINSPIQRYELRFRYASSRDARVILVTGAASTGVGGQVSNMPLQK 556
Qy 587 TMSANESLTSQSPFAPFP-----VGISASGSQTAGISISNNAGRQTFFHFKIE 635
Db 557 TMEIGENLTSRTFRYDFSNPFSFRANPDIIGISEQLFGAG-SISSG-----ELYIDKIE 611
Qy 636 FIPITATFEAYDLERAQEAVALFTWNPRLRTDVTYHI DOVSNLVACLSDDEFCLDE 695
Db 612 IILADATFEASDLERAQKAVNALFTSSNQIGLKTDTYDHI DOVSNLVCLSDDEFCLDE 671
Qy 696 KRELLEKVKYAKRLSDERNLLQDPNFTSINKQDPFI STNEQSNFTSTHEQSEHGHWGSEN 755
Db 672 KRELSEKVKAKRLSDERNLLQDPNFGINRQPD-----RCWRGSTD 713
Qy 756 ITIQEGNDVPKENYVTLPGTFNECYTYLYQKIGESLKYATRYQLRGYIEDSDLEIYL 815
Db 714 ITIQGGDDVPKENYVTLPGTVDECYPTLYQKIDESKLKAYTRYELRGYIEDSDLEIYL 773
Qy 816 IRYNAKHETLDVPGETESVWPLSVESPIGRGCEPNRCAPHFENWPDLDSCSDGDEKCAHHS 875
Db 774 IRYNAKHEIYVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSDGDEKCAHHS 833
Qy 876 HPSLDDIDIGCTDLHENLGVWVPKIKTOEGHARLGNLEFTEBKPLLGEALSRVKRAEKK 935
Db 834 HHFTLDDVGCTDLNEDLGVWVIFKIKTOGHARLGNLEFTEBKPLLGEALSRVKRAEKK 893
Qy 936 WRDKREKLOLETKRVTYTEAKEAVDALFVDSQYNRLOADTNIGMIHAADKLVRHIREAYLS 995
Db 894 WRDKREKLOLETNIVYKEAKESVDALFVNSQYDRLOQVDTNAMIHAADKVRHIREAYLP 953
Qy 996 ELSVIPGVNAEIPFELEGRIITAILSLYDARNVKNQDPNNGLACWNVKGHVDV-QQSHHR 1054
Db 954 ELSVIPGVNAEIPFELEGRIIFTAYSLYDARNVKNQDPNNGLACWNVKGHVDVEEQNNHR 1013
Qy 1055 SVLVIPPEWEAEVSQAVRVCGRGYILRVATYKEGYGGCVTHIEIENNTDELKFNCEEE 1114
Db 1014 SVLVIPPEWEAEVSQAVRVCGRGYILRVATYKEGYGGCVTHIEIENNTDELKFNCEVEE 1073
Qy 1115 EYVPTDTGTGNDYTA-----HQTAVCNRNAGYDAYEDVDTASVNYKPTYEEETDVR 1170
Db 1074 EYVFNNTVTCNNYTGTOEYEGT--YTSRQGYDEAYGNPNPSVPADYASVYEEKSYTDGR 1131
Qy 1171 RDNHCEYDRGVNTPPLPAGWMTKELYFPBTDKWIIEIGETEGKFTVDSVELLLMEE 1228
Db 1132 RENPCSNRGYGDYTPLPAGVYTKDLEYFPBTDKWIIEIGETEGFTVDSVELLLMEE 1189

Search completed: April 21, 2005, 04:16:15

Job time : 139 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 20, 2005, 16:15:00 ; Search time 15262 Seconds
(without alignments)
11705.830 Million cell updates/sec

Title: US-10-614-524-1

Perfect score: 3687
Sequence: 1 ttgactcaataggaaaaa.....tactccttatggaggaatag 3687

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*
1: gb_ba.*
2: gb_hgt.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3687	100.0	3687	6	AX189649
2	3666.2	99.4	4173	6	AR359382
3	3666.2	99.4	4173	6	AX098667
4	3266.6	88.6	3684	1	AF077326
5	3266.6	88.6	3684	6	I90319
6	3260.2	88.4	3684	6	AR359400
7	3260.2	88.4	3684	6	AX098692
8	3136.8	85.1	3687	1	X06711 B. thuringi
9	3135.2	85.0	3687	1	AF368257
10	3133.6	85.0	4074	1	BTCRY1BA2
11	3133.6	85.0	4074	6	I42103
12	3133.6	85.0	4798	1	AF363025
13	2687.2	72.9	3934	1	BACCRYIE
14	2687.2	72.9	3934	6	AR068828
15	2687.2	72.9	3934	6	I38760
16	2687.2	72.9	3934	6	I70138
17	2687.2	71.3	3627	6	AX138580
18	2630.2	71.3	3627	6	AX146772
19	2579.2	70.0	8306	1	BTU70726

20	2563.2	69.5	3696	1	AY138457
21	2544.4	69.0	3663	6	AX088012
22	2541.2	68.9	3663	6	AX088010
23	2384.2	64.7	3624	6	AX138578
24	2384.2	64.7	3624	6	AX146770
25	2271.6	61.6	3842	1	BTMCRYIBC
26	2145	58.2	2549	1	AY570734
27	2004.8	54.4	3651	6	AX138576
28	2004.8	54.4	3651	6	AX146768
29	2000.4	54.3	4623	1	BTU28801
30	1796.4	48.7	3525	1	BACCRYIEB
31	1793.4	48.6	3522	6	AR085762
32	1793.4	48.6	3522	6	I11609
33	1793.4	48.6	3522	6	I73040
34	1791.8	48.6	3522	6	AR362261
35	1790.2	48.6	3522	6	A27529
36	1662	45.1	4106	1	BACCRYIC
37	1662	45.1	4106	6	I82521
38	1662	45.1	4106	6	I93759
39	1581.6	42.9	3558	6	AR451656
40	1581.6	42.9	3558	6	BD090512
41	1501	40.7	3766	6	BTU31527
42	1495.6	40.6	3624	6	AR029509
43	1495.6	40.6	3624	6	AR098462
44	1495.6	40.6	3624	6	BD194455
45	1495.6	40.6	3624	6	I41422

ALIGNMENTS

RESULT 1
AX189649
LOCUS AX189649 3687 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 1 from Patent WO0147952.
ACCESSION AX189649
VERSION AX189649.1 GI:15143038
KEYWORDS
SOURCE Bacillus thuringiensis
ORGANISM Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
REFERENCE 1
AUTHORS Arnaut, G., Boets, A., Damme, N., Mathieu, E., Vanneste, S. and van Rie, J.
TITLE Insecticidal proteins from Bacillus thuringiensis
JOURNAL Patent: WO 0147952-A 1 05-JUL-2001;
Aventis CropScience N.V. (BE)
FEATURES
source
1..3687
/organism="Bacillus thuringiensis"
/mol_type="unassigned DNA"
/db_xref="taxon:1428"
1..3687
/note="unnamed protein product"
/codon_start=1
/transl_table=11
/protein_id="CAC50778.1"
/db_xref="GI:15143039"
/translations="MTSNRKNENEINALSIPAVSNHSTOMDLSPDARIEDSLCIAEG
NNINPLVASTVQTGINAGRIVLGVFPAGQIASFYSLVGLWPRGRDQWEIFLE
HVLDINQQTENARTALRQLQSGSFAYQOQLEDWLENRDDARTSTVLYTQYIA
LELDFLNMPFLAIRQVEPLLVYQAQANHLILLDLASLFGSEFGTSQEIQRYVE
ROYEOTRDYSDYCVENYTGNSLRGTNAASWRYNQFRDLTLGVLDLVALPPSYDT
RVTPTNSAQLTREVTDTAIGATGVNWSMWNYNNAAPSJALETAVIRSPHLLDLE
QLTFTSSRSWASATRMVYWRGHTIQSRPIGGGLNTSTHGSTNTSINPRLSFRSDV
WTPEYAGVLLWGIYILEPHTVTRFNFQNTFERGTANYSQPYESQGLQKDE
TELPETTERPNYESHRLSHIGLSRVHPVSVSWTHRSADRTNTISDSITQIP
LVKSFNLNGSTSVVSGPFTGGDIIRTNVNGSVLSMGLNFNTSLQRYVRVRAASQ
TWLVRTVVGSTTFDQGFPTMSANESLTSQSFRFAEPVGISAGSQTAGISINNA
GROTFPHDKIEFIPITATFAEYDLERAQAVNALFTNTPRRLKTDVTDYHIDQVSN
LVACLSEDFCLDEKLEKLVKAKLSRDLNLLQDPNFTSINKQDPFISTNEQSNFT
SIHQEHEHGWGSGENITIQEGNDVFKENYVTLPGTFNECYPTLYLQKIGSELSKAYTR

YQLRGVLDSDQLELYLIVNAKHDTLVPCTESVSPVGRCEINRCAPHEI
 VNPEDSCSGFKKASHHSHSLDITGDTLHNIQVSVFVTKIOWEABHGLNIE
 FIEEKLPGALSRVKEAKWRDKRQLETFEETAEADVALPDSQVNRLOA
 DTNIGMIAKLAVHIREALYSLSVLSVGNATIEFEELGRIITALPDSQVNRLOA
 DNGENGLACMVNKHVDVQSHRSVYLPBWEAISEQVAPGGRGLVLTVAAYGE
 YGECVGTIELENNITDLQCKRCEBEVYPTGTGNCDSVAHQCTACVNSRNGYED
 YEVDITANVYKPTPEEYTVDRNHCNEVDYRGVYVNPPLPAGYMWTKLEYEPBTDK
 VWIEIGTEGKFLVDSVLELLMVE"

ORIGIN

```
Query Match      100.0%; Score 3687; DB 6; Length 3687;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3687; Conservative 0; Mismatches 0; Indels 0;
```

QY	1	TTGACTTCAAATAGAGAAAATAGAGAAATGAAATTAATAATGCTTTATCGATTCCAGCTGTA	60
Db	1	TTGACTTCAAATAGAGAAAATAGAGAAATGAAATTAATAATGCTTTATCGATTCCAGCTGTA	60
QY	61	TGCAATCATTTCCACAAATGGAATCTATCACAGATGCTCGTATTGAGGAATCTTTGTGT	120
Db	61	TGCAATCATTTCCACAAATGGAATCTATCACAGATGCTCGTATTGAGGAATCTTTGTGT	120
QY	121	ATAGCCGAGGGGAATAATATAAATCCACTTTTAGCGCATCAACAGTCCAAACGGGTATT	180
Db	121	ATAGCCGAGGGGAATAATATAAATCCACTTTTAGCGCATCAACAGTCCAAACGGGTATT	180
QY	181	AACATAGCTGGTAGAATACTAGGTGTATTAGGCGCTACCGTTTCTCGACAAATAGTCTGT	240
Db	181	AACATAGCTGGTAGAATACTAGGTGTATTAGGCGCTACCGTTTCTCGACAAATAGTCTGT	240
QY	241	TTTTATAGTTTTCTTTGTTGGTGAATTATGGCCCGCGCAGAGATCAGTGGGAAATTTTC	300
Db	241	TTTTATAGTTTTCTTTGTTGGTGAATTATGGCCCGCGCAGAGATCAGTGGGAAATTTTC	300
QY	301	CTAGAACATGTCGAACAACATTATAAATCAACAAATAACAGAAATGCTAGGAATACGGCA	360
Db	301	CTAGAACATGTCGAACAACATTATAAATCAACAAATAACAGAAATGCTAGGAATACGGCA	360
QY	361	CTTGCTCGAATACAAAGTTTAGGAGATTCCTTTAGAGCCTTCAACAGTCACTTTGAAGAT	420
Db	361	CTTGCTCGAATACAAAGTTTAGGAGATTCCTTTAGAGCCTTCAACAGTCACTTTGAAGAT	420
QY	421	TGGCTAGAAAAACCGTGATGATGCAAGAACGAGAAGTGTCTTTATACCCAATATATAGCC	480
Db	421	TGGCTAGAAAAACCGTGATGATGCAAGAACGAGAAGTGTCTTTATACCCAATATATAGCC	480
QY	481	TTAGAACTTGATTTTCTTAATGCGATGCGCTTTTCGCAATTAGAAACCAAGAAGTTCCA	540
Db	481	TTAGAACTTGATTTTCTTAATGCGATGCGCTTTTCGCAATTAGAAACCAAGAAGTTCCA	540
QY	541	TTTAAATGGTATATGCTCAAGCTGCAAAATTAACCTTATTTATGAGAGATGCTCT	600
Db	541	TTTAAATGGTATATGCTCAAGCTGCAAAATTAACCTTATTTATGAGAGATGCTCT	600
QY	601	CTTTTTGGTAGTAATTTGGCGTTACATCGCAGGAATTCAAAGTTTATATGAGCCCAA	660
Db	601	CTTTTTGGTAGTAATTTGGCGTTACATCGCAGGAATTCAAAGTTTATATGAGCCCAA	660
QY	661	GTGGAACAAAACGAGAGATTAATTCGACTATTGCGTAGAATGGTATAATACAGTCTTAAT	720
Db	661	GTGGAACAAAACGAGAGATTAATTCGACTATTGCGTAGAATGGTATAATACAGTCTTAAT	720
QY	721	AGCTTTAGAGGGAACAAATGCGCGAAGTTGGGTGGTATAATCAATTCGTTAGAGATCTA	780
Db	721	AGCTTTAGAGGGAACAAATGCGCGAAGTTGGGTGGTATAATCAATTCGTTAGAGATCTA	780
QY	781	AGCTTTAGGGGTATTAGATCTAGTGGCACTATTCCTCAAGCTATGACACTCGCACTTATCCA	840
Db	781	AGCTTTAGGGGTATTAGATCTAGTGGCACTATTCCTCAAGCTATGACACTCGCACTTATCCA	840
QY	841	ATAAATAACGAGTGTCAAGTTAAACAGGGAAGTTTATACAGACGCAATTTGAGCAACAGGG	900
Db	841	ATAAATAACGAGTGTCAAGTTAAACAGGGAAGTTTATACAGACGCAATTTGAGCAACAGGG	900

Qy	1	TTGACTTCAAATAGGAAAAATGAGAAATTAATAATGCTTTATCGATTCAGCTGTA	60
Dh <td>1</td> <th>TTGACTTCAAATAGGAAAAATGAGAAATTAATAATGCTTTATCGATTCAGCTGTA</th> <th>60</th>	1	TTGACTTCAAATAGGAAAAATGAGAAATTAATAATGCTTTATCGATTCAGCTGTA	60

QY 61 TCGAATCATTCACACAAATGGATCTATACACAGATGCTCGTATGTAGGATCTTTGTGT 120
 Db 61 TCGAATCATTCACACAAATGGATCTATACACAGATGCTCGTATGTAGGATCTTTGTGT 120
 QY 121 ATAGCCGAGGGGATATATCAATCCACTTGTGTAGCGCATCAACAGTCCAAACGGGTATT 180
 Db 121 ATAGCCGAGGGGATATATCAATCCACTTGTGTAGCGCATCAACAGTCCAAACGGGTATT 180
 QY 181 AACATAGCTGGTAGAACTACTAGGTGTATTAGGCGTACCGTTTGTGCACAAAATAGCTAGT 240
 Db 181 AACATAGCTGGTAGAACTACTAGGTGTATTAGGCGTACCGTTTGTGCACAAAATAGCTAGT 240
 QY 241 TTTTATAGTTTTCTTGTGTGTAATTAATGCGCCGCGCAGAGATCAGTGGGAAATTTTC 300
 Db 241 TTTTATAGTTTTCTTGTGTGTAATTAATGCGCCGCGCAGAGATCAGTGGGAAATTTTC 300
 QY 301 CTAGAACATGTCGAACAACTTATAAATCAACAAATAACAGAAATGCTAGGAATACGGCA 360
 Db 301 CTAGAACATGTCGAACAACTTATAAATCAACAAATAACAGAAATGCTAGGAATACGGCA 360
 QY 361 CTGCTCGATTACAAGGTTTAGGAGATTCTTTTAGAGCCCTATCAACAGTCACTTGAAGAT 420
 Db 361 CTGCTCGATTACAAGGTTTAGGAGATTCTTTTAGAGCCCTATCAACAGTCACTTGAAGAT 420
 QY 421 TGGCTAGAAAACCGTGATGATGCAAGAAACGAGAAGTGTCTTTATACCCCAATATAGCC 480
 Db 421 TGGCTAGAAAACCGTGATGATGCAAGAAACGAGAAGTGTCTTTATACCCCAATATAGCC 480
 QY 481 TTAGAACCTTGAATTTCTTAAATGCGATGCGCGCTTTTCGCAATTAAGAACCAAGAGTCCA 540
 Db 481 TTAGAACCTTGAATTTCTTAAATGCGATGCGCGCTTTTCGCAATTAAGAACCAAGAGTCCA 540
 QY 541 TTATTAATGCTATATGCTCAAGCTGCAAAATTTACACCTATTTATTTAGAGAGTGCCTCT 600
 Db 541 TTATTAATGCTATATGCTCAAGCTGCAAAATTTACACCTATTTATTTAGAGAGTGCCTCT 600
 QY 601 CTTTTTGGTAGTGAATTTGGGCTTACATCGCAGAAATCAACGTTATATATAGCGCCAA 660
 Db 601 CTTTTTGGTAGTGAATTTGGGCTTACATCGCAGAAATCAACGTTATATATAGCGCCAA 660
 QY 661 GTGGAACAAACGAGAGATTTCCGACTATTTGGTAGAATGGTATATATACAGTCTTAAT 720
 Db 661 GTGGAACAAACGAGAGATTTCCGACTATTTGGTAGAATGGTATATATACAGTCTTAAT 720
 QY 721 AGCTTGAGAGGCAAAATGCGCAAGTTGGGTGGTGTATTAATCAATTTCCGTAGAGATCTA 780
 Db 721 AGCTTGAGAGGCAAAATGCGCAAGTTGGGTGGTGTATTAATCAATTTCCGTAGAGATCTA 780
 QY 781 ACGTTAGGGTATTAGATCTAGTGGCACTATTTCCCAAGCTATGACACTCGCACTTATCCA 840
 Db 781 ACGTTAGGGTATTAGATCTAGTGGCACTATTTCCCAAGCTATGACACTCGCACTTATCCA 840
 QY 841 ATAAATACGAGTCTCAGTTTAAACAGGGAAGTTTATACAGACGCAATTTGAGCAACAGG 900
 Db 841 ATAAATACGAGTCTCAGTTTAAACAGGGAAGTTTATACAGACGCAATTTGAGCAACAGG 900
 QY 901 GTAATATGCAAGTATGAATTTGGTATAATAATGCACCTTCGTTTTCGGCTATAGAG 960
 Db 901 GTAATATGCAAGTATGAATTTGGTATAATAATGCACCTTCGTTTTCGGCTATAGAG 960
 QY 961 ACTGCGGTTATCGGAAGCCGCACTACTACTGATTTTCTAGAAACAACTTATTTTATG 1020
 Db 961 ACTGCGGTTATCGGAAGCCGCACTACTACTGATTTTCTAGAAACAACTTATTTTATG 1020
 QY 1021 ACTTCATCAGATGAGTGTCTAGGCATATGACTTACTTGGCGGGGACACAAATTCAA 1080
 Db 1021 ACTTCATCAGATGAGTGTCTAGGCATATGACTTACTTGGCGGGGACACAAATTCAA 1080
 QY 1081 TCTCGGCCAATAGAGCGGATTAATACCTCAACGATGGGTCTACCAATCTTCTATT 1140
 Db 1081 TCTCGGCCAATAGAGCGGATTAATACCTCAACGATGGGTCTACCAATCTTCTATT 1140
 QY 1141 AATCCTGTAAGATTATCATTTCTCTCTCGAGACGTATATTGGACTGAATCATATGACGGA 1200

Db 1141 AATCCTGTAAGATTATCATTTCTCTCTCGAGACGTATATTGGACTGAATCATATGCAGGA 1200
 QY 1201 GTGCTTCTATGGGGAATTTTACCTTTGAAACCTTATTTCATGGTGTCCCTACTGTTAGATTTAAT 1260
 Db 1201 GTGCTTCTATGGGGAATTTTACCTTTGAAACCTTATTTCATGGTGTCCCTACTGTTAGATTTAAT 1260
 QY 1261 TTTAGGAACCTCTCAGAAATACTTTTGAAGAGGTACTGCTAACTATATAGTCAACCTATGAG 1320
 Db 1261 TTTAGGAACCTCTCAGAAATACTTTTGAAGAGGTACTGCTAACTATATAGTCAACCTATGAG 1320
 QY 1321 TCACTGGGCTTCAATTTAAAGATTCAGAAATCGAATTTACCAAGAAACAAACAGAACGA 1380
 Db 1321 TCACTGGGCTTCAATTTAAAGATTCAGAAATCGAATTTACCAAGAAACAAACAGAACGA 1380
 QY 1381 CCAAAATTAATGAATCATATAGTCTATAGTTATCTCAGATAGGGCTCAATTCACAACTTAGG 1440
 Db 1381 CCAAAATTAATGAATCATATAGTCTATAGTTATCTCAGATAGGGCTCAATTCACAACTTAGG 1440
 QY 1441 GTGCATGTACAGTATATTCTTGGAGCGCACCGTAGTGCAGATCGTACAAATACCATTAGT 1500
 Db 1441 GTGCATGTACAGTATATTCTTGGAGCGCACCGTAGTGCAGATCGTACAAATACCATTAGT 1500
 QY 1501 TCAGATAGCAATAACAAATACCATTTGGTAAATCAATTCACCTTAATTCAGGTACTCT 1560
 Db 1501 TCAGATAGCAATAACAAATACCATTTGGTAAATCAATTCACCTTAATTCAGGTACTCT 1560
 QY 1561 GTAGTCAGTGGCCAGGATTTACAGAGGGGATATTAATCCGAACTAACGTTTAATGGTAGT 1620
 Db 1561 GTAGTCAGTGGCCAGGATTTACAGAGGGGATATTAATCCGAACTAACGTTTAATGGTAGT 1620
 QY 1621 GTACTAAGTAGTGGTCTTAATTTTAAATACATCAATTCAGCGGTATCCGCTGAGAGTT 1680
 Db 1621 GTACTAAGTAGTGGTCTTAATTTTAAATACATCAATTCAGCGGTATCCGCTGAGAGTT 1680
 QY 1681 CGTTATGCTGCTTCTCAACAAATGGTCTGAGGGTAACTGTGCGAGGAGTACTACTTTT 1740
 Db 1681 CGTTATGCTGCTTCTCAACAAATGGTCTGAGGGTAACTGTGCGAGGAGTACTACTTTT 1740
 QY 1741 GATCAAGGATTCCTCTAGTACTATGAGTCAAAATGAGTCTTTGACATCTCAATCATTTAGA 1800
 Db 1741 GATCAAGGATTCCTCTAGTACTATGAGTCAAAATGAGTCTTTGACATCTCAATCATTTAGA 1800
 QY 1801 TTTGCAAGATTTCTCTGTAGTATTAGTGCATCTGGCAGTCAAACTGCTGGAATAAGTATA 1860
 Db 1801 TTTGCAAGATTTCTCTGTAGTATTAGTGCATCTGGCAGTCAAACTGCTGGAATAAGTATA 1860
 QY 1861 AGTAATAATGCAAGTACAAACGTTTCACTTTGATAAATTTGAATTCATTTCCAATTAAT 1920
 Db 1861 AGTAATAATGCAAGTACAAACGTTTCACTTTGATAAATTTGAATTCATTTCCAATTAAT 1920
 QY 1921 GCAACCTTCAAGCAGAAATACGATTTTAGAAGGGCGCAAGGGCGGTGAATGCTCTGTTT 1980
 Db 1921 GCAACCTTCAAGCAGAAATACGATTTTAGAAGGGCGCAAGGGCGGTGAATGCTCTGTTT 1980
 QY 1981 ACTAATAACGAATCCAAAGAGATTGAAACAGATGTGACAGATTTATCATATTGATCAAGTA 2040
 Db 1981 ACTAATAACGAATCCAAAGAGATTGAAACAGATGTGACAGATTTATCATATTGATCAAGTA 2040
 QY 2041 TCCAAATTTAGTGGCGTGTATTCGGATGAATTTCTGCTTAGATGAAAAGAGAGAAATTAAT 2100
 Db 2041 TCCAAATTTAGTGGCGTGTATTCGGATGAATTTCTGCTTAGATGAAAAGAGAGAAATTAAT 2100
 QY 2101 GAGAAAGTGAATATATGCGAAACGACTCAGTGTGAAAGAACTTACTTCCAAAGATCCAAAC 2160
 Db 2101 GAGAAAGTGAATATATGCGAAACGACTCAGTGTGAAAGAACTTACTTCCAAAGATCCAAAC 2160
 QY 2161 TTCAATCCATCAATTAAGCAACCAAGTCTTCAATATCTAATGAGCAATCGAATTTTCA 2220
 Db 2161 TTCAATCCATCAATTAAGCAACCAAGTCTTCAATATCTAATGAGCAATCGAATTTTCA 2220
 QY 2221 TCTATCCATGAACAACTGCAATGATGTTGGGAGTGAGAACATTACAATCCAGGAA 2280


```
Db 2221 TCTATCCATGAACAATCTGAACATGGATGGTGGGAAGTGAGAACATTTACAATCCAGAA 2280
Qy 2281 GGAATGACGTATTTAAAGAGATTACGTCACTACCGGGGACTTTTAAATGAGTGTAT 2340
Db 2281 GGAATGACGTATTTAAAGAGATTACGTCACTACCGGGGACTTTTAAATGAGTGTAT 2340
Qy 2341 CCGACGTATTTATATCAAAAATAGGAGAGTCGGAATTTAAAGCTTATATCTCGTACCAA 2400
Db 2341 CCGACGTATTTATATCAAAAATAGGAGAGTCGGAATTTAAAGCTTATATCTCGTACCAA 2400
Qy 2401 TTAAGAGGTATATTTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGTATAATGCG 2460
Db 2401 TTAAGAGGTATATTTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGTATAATGCG 2460
Qy 2461 AAACATGAACATTGGATGTTCCAGGTACCGAGTCGGATGCGCGCTTTTCAGTTGAAAGC 2520
Db 2461 AAACATGAACATTGGATGTTCCAGGTACCGAGTCGGATGCGCGCTTTTCAGTTGAAAGC 2520
Qy 2521 CCAATCGGAAGTCCGAGAACCGAATCGATGCGCACCAATTTTGAATGGAATCCCTGAT 2580
Db 2521 CCAATCGGAAGTCCGAGAACCGAATCGATGCGCACCAATTTTGAATGGAATCCCTGAT 2580
Qy 2581 CTAGATTGTTCTCGACAGATGAGAAAAATGTCGCATCATTCGCCATCATTTCTCTTTG 2640
Db 2581 CTAGATTGTTCTCGACAGATGAGAAAAATGTCGCATCATTCGCCATCATTTCTCTTTG 2640
Qy 2641 GATATTGATATTGGATGCACAGACTTGCATCAGAACTAGGCGTGTGGGTGTTATCAAG 2700
Db 2641 GATATTGATATTGGATGCACAGACTTGCATCAGAACTAGGCGTGTGGGTGTTATCAAG 2700
Qy 2701 ATTAAGACGAGGAGGTGATGCAAGACTAGGGAATCTGGAATTTATGAGAGAAACCA 2760
Db 2701 ATTAAGACGAGGAGGTGATGCAAGACTAGGGAATCTGGAATTTATGAGAGAAACCA 2760
Qy 2761 TTATTAGGAGACGACTGTCGTGTCAGAGACGACAGAAAAAATGCGAGACAAACGT 2820
Db 2761 TTATTAGGAGACGACTGTCGTGTCAGAGACGACAGAAAAAATGCGAGACAAACGT 2820
Qy 2821 GAAAAACTACAATTGAAAAACAAACGAGTATATACAGAGGCAAAAGCTGTGGATGCT 2880
Db 2821 GAAAAACTACAATTGAAAAACAAACGAGTATATACAGAGGCAAAAGCTGTGGATGCT 2880
Qy 2881 TTATTGATGATCTCAATATATAGATTACAGCGGATCAACACATTTGGATGATTCAT 2940
Db 2881 TTATTGATGATCTCAATATATAGATTACAGCGGATCAACACATTTGGATGATTCAT 2940
Qy 2941 GCGCAGATAACTGTTTCATCGAATTCGAGAGCTTATCTGTCAGAAATATCTGTTATC 3000
Db 2941 GCGCAGATAACTGTTTCATCGAATTCGAGAGCTTATCTGTCAGAAATATCTGTTATC 3000
Qy 3001 CCGGGTGAATGCGGAAATTTTGAAGAAATTTAGAGGTCGCAATTCACCTGCAATCTCC 3060
Db 3001 CCGGGTGAATGCGGAAATTTTGAAGAAATTTAGAGGTCGCAATTCACCTGCAATCTCC 3060
Qy 3061 CTATACGATCGGAATATGCTGTTAAATATGATGATTTTAAATGATGATGATGCTG 3120
Db 3061 CTATACGATCGGAATATGCTGTTAAATATGATGATTTTAAATGATGATGATGCTG 3120
Qy 3121 AATGTAAGGGCATGTAGATGTACACAGGCCATCACCGTCTGCTGTTGTTATCCCA 3180
Db 3121 AATGTAAGGGCATGTAGATGTACACAGGCCATCACCGTCTGCTGTTGTTATCCCA 3180
Qy 3181 GAATGGAAGCAGAAAGTGTACAGACAGTTCCGCTGTCGCGGGCGTGGCTATATCTTC 3240
Db 3181 GAATGGAAGCAGAAAGTGTACAGACAGTTCCGCTGTCGCGGGCGTGGCTATATCTTC 3240
Qy 3241 CGTGTACAGCGTACAAAGAGGATATGAGAGGTTGTGTAAACGATCCATGAATCCGAG 3300
Db 3241 CGTGTACAGCGTACAAAGAGGATATGAGAGGTTGTGTAAACGATCCATGAATCCGAG 3300
Qy 3301 AACAAATACAGCGAACTAAATTTAAATACTGTGAAGAGGAGTGTATCCACCGAT 3360
Db 3301 AACAAATACAGCGAACTAAATTTAAATACTGTGAAGAGGAGTGTATCCACCGAT 3360
```

RESULT 3

```
AX098667 LOCUS 4173 bp DNA linear PAT 02-APR-2001
DEFINITION Sequence 37 from Patent WO0119859.
ACCESSION AX098667
VERSION AX098667.1 GI:13537912
KEYWORDS Bacillus thuringiensis
SOURCE Bacillus thuringiensis
ORGANISM Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
```

REFERENCE

```
1. Baum, J.A., Chu, C.R., Donovan, W.P., Gilmer, A.J. and Rupar, M.J.
Lepidopteran-active bacillus thuringiensis delta-endotoxin
compositions and methods of use
Patent: WO 0119859-A 37 22-MAR-2001,
MONSANTO COMPANY (US)
```

FEATURES

```
source
1. 4173
/organism="Bacillus thuringiensis"
/mol_type="unassigned DNA"
/db_xref="taxon:1428"
1. 3687
/notes="unnamed protein product"
/codon_start=1
/transl_table=11
/protein_id="CAC35766.1"
/db_xref="GI:13537913"
```

```
/translation="MISNRKNEIINALSIPAVSHSTQMDLSPDRIEDSLCIARG
NNINPLVSTAVQTGINIAGRIILVIGVPAGQIASFYSLVGLMWRGRDQMEIFLE
HVEQLNQQITENARNTALRQLGDSFRAYQQSLDLENDLDRATSLVLYTQYTA
LEUDFLNAPLFAIRNOEVLPLMVAQAANLHLLLDASLFGSEFLGTQEIQRYYE
ROYEQTRDYSDYVWYNTGLNSLRGTNAASWYRNVQFRDLTLGLVLDLVALPSYDT
RPTYNISQALTREVTDAIGATGYNWASNNWNNAPSAIETAVIRSPHLLDLE
QLTIFTSRSRSATRWGHTIQRPIGGGLNTSTHGSTNTSINPVRSLPFSRDV
WYTESAGVLLWGIYLEPIHGVPVTRFRNPQNTFERTGNTANSQPYESPLQKDE
TELPPTTTPPNYSYSHRLSLTISQSRVHVYVSWTHRSADRTNTISDSITQIP
LVKSFNLNGLSVSGPFGDIIRTNVNGSVLSMGLNPNFTSLQRYRVRVRAASQ
TWLVRYVGSSTTFDQGFSTMSANSLTSQSFRFAEPVGIISASQSTAGISLNNNA
GRQTFHDKTFIPITATFEAYDLERAQAVNALFTNTPRLKTDVTDYHDQVSN
LVACDEFCLDEKRELLEKVKAKRLSDERNLLQDPNFTSINKPQFISTNEQSTF
SIHQESEHWGWSENITIQEKNVFRKYNVTLFPTNECYTLYLQKIGSELKAYTR
YQLRGVTEDSQDLEIYLLIRNKHETLDVPGTESVMPLESVPSIGRCGNRCAPHE
WNPDLDCSRDGEKKAHHFSLDIDIGCTDLHENLGVWVFKITQEGHARGNLUE
FIEKPLLLGALSVRKAEKKWRDKLETKRVYVTEAKEAVDALFVDSQVNRLOA
DTNIGHMHAADKLVRIRIAYLSLSVPGVNAEIIPEELSGRIITSLISLDARNVVKQ
GDFNGLACNVKGVHDVQOQSHRSVLVPEWEAEVSQAVRVCPRGRIILRVYTKSG
```

YGBGCVTHIEIENNTDELKFKNCEBEEVYPTDGTGNDYTAHOGTAACNSRNAGYBDA
YEVDTTASVNYKYTEBEYTDVRRDNHCEYDRGYNYPPLPAGYVTKELEYFPETDK
WVIEIGTEGTFIVDSIELLLMBE"

ORIGIN

Query Match		99.4%; Score 3666.2; DB 6; Length 4173;
Best Local Similarity		99.6%; Pred. No. 0;
Matches 3674; Conservative		0; Mismatches 13; Indels 0; Gaps 0;
Qy	1	TTGACTTCAAAATAGGAAAATGAGAATGAATATATAATGCTTTATCGATTCCAGCTGTGA 60
Db	1	TTGACTTCAAAATAGGAAAATGAGAATGAATATATAATGCTTTATCGATTCCAGCTGTGA 60
Qy	61	TGCAATCATTTCCACACAAATGAGTCTATCACAGATGCTCGTATGAGGATTTCTTTGTGT 120
Db	61	TGCAATCATTTCCACACAAATGAGTCTATCACAGATGCTCGTATGAGGATTTCTTTGTGT 120
Qy	121	ATAGCCGAGGGGAATATATCAATCCACTGTTAGCGCATCAACAGTCCAAACGGGTATT 180
Db	121	ATAGCCGAGGGGAATATATCAATCCACTGTTAGCGCATCAACAGTCCAAACGGGTATT 180
Qy	181	AACATAGCTGCTAGAACTACTAGGTGATATTAGGGGTACCGTTTCTGGACAAATAGCTAGT 240
Db	181	AACATAGCTGCTAGAACTACTAGGTGATATTAGGGGTACCGTTTCTGGACAAATAGCTAGT 240
Qy	241	TTTTATAGTTTTCTTGTGTGTAATTATGCCCCGGCGGAGAGATCAGTGGGAAATTTTC 300
Db	241	TTTTATAGTTTTCTTGTGTGTAATTATGCCCCGGCGGAGAGATCAGTGGGAAATTTTC 300
Qy	301	CTAGAACATGTCGAACAACTTATAATCAACAATAACAGAAAATGCTAGGAATACGGCA 360
Db	301	CTAGAACATGTCGAACAACTTATAATCAACAATAACAGAAAATGCTAGGAATACGGCA 360
Qy	361	CTTGCTCGATTACAAGTTTAGAGATTCTTTAGAGCCCTATCAACAGTCACTTGAAGAT 420
Db	361	CTTGCTCGATTACAAGTTTAGAGATTCTTTAGAGCCCTATCAACAGTCACTTGAAGAT 420
Qy	421	TGGCTAGAAAACCGTGATGTCAGAAACGAGAAAGTGTCTTTATACCCAAATATAGCC 480
Db	421	TGGCTAGAAAACCGTGATGTCAGAAACGAGAAAGTGTCTTTATACCCAAATATAGCC 480
Qy	481	TTAGAACTTGATTTCTTAATGCGATGCCCTTTTCGCAATTAGAAACGAAGTTCCA 540
Db	481	TTAGAACTTGATTTCTTAATGCGATGCCCTTTTCGCAATTAGAAACGAAGTTCCA 540
Qy	541	TTAATTAATGCTATGCTCAAGTGCAGATTTTACACCTATTATTATTGAGAGATGCTCT 600
Db	541	TTAATTAATGCTATGCTCAAGTGCAGATTTTACACCTATTATTATTGAGAGATGCTCT 600
Qy	601	CTTTTGGTATGAAATTTGGGCTTACATCGCAGGAAATTCACGTTATTATGAGCGCCAA 660
Db	601	CTTTTGGTATGAAATTTGGGCTTACATCGCAGGAAATTCACGTTATTATGAGCGCCAA 660
Qy	661	GTGGAACAAACGAGAGATTATTCGGACTATTGGTAGAATGGTATATACAGTCTAAAT 720
Db	661	GTGGAACAAACGAGAGATTATTCGGACTATTGGTAGAATGGTATATACAGTCTAAAT 720
Qy	721	AGCTTGAGAGGGAACAATGCGCAAGTTGGTGGTTTATAATCAATTCGCTAGAGATCTA 780
Db	721	AGCTTGAGAGGGAACAATGCGCAAGTTGGTGGTTTATAATCAATTCGCTAGAGATCTA 780
Qy	781	ACGTTAGGGGTATTAGATCTAGTGGCACTATTCCTCAAGCTATGACACTCTATATCCA 840
Db	781	ACGTTAGGGGTATTAGATCTAGTGGCACTATTCCTCAAGCTATGACACTCTATATCCA 840
Qy	841	ATAAATACGAGTCTCAGTTTAAAGGGAAGTTTATACAGACCAATGGAGCAACAGGG 900
Db	841	ATAAATACGAGTCTCAGTTTAAAGGGAAGTTTATACAGACCAATGGAGCAACAGGG 900
Qy	901	GTAATATGCAAGTATGAATGGTATAATAATGCACTTCGTTTTCGCTATATAGAG 960
Db	901	GTAATATGCAAGTATGAATGGTATAATAATGCACTTCGTTTTCGCTATATAGAG 960

Qy	961	ACTGCGGTTATCCGAAGCCGCACTACTCTGATTTTCTAGAAACAATTCAATTTTATG 1020
Db	961	ACTGCGGTTATCCGAAGCCGCACTACTCTGATTTTCTAGAAACAATTCAATTTTATG 1020
Qy	1021	ACTTCATCAGATGGAGTCTACTAGGCATATGACTTACTGGGGGGGACACAATTCAA 1080
Db	1021	ACTTCATCAGATGGAGTCTACTAGGCATATGACTTACTGGGGGGGACACAATTCAA 1080
Qy	1081	TCCTCGGCCAATAGGAGCGGATTAATAATACCTCAACATGGGTCTACCAATATCTTATT 1140
Db	1081	TCCTCGGCCAATAGGAGCGGATTAATAATACCTCAACATGGGTCTACCAATATCTTATT 1140
Qy	1141	AATCTCTGTAAGTATATCACTTCTCTCGAGACGTATATTGGACTGAATCATATGAGGA 1200
Db	1141	AATCTCTGTAAGTATATCACTTCTCTCGAGACGTATATTGGACTGAATCATATGAGGA 1200
Qy	1201	GTGCTTCTATGGGGAATTTACCTTGAACCTTATTCATGGGTGCCCTACTGTTAGATTAAT 1260
Db	1201	GTGCTTCTATGGGGAATTTACCTTGAACCTTATTCATGGGTGCCCTACTGTTAGATTAAT 1260
Qy	1261	TTTAGGAACCTCAGAAATATCTTTTGAAGAGGTACTGCTAACTATATAGTCAACCTATGAG 1320
Db	1261	TTTAGGAACCTCAGAAATATCTTTTGAAGAGGTACTGCTAACTATATAGTCAACCTATGAG 1320
Qy	1321	TCACCTGGGCTTCAATTAAGAAATCAGAAATCGAATACCAACAGAAACAACAGAACGA 1380
Db	1321	TCACCTGGGCTTCAATTAAGAAATCAGAAATCGAATACCAACAGAAACAACAGAACGA 1380
Qy	1381	CGAAATATGAAATCATATAGTCAATAGTTCATCATAGGGCTCATTTTCAATCTAGG 1440
Db	1381	CGAAATATGAAATCATATAGTCAATAGTTCATCATAGGGCTCATTTTCAATCTAGG 1440
Qy	1441	GTGCATGTACCAAGTATATTTTGGAGCGCACCGTAGTGCAGATCGTACAAATACCATTAGT 1500
Db	1441	GTGCATGTACCAAGTATATTTTGGAGCGCACCGTAGTGCAGATCGTACAAATACCATTAGT 1500
Qy	1501	TCAGATAGCAATACAAATACCAATTCGTTGTAATCATCTTAACTTAACTTAACTTAACT 1560
Db	1501	TCAGATAGCAATACAAATACCAATTCGTTGTAATCATCTTAACTTAACTTAACTTAACT 1560
Qy	1561	GTAGTCAGTGGGCCAGGATTTACAGAGGGGATATTAATCCGAACTAACCGTTAATGGTAGT 1620
Db	1561	GTAGTCAGTGGGCCAGGATTTACAGAGGGGATATTAATCCGAACTAACCGTTAATGGTAGT 1620
Qy	1621	GTACTAAGTATGGGTCTTAAATTTTAAATATACATCAATACAGCGGTATCGCGTGAAGTT 1680
Db	1621	GTACTAAGTATGGGTCTTAAATTTTAAATATACATCAATACAGCGGTATCGCGTGAAGTT 1680
Qy	1681	CGTTATGCTGCTCTCAAAACAATGGTCTCGAGGGTAACTGTCGAGGGAGTACTACTTTT 1740
Db	1681	CGTTATGCTGCTCTCAAAACAATGGTCTCGAGGGTAACTGTCGAGGGAGTACTACTTTT 1740
Qy	1741	GATCAAGGATTCCTAGTACTATGAGTCAAAATGAGTCTTTGACATCTCAATCATTTAGA 1800
Db	1741	GATCAAGGATTCCTAGTACTATGAGTCAAAATGAGTCTTTGACATCTCAATCATTTAGA 1800
Qy	1801	TTTGCAAGAAATTTCTCTAGGTATTTAGTGCATCTGGCAGTCAAACTGCTGGAATAAGTATA 1860
Db	1801	TTTGCAAGAAATTTCTCTAGGTATTTAGTGCATCTGGCAGTCAAACTGCTGGAATAAGTATA 1860
Qy	1861	AGTAATATGAGGTAGACAACGTTTCTCTTTGATAAAATTTGAATTTCAATTTCAATTTACT 1920
Db	1861	AGTAATATGAGGTAGACAACGTTTCTCTTTGATAAAATTTGAATTTCAATTTCAATTTACT 1920
Qy	1921	GCAACCTTCGAGACAGAAATACGATTTTAGAAAGGGCCCAAGAGCGGTGAATGCTCTGTTT 1980
Db	1921	GCAACCTTCGAGACAGAAATACGATTTTAGAAAGGGCCCAAGAGCGGTGAATGCTCTGTTT 1980
Qy	1981	ACTAATACGAATCCAAAGAGATTGAAAAACAGATGTGACAGATTATCATATTGATCAAGTA 2040
Db	1981	ACTAATACGAATCCAAAGAGATTGAAAAACAGATGTGACAGATTATCATATTGATCAAGTA 2040
Qy	2041	TCCAATTTAGTGGCGTGTATTTCGGATGAATCTGCTGTAGTCAAAAGAGAGATTTACTT 2100

Db 2041 TCCAAATTTAGTGGCGTGTATCGGATGAATCTGCTTAGATGAAGAAGAGATTAATT 2100
Qy
2101 GAGAAAGTGAAATATGCGAAACGACTCAGTGATGAAAGAACTTATCTCCAGAGTCCAAC 2160
Db 2101 GAGAAAGTGAAATATGCGAAACGACTCAGTGATGAAAGAACTTATCTCCAGAGTCCAAC 2160
Qy 2161 TCCATATCCATCAATAGAACACAGACTTCATATCTACTAATGAGCAATCGAATTTTCA 2220
Db 2161 TCCATATCCATCAATAGAACACAGACTTCATATCTACTAATGAGCAATCGAATTTTCA 2220
Qy 2221 TCTATCATGAACAATCTGAACATGGATGGTGGGAAGTGAGAACATTTACAATCCAGGAA 2280
Db 2221 TCTATCATGAACAATCTGAACATGGATGGTGGGAAGTGAGAACATTTACAATCCAGGAA 2280
Qy 2281 GGAATGACGTATTTAAAGAAATTAAGTCACTACCGGGGACTTTTAATAGTGTAT 2340
Db 2281 GGAATGACGTATTTAAAGAAATTAAGTCACTACCGGGGACTTTTAATAGTGTAT 2340
Qy 2341 CCGACGTATTTATCAAAAATAGGAGAGTCCGAATTTAAAGCTTATCTCGTACCAA 2400
Db 2341 CCGACGTATTTATCAAAAATAGGAGAGTCCGAATTTAAAGCTTATCTCGTACCAA 2400
Qy 2401 TTAAGAGGTATATTGAAGATAGTCAAGATTTAGAGATATATTGATTCGTTTAAATGCG 2460
Db 2401 TTAAGAGGTATATTGAAGATAGTCAAGATTTAGAGATATATTGATTCGTTTAAATGCG 2460
Qy 2461 AAACATGAACATTTGGATGTTTCCAGGTACCGAGTCCGATGGCGCTTTTCAAGTGAAGC 2520
Db 2461 AAACATGAACATTTGGATGTTTCCAGGTACCGAGTCCGATGGCGCTTTTCAAGTGAAGC 2520
Qy 2521 CCAATCGAAGGTGCGGAGAACCGAATTCGATCGCACACATTTTGAATGGAATCCTGAT 2580
Db 2521 CCAATCGAAGGTGCGGAGAACCGAATTCGATCGCACACATTTTGAATGGAATCCTGAT 2580
Qy 2581 CTAGATTGTTCTCGACAGATGGAGAAATGTCGCGCATATCCCATCATTTCTCTTTG 2640
Db 2581 CTAGATTGTTCTCGACAGATGGAGAAATGTCGCGCATATCCCATCATTTCTCTTTG 2640
Qy 2641 GATATTGATATTGGATGCACAGACTTGCATGAGAAATCTAGCGGTGCGGTGATTTCAAG 2700
Db 2641 GATATTGATATTGGATGCACAGACTTGCATGAGAAATCTAGCGGTGCGGTGATTTCAAG 2700
Qy 2701 ATTAAGACGAGGAAGTGTATGCAAGACTAGGAAATCTGGAATTTATGAAGAGAAACCA 2760
Db 2701 ATTAAGACGAGGAAGTGTATGCAAGACTAGGAAATCTGGAATTTATGAAGAGAAACCA 2760
Qy 2761 TTATTAGGAGAGCACTGTCTCGTGTGAAGAGAGCAGAGAAATGCGAGACAAACGT 2820
Db 2761 TTATTAGGAGAGCACTGTCTCGTGTGAAGAGAGCAGAGAAATGCGAGACAAACGT 2820
Qy 2821 GAAAACTTACAATTTGGAACCAAAACGAGTATATACAGAGGCAAAAGAGCTGTGATGCT 2880
Db 2821 GAAAACTTACAATTTGGAACCAAAACGAGTATATACAGAGGCAAAAGAGCTGTGATGCT 2880
Qy 2881 TTATTTGTAGATCTCAATATAATAGATTAACAGCGGATCAAAACATTTGCGATGATTCAT 2940
Db 2881 TTATTTGTAGATCTCAATATAATAGATTAACAGCGGATCAAAACATTTGCGATGATTCAT 2940
Qy 2941 CCGGACAGATAAATTTGTTATCGAATTTGAGAGGCTTATCTGTCAGAAATTTATCTGTTATC 3000
Db 2941 CCGGACAGATAAATTTGTTATCGAATTTGAGAGGCTTATCTGTCAGAAATTTATCTGTTATC 3000
Qy 3001 CCGGCTGTAAATGCGGAAATTTTGAAGAAATTTAGAAAGTCCGATTTATCTGCAATCTCC 3060
Db 3001 CCGGCTGTAAATGCGGAAATTTTGAAGAAATTTAGAAAGTCCGATTTATCTGCAATCTCC 3060
Qy 3061 CTATACGATCGAGAAATGCTGTTTAAAGATGTTTAAATGATGATGATGATGATGATGATG 3120
Db 3061 CTATACGATCGAGAAATGCTGTTTAAAGATGTTTAAATGATGATGATGATGATGATGATG 3120
Qy 3121 AATGTAAGGCGCATGTAGATGTAACAAGAGCCATCACCGTTCCTGCTTGTATATCCCA 3180

Db 3121 AATGTAAGGCGCATGTAGATGTAACAAGAGCCATCACCGTTCCTGCTTGTATATCCCA 3180
Qy 3181 GAATGGGAAGCAGAAGTGTCTCAAGCAGTTCGCGTCTGTCCGGGCGTGCCTATATCTC 3240
Db 3181 GAATGGGAAGCAGAAGTGTCTCAAGCAGTTCGCGTCTGTCCGGGCGTGCCTATATCTC 3240
Qy 3241 CGTGTCAACGCTACAAAGAGGATATGAGAGGTTGTCTAAAGTCCATGAATCGAG 3300
Db 3241 CGTGTCAACGCTACAAAGAGGATATGAGAGGTTGTCTAAAGTCCATGAATCGAG 3300
Qy 3301 AACAAATACAGACGAATCTAAATTTAAAACTGTGAAGAGGAGTGTATCCAAACGGAT 3360
Db 3301 AACAAATACAGACGAATCTAAATTTAAAACTGTGAAGAGGAGTGTATCCAAACGGAT 3360
Qy 3361 ACAGGAACGTGTATGATTAATCTGCACACCAAGGTACAGCAGTATGTAATTTCCCGTAA 3420
Db 3361 ACAGGAACGTGTATGATTAATCTGCACACCAAGGTACAGCAGTATGTAATTTCCCGTAA 3420
Qy 3421 GCTGGATATGAGCATCATATGAAGTTGTACTACAGCATCTGTTAATTTACAAACCGACT 3480
Db 3421 GCTGGATATGAGCATCATATGAAGTTGTACTACAGCATCTGTTAATTTACAAACCGACT 3480
Qy 3481 TATCAAGAAAGAAACGATATACAGATGTACGAAGAGATAATCAITTTGTAATATGACAGAGG 3540
Db 3481 TATCAAGAAAGAAACGATATACAGATGTACGAAGAGATAATCAITTTGTAATATGACAGAGG 3540
Qy 3541 TATGTGAATTTATCCACATACAGCTGGTTATATGACAAAGAAATTTAGAAATTTCTCCCA 3600
Db 3541 TATGTGAATTTATCCACATACAGCTGGTTATATGACAAAGAAATTTAGAAATTTCTCCCA 3600
Qy 3601 GAAACCGATGAAGTATGATTTGAGATTGGAGAAACCGAAGGAGTATTATTGTAGACAGC 3660
Db 3601 GAAACCGATGAAGTATGATTTGAGATTGGAGAAACCGAAGGAGTATTATTGTAGACAGC 3660
Qy 3661 GTGGAATTTACTCTCTTATGAGGAATAG 3687
Db 3661 ATAGAATTACTCTTATGAGGAATAG 3687

RESULT 4

AF077326 LOCUS 3684 bp DNA linear BCT 26-AUG-1998
DEFINITION Bacillus thuringiensis CryIb delta-endotoxin gene, complete cds.
ACCESSION AF077326
VERSION AF077326.1 GI:3360518
KEYWORDS
SOURCE
ORGANISM
Bacillus thuringiensis
Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
REFERENCE 1 (bases 1 to 3684)
AUTHORS Payne, J., Cummings, D.A., Cannon, R.J.C., Narva, K.E. and Stelman, S.J.
TITLE Bacillus thuringiensis genes encoding lepidopteran-active toxins
JOURNAL Patent: US 5723758 03-MAR-1998; Mycogen Corporation; San Diego, CA
REFERENCE 2 (bases 1 to 3684)
AUTHORS Stelman, S.J.
TITLE Direct Submission
JOURNAL Submitted (08-JUL-1998) Molecular Biology, Mycogen Corporation, 5501 Oberlin Dr., San Diego, CA 92121, USA
FEATURES
source
1.3684
/organism="Bacillus thuringiensis"
/mol_type="genomic DNA"
/strain="PS158C2"
/db_xref="taxon:1428"
/plasmid="pMYC2383"
1.3684
/codon_start=1
/transl_table=11
/product="CryIb delta-endotoxin"
/protein_id="AAC32850.1"
/db_xref="GI:3360519"
CDS

/translation="WTSNRKNEIINALSPAVNSHSAQWNLSDARIEDSICAE
NLDPFVSAVQTGINIARILGVGFAGQASFYVLSGELWDRDPWEI
HVLQITQVNTENRAGILQGLNSFRAGYQOSLEDNRDADRSTRVLT
LEIDFLNAMPFAIRNQEVPLVAQANLILDRASLFGSEGLTQSEYRVE
ROKEDRSDYCAWNTVPLGLNLGTNAESWLRNQYRDLTLGVLDIALP
RVYPMNTSAOLTRIEIYDPIGRNAPSGFASPTMENNAPSAEIAVRP
PEQLTIPSVLSRNSQYNNVYWHRLSRTIRGLSTSTHGNTSTINP
DVYRTSFAGINILLTIPVGVPMFNRNPLNSGLSLYITGYTGVLQF
LEPETTERNSYSGHRLSNTLISGNTLRAPYSWTHRGADRTNISD
KGFNLNRSYSVSGPFGTDIINTVNGSVLSMNFNTSLQURVRVRA
MLVRVYGGSTTDDQGFPTSMANSLTOSQRPRAEPVGISAGSOTAG
RQTHEDKIBFIPITLAEAYDLRAQEAVALPTNTPRRLTGTVDTH
VACUDEFCLDEKRELLKAYKSLDERNLQDPNTSINKQDPTISNEOS
IRHQSEHGWSQSLIPIQBNDFKENVYLPFTGNETPYTKLGEALKAY
QLSQTSDSQSLIYILIRNKHETLDVPTGSEVMPLESPIGRCEPNR
NPDLDCRDEKCAHSHHSLFDLGVGILHENYVWVFKLTQSEHARL
IESKPLGALSRVKAKEKRDKEKLOLTKRIVYATEAKVALFVDSQ
TNTGMHAADKLVRHREAYLSELSVIPFNVAITFEELBGRITAIL
DNNGLCAMWKNVDKQSHRSVLPIPEWAEASQVRCVPGRVILYAT
GEGCVTITENNTDNDKCEBSEVYPTDGTGNTAHQGTAAICSNRAG
WDTTASVYPISEBETVTDVRRDNNHCYDRGYVNPVPVAGYVTKEL
YBRTGTEKPFPIVDSVLEIAME"

ORIGIN

Query Match	88.6%;	Score 3266.6;	DB 1;	Length 3684;
Best Local Similarity	93.4%;	Pred. No. 0;		

QY	1	TTGACTTCAATAGGAAAAATGAGAAATGAATTTATAAATGCTTTATTCGATTCAGTCTGA 60
DB	1	TTGACTTCAATAGGAAAAATGAGAAATGAATTTATAAATGCTTTATTCGATTCAGTCTGA 60
QY	61	TCGAATCATTTCCACACAAATGGATCTATCACAGATGCTCGTATTGAGGATTCTTTTGCT 120
DB	61	TCGAATCATTTCCGACAAATGAATCTATCAACGATGCTCGTATTGAGAGTAGCTTGCT 120
QY	121	ATAGCGGAGGGAATAATATCAATCCACTTGTATTAGCGCATCAACAGTCCAAACGGGTATT 180
DB	121	ATAGCGGAGGGAAACAATATCGATCCATTTGTTAGCGCATCAACAGTCCAAACGGGTATT 180
QY	181	AACATAGCTGGTAGAATACTAGGTGCTATTATAGGCGTACCGTTTCTCGACAAATAGCTAGT 240
DB	181	AACATAGCTGGTAGAATACTAGGTGCTATTATAGGCGTACCGTTTCTCGACAAATAGCTAGT 240
QY	241	TTTTATAGTTTCTTTGTTGGTGAATTTATGCCCCGCGGCAGAGATCAGTGGGAAATTTTC 300
DB	241	TTTTATAGTTTCTTTGTTGGTGAATTTATGCCCCGCGGCAGAGATCCTTTGGGAAATTTTC 300
QY	301	CTAGACATGTCGACACACTTTATAATTCACAAATACAGAAATGCTAGGATACGGCA 360
DB	301	CTAGAACATGTCGAAACAATTTATAGACACACAGTAAACAGAAATATCTAGGGATACGGCT 360
QY	361	CTTGCTCGAATTACAAGGTTTAGGAGATTCTCTTTAGAGCCTTATCAACAGATCATTGGAAGT 420
DB	361	CTTGCTCGAATTACAAGGTTTAGGAAAATTCCTTTAGAGCCTTATCAACAGATCATTGGAAGT 420
QY	421	TGGCTAGAAAACCGTGATGATGCAAGAACGAGAAGTGTCTTTATACCCTAATATATAGCC 480
DB	421	TGGCTAGAAAACCGTGATGATGCAAGAACGAGAAGTGTCTTTATACCCTAATATATAGCC 480
QY	481	TTTAGAACTTGATTTTCTTTAAATGCGATGCGGCTTTTCGAATTAGAAACCAAGAAGTTCCA 540
DB	481	TTTAGAACTTGATTTTCTTTAAATGCGATGCGGCTTTTCGAATTAGAAACCAAGNAGTTCCA 540
QY	541	TTATTAAATGGTATATGCTCAAGCTGCAAAATTTACACCTATTTATTGAGAGATGCTCT 600
DB	541	TTATTAAATGGTATATGCTCAAGCTGCAAAATTTACACCTATTTATTGAGAGATGCTCT 600
QY	601	CTTTTTGGTAGTGAATTTGGGCTTACATCCGAGAAATTCACGTTATTATTGAGCGCCAA 660
DB	601	CTTTTTGGTAGTGAATTTGGGCTTACATCCAGAAATTCACGTTATTATTGAGCGCCAA 660
QY	661	GTGGACAAACGAGAGATTATTTCGACCTATTGCGTAGAATGGTATATATACAGGTCTAAAT 720

Db 1732 ACTTTTGCATCAAGGATCCCTAGTACTATGAGTGCATAATGAGTCTTTGACATCTCAATCA 1791
 Qy 1795 TTTAGATTTGCAGAAATTCCTGTAGGTATTAGTGCATCTGCGAGTCAAACTGCTGGAATA 1854
 Db 1792 TTTAGATTTGCAGAAATTCCTGTAGGTATTAGTGCATCTGCGAGTCAAACTGCTGGAATA 1851
 Qy 1855 AGTATAGTAAATATGAGGTAGACAAACGTTTCACTTTGATATAAAATGGAATTCATTCCA 1914
 Db 1852 AGTATAGTAAATATGAGGTAGACAAACGTTTCACTTTGATATAAAATGGAATTCATTCCA 1911
 Qy 1915 ATTACTCCAACTTCGAAGCAGAAATACGATTTAGAAAGGCGCAAGAGGCGGTGAATGCT 1974
 Db 1912 ATTACTCCAACTTCGAAGCAGAAATACGATTTAGAAAGGCGCAAGAGGCGGTGAATGCT 1971
 Qy 1975 CTGTTTACTAATACGAATCCAAAGAAATTTGAAAACAGATGTGACAGATTTATCATATTGAT 2034
 Db 1972 CTGTTTACTAATACGAATCCAAAGAGTTTGA AAAACAGGTGTGACAGATTTATCATATTGAT 2031
 Qy 2035 CAAGTATCCAAATTTAGTGGCGTGTATTATCGATGAATTTCTGCTTAGATGAAGAGAGAA 2094
 Db 2032 GAAGTATCCAAATTTAGTGGCGTGTATTATCGATGAATTTCTGCTTAGATGAAGAGAGAA 2091
 Qy 2095 TTAATCTCAGAAAGTGAATATGCGAAACGACTCAGTGCATGAAAGAACTTTACTCCAGAT 2154
 Db 2092 TTAATCTCAGAAAGTGAATATGCGAAACGACTCAGTGCATGAAAGAACTTTACTCCAGAT 2151
 Qy 2155 CCAAACTTCACATCCATCAATAGCAACAGAGCTTCATATCTACTATGAGCAATCGAAT 2214
 Db 2152 CCAAACTTCACATCCATCAATAGCAACAGAGCTTCATATCTACTATGAGCAATCGAAT 2211
 Qy 2215 TTCAATCTATCCATGAACATCTGAACATGAGTGGTGGGAGTGAACATTTACCAATC 2274
 Db 2212 TTCAATCTATCCATGAACATCTGAACATGAGTGGTGGGAGTGAACATTTACCAATC 2271
 Qy 2275 CAGAGGAATGACGATTTAAAGCAATTTAGTGCACATCTACCGGAGCTTTTATGAG 2334
 Db 2272 CAGAGGAATGACGATTTAAAGCAATTTAGTGCACATCTACCGGAGCTTTTATGAG 2331
 Qy 2335 TGTATCCGACGTTATTTATCAAAAATAGGAGAGTCCGAATTTAAAGCTTATACCTCGC 2394
 Db 2332 TGTATCCGACGTTATTTATCAAAAATAGGAGAGTCCGAATTTAAAGCTTATACCTCGC 2391
 Qy 2395 TACCAATTAAGAGGTATATTTGAAGATGATCAAGATTTAGAGATATATTTGATTCGTTAT 2454
 Db 2392 TACCAATTAAGAGGTATATTTGAAGATGATCAAGATTTAGAGATATATTTGATTCGTTAT 2451
 Qy 2455 AATCCGAAACATGAAACATTTGATGTTTCCAGGTACCGAGTCCGATGCGCGCTTTTCAGTT 2514
 Db 2452 AATCCGAAACATGAAACATTTGATGTTTCCAGGTACCGAGTCCGATGCGCGCTTTTCAGTT 2511
 Qy 2515 GAAAGCCCAATCCGAAGGTGCGAGAACCGAATCGATCGCCACCAATTTTGAATGGAAT 2574
 Db 2512 GAAAGCCCAATCCGAAGGTGCGAGAACCGAATCGATCGCCACCAATTTTGAATGGAAT 2571
 Qy 2575 CCTGATCTAGATTTCTCCTCAGAGATGGAGAAAATGTGCGCATCATTTCCCATCAATTC 2634
 Db 2572 CCTGATCTAGATTTCTCCTCAGAGATGGAGAAAATGTGCGCATCATTTCCCATCAATTC 2631
 Qy 2635 TCTTTGATATTTGATTTGATGCACAGACTTGCATGAGAAATCTAGCGGTGTGGTGGA 2694
 Db 2632 TCTTTGATATTTGATTTGATGTCATAGACTTGCATGAGAACTTAGCGGTGTGGTGGA 2691
 Qy 2695 TTAAGATTTAAGCGAGGAGGTTCATGAGACTTAGGAACTCGGAATTTTATTTGAAGAG 2754
 Db 2692 TTAAGATTTAAGCGAGGAGGTTCATGAGACTTAGGAACTCGGAATTTTATTTGAAGAG 2751
 Qy 2755 AAACCATTTATTAGAGAGCACTCTCTGCTGTAAGAGAGCAGAGAAAATGGAGAGAC 2814
 Db 2752 AAACCATTTATTAGAGAGCACTCTCTGCTGTAAGAGAGCAGAGAAAATGGAGAGAC 2811
 Qy 2815 AAACGTGAAAACCTACAAATTTGAAAACAAAACGAGTATATACAGAGGCAAAAGAGCTGTG 2874
 Db 2812 AAACGTGAAAACCTACAAATTTGAAAACAAAACGAGTATATACAGAGGCAAAAGAGCTGTG 2871

Qy 2875 GATGCTTTTATTGTAGATTTCTCAATATAATAGATTTACAAGCGGATACAAACATTTGGCATG 2934
 Db 2872 GATGCTTTTATTGTAGATTTCTCAATATAATAGATTTACAAGCGGATACAAACATTTGGCATG 2931
 Qy 2935 ATTATCATGCGGAGATTAACACTTTGTTTCAATTCGAGAGGCTTATCTGTGAGAAATATCT 2994
 Db 2932 ATTATCATGCGGAGATTAACACTTTGTTTCAATTCGAGAGGCTTATCTTTGAGAAATATCT 2991
 Qy 2995 GTTATCCCGGCTGTAATTCGGAATTTTTTGAAGAAATTTAGAAAGTGCATTTATCACTGCA 3054
 Db 2992 GTTATCCCGGCTGTAATTCGGAATTTTTTGAAGAAATTTAGAAAGTGCATTTATCACTGCA 3051
 Qy 3055 ATCTCCCTATACGATGCGAGAAATGTCGTTTAAATAAGTGGTATTTTAAATAGATTTAGCA 3114
 Db 3052 ATCTCCCTATACGATGCGAGAAATGTCGTTTAAATAAGTGGTATTTTAAATAGATTTAGCA 3111
 Qy 3115 TGTGGAATGTAAAGGCGCATGTAGATGTACACAGAGCCATCACCGTCTCTGCTCTGTTGT 3174
 Db 3112 TGTGGAATGTAAAGGCGCATGTAGATGTACACAGAGCCATCACCGTCTCTGCTCTGTTGT 3171
 Qy 3175 ATCCCAATTTGGGAAGCAGAAAGTGTCAACAGCAGTTCGCGTCTGTCGCGGCGTGGCTAT 3234
 Db 3172 ATCCCAATTTGGGAAGCAGAAAGTGTCAACAGCAGTTCGCGTCTGTCGCGGCGTGGCTAT 3231
 Qy 3235 ATCTCTCGTGTCAAGCGTACAAAGAGGATATGGAGAGGTTGTGTAAACGATCCATGAA 3294
 Db 3232 ATCTCTCGTGTCAAGCGTACAAAGAGGATATGGAGAGGTTGTGTAAACGATCCATGAA 3291
 Qy 3295 ATCGAGAACTATACAGACGAACTAAAATTTTAAACCTGTGAAGAGAGGAGTGTATCCA 3354
 Db 3292 ATCGAGAACTATACAGACGAACTAAAATTTTAAACCTGTGAAGAGAGGAGTGTATCCA 3351
 Qy 3355 ACCGATACAGAACTGTATGATTTACTGTCACCAAGGTACAGCAGTATGTAATTC 3414
 Db 3352 ACCGATACAGAACTGTATGATTTACTGTCACCAAGGTACAGCAGTATGTAATTC 3411
 Qy 3415 CGTAATCTGGATATGAGGATGCATATGAAGTTGATATCTACAGCATCTGTTAATTAACAA 3474
 Db 3412 CGTAATCTGGATATGAGGATGCATATGAAGTTGATATCTACAGCATCTGTTAATTAACAA 3471
 Qy 3475 CCGACTTATGAAGAGAACTATACAGATGTACAGAGATTAATCAATTTGTAATATGAC 3534
 Db 3472 CCGACTTATGAAGAGAACTATACAGATGTACAGAGATTAATCAATTTGTAATATGAC 3531
 Qy 3535 AGAGGTATGTGAATTTATCCACCTACAGCTGGTTATATGACAAAGAAATTAAGAATAC 3594
 Db 3532 AGAGGTATGTGAATTTATCCACCTACAGCTGGTTATATGACAAAGAAATTAAGAATAC 3591
 Qy 3595 TTCCCGAAACCCGATTAAGGTATGGAATTTGAGATTTGGAGAAACGGAAGGAAAGTTTATTTGA 3654
 Db 3592 TTCCCGAAACCCGATTAAGGTATGGAATTTGAGATTTGGAGAAACGGAAGGAAAGTTTATTTGA 3651
 Qy 3655 GACAGGTGGAATTTACTCTCTTATGGAGGAATAG 3687
 Db 3652 GACAGGTGGAATTTACTCTCTTATGGAGGAATAG 3684

RESULT 5
 190319
 LOCUS
 DEFINITION
 190319
 ACCESSION
 VERSION
 190319.1
 GI:3410259
 KEYWORDS
 SOURCE
 Unknown.
 ORGANISM
 Unclassified.
 1 (bases 1 to 3684)
 PAYNE, J., Cummings, D.A., Cannon, R.J.C., Narva, K.E. and Stelman, S.
 Bacillus thuringiensis genes encoding lepidopteran-active toxins
 Patent: US 5723758-A 7 03-MAR-1998;
 Location/Qualifiers

190319
 Sequence 7 from patent US 5723758.
 190319
 190319.1
 GI:3410259

3684 bp
 DNA
 linear
 PAT 10-AUG-1998

Qy	955	ATAGAGACTCGGGTTATCCGAAGCCGCATCTACTACTTGTGATTTTCTAGAACCAACTTCAAAATT	101
Db	961	ATAGAGGCTCGCGTTATTTAGGCGCTCCGCATCTACTCTTGAATTTTCCAGAACAAGCTTCAAAATT	102
Qy	1015	TTTAGCACATTCATCACGATCGAGTGCTACTAGGCATATGACTTACTTGGCGGGGCACACA	1074
Db	1021	TTTCAAGCTATTAAGTCGATCGAGGTATATCTCAATATATGAAATTTACTGGGTGGGACATAGA	1080
Qy	1075	ATTCAATCTTCGGCCAATAGGAGGCGGATTAAATACCTCAACGCATGGGTCTACCAATACT	1134
Db	1081	CTTGAATCGGAACAATAAGGGGTCATTAAAGTACCTCGACACACGGAATATACCAATACT	1140
Qy	1135	TCTATTAATCCTGTAGATTATCATCTCTCTCGAGACGTATATTGGACTGAATCATAT	1194
Db	1141	TCTATTAATCCTGTAAACATTTACAGTTTACATCTCGAGACGTTTTATAGAACAGAAATCATTT	1200
Qy	1195	GCAGGAGTCTTCTATCGGGAAATTTACCTTGAACCTTATTTCATGGTGTCCCTACTGTGTAGA	1254
Db	1201	GCAGGGATAAATAT-----ACTTCTAACTACTCTCTGTGAATGGAGTACCTTGGGCTAGA	1254
Qy	1255	TTTAAATTTAGGAACCTTCAGAAATCTTTTGAAGAGGTTACTCTCTAACTATAGTCAACCC	1314
Db	1255	TTTAAATTGGAGAAATCCCTGAAATTTCTCT--AGAGTAGCCCTTCTCTATATCTATAGG	1311
Qy	1315	TATGAGTCACCTGGGCTTCAATTTAAAGATTTCAGAACTGAAATACCAACAGAAAAACA	1374
Db	1312	TATACTGGAGTGGGACACAACCTATTTTGATTCAGAACTGAAATAGCACAGAAAAACA	1371
Qy	1375	GAACGACCAATTTATGAATCATATAGTCATAGTGTATCTCACATAGGCTCATTTCCACA	1434
Db	1372	GAACGACCAATTTATGAATCTTACAGTCATAGAAATATCTTAATATAGACTAAATATCAGGA	1431
Qy	1435	TCTAGGTCATGTACCAGTATATCTTGGACGACCGTAGTCAGATCGTACAAATACC	1494
Db	1432	AACACTTGGAGACACAGTATATTTCTTGGACGACCGTAGTCAGATCGTACAAATACC	1491
Qy	1495	ATTAGTTTCAGATAGCATAAACACAATAACCAATCGGTAAAAATCAATCAACCTTAATCAGGT	1554
Db	1492	ATTAGTTTCAGATAGCATAAACACAATAACCAATCGGTAAAAATCAATCAACCTTAATCAGGT	1551
Qy	1555	ACCTCTGTAGTCAGTGGCCGAGATTTACAGGAGGGGATATAATCCGAACCTAACGTTAAT	1614
Db	1552	ACCTCTGTAGTCAGTGGCCGAGATTTACAGGAGGGGATATAATCCGAACCTAACGTTAAT	1611
Qy	1615	GGTAGTCTACTAAGTATGGGTCCTTAATTTTAAATAACATCAATTCACGCGGTATCGCGTG	1674
Db	1612	GGTAGTGTACTAAGTATGGGTCCTTAATTTTAAATAACATCAATTCACGCGGTATCGCGTG	1671
Qy	1675	AGAGTTCGTTATGCTGTCTCTAAAACAAATGGTCTCGAGGGTAACTGTGCGAGGGAGTACT	1734
Db	1672	AGAGTTCGTTATGCTGTCTCTAAAACAAATGGTCTCGAGGGTAACTGTGCGAGGGAGTACT	1731
Qy	1735	ACGTTTGTATCAAGGATTCCTTAGTACTATAGTGTGCAAAATGAGTCTTTTGACATCTCAATCA	1794
Db	1732	ACTTTTGATCAAGGATTCCTTAGTACTATGAGTGTCAAAATGAGTCTTTTGACATCTCAATCA	1791
Qy	1795	TTTATAGTTTCGAAATTTCTGTAGGTATTTAGTGCATCTGGCAGTCAAACTGCTCGGAATA	1854
Db	1792	TTTATAGTTTCGAAATTTCTGTAGGTATTTAGTGCATCTGGCAGTCAAACTGCTCGGAATA	1851
Qy	1855	AGTATAGTAAATATGCAAGTACAAAAACGTTTTCACCTTTGATAAAAATGAAATTCATTCCA	1914
Db	1852	AGTATAGTAAATATGCAAGTACAAAAACGTTTTCACCTTTGATAAAAATGAAATTCATTCCA	1911
Qy	1915	ATTACTGCAACCTTTCGAAGCAGAAATTCAGATTTAGAAAGGGCGCAGAGCGGTGAATGCT	1974
Db	1912	ATTACTGCAACCTTTCGAAGCAGAAATTCAGATTTAGAAAGGGCGCAGAGCGGTGAATGCT	1971
Qy	1975	CTGTTTACTAATACGAAATCCAGAAAGTTGAAACACAGATGCTGCAGATTAATCATATTGAT	2034
Db	1972	CTGTTTACTAATACGAAATCCAGAAAGTTGAAACACAGATGCTGCAGATTAATCATATTGAT	2031
Qy	2035	CAAGTATCCAAATTTAGTGGCGTGTATTATCGGATGAAATTTCTGCTTTAGATGAAAAAGAGAA	2094

```
Db 2032 GAAGTATCCAAATTTAGTGGCGTGTATCGATGAAATCTGCTTGGATGAAGAAGAGAGAA 2091
Qy 2095 TTACTTGAGAAAGTGAATATGCGAAACGACTCAGTGCATGAAAGAAACTTACTTCCAAGAT 2154
Db 2092 TTACTTGAGAAAGTGAATATGCGAAACGACTCAGTGCATGAAAGAAACTTACTTCCAAGAT 2151
Qy 2155 CCAAACTTCATCCATCCATTAAGCAACACAGACTTCATATCTACTATGAGCAATCGAAT 2214
Db 2152 CCAAACTTCATCCATCCATTAAGCAACACAGACTTCATATCTACTATGAGCAATCGAAT 2211
Qy 2215 TTCACTCTATCCATGAACCAATCTGAACATGAGTGGGGAAGTGAAGACATTTACAATC 2274
Db 2212 TTCACTCTATCCATGAACCAATCTGAACATGAGTGGGGAAGTGAAGACATTTACAATC 2271
Qy 2275 CAGGAAGGAATGACGTATTTAAAGAGAAATTCACGTACACCTACCGGGGACTTTTAATGAG 2334
Db 2272 CAGGAAGGAATGACGTATTTAAAGAGAAATTCACGTACACCTACCGGGGACTTTTAATGAG 2331
Qy 2335 TGTATCCGAGGTATTTATATCAAAAAATAGGAGAGTCCGAAATTAAGGCTTTATCTCGC 2394
Db 2332 TGTATCCGAGGTATTTATATCAAAAAATAGGAGAGTCCGAAATTTAAAGGCTTTATCTCGC 2391
Qy 2395 TACCAATTAAGAGGTATTTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGTTAT 2454
Db 2392 TACCAATTAAGTGGCTATTTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGTTAT 2451
Qy 2455 AATCGGAAACATGAACCAATTTGGATGTTCCAGGTACCGAGTCCGATATGCGCGCTTTCAAGT 2514
Db 2452 AATCGGAAACATGAACCAATTTGGATGTTCCAGGTACCGAGTCCGATATGCGCGCTTTCAAGT 2511
Qy 2515 GAAAGCCCAATCGGAAGTGGGAGAACCGAATCGATCGGCACACATTTTGAATGGAAT 2574
Db 2512 GAAAGCCCAATCGGAAGTGGGAGAACCGAATCGATCGGCACACATTTTGAATGGAAT 2571
Qy 2575 CCTGATCTAGATGTTCTCGAGAGATGGAGAAAATGTCGCGATCATTCCTCATCTTC 2634
Db 2572 CCTGATCTAGATGTTCTCGAGAGATGGAGAAAATGTCGCGATCATTCCTCATCTTC 2631
Qy 2635 TCTTTGGATATTGATTTGGATGCACAGACTTGCATGAGAACTTAGCGGTGGTGGTA 2694
Db 2632 TCTTTGGATATTGATTTGGATGCATAGACTTGCATGAGAACTTAGCGGTGGTGGTA 2691
Qy 2695 TTCAAGATTAAGACCGCAGGAGGTTCATCAAGACTAGCGAATCTGGAATTTATGAAGAG 2754
Db 2692 TTCAAGATTAAGACCGCAGGAGGTTCATCAAGACTAGCGAATCTGGAATTTATGAAGAG 2751
Qy 2755 AAACCATTTATGAGAGAGCACTCTCTGCTGTAAGAGCAGAGAAAATGAGAGAC 2814
Db 2752 AAACCATTTATGAGAGAGCACTCTCTGCTGTAAGAGCAGAGAAAATGAGAGAC 2811
Qy 2815 AAACGTGAAAACTACAAATTTGAAACAAACGAGTATATACAGAGGCAAAAGAGCTGTG 2874
Db 2812 AAACGTGAAAACTACAAATTTGAAACAAACGAGTATATACAGAGGCAAAAGAGCTGTG 2871
Qy 2875 GATGCTTTATTTGATGATTTCTCAATATAATAGATTACAAGCGGATACAAACATTTGGCATG 2934
Db 2872 GATGCTTTATTTGATGATTTCTCAATATAATAGATTACAAGCGGATACAAACATTTGGCATG 2931
Qy 2935 ATTATCGGCGAGATAAATCTGTTTCATCGAATTCGAGAGGCTTATCTGTCAGAAATATCT 2994
Db 2932 ATTATCGGCGAGATAAATCTGTTTCATCGAATTCGAGAGGCGTATCTTTCAGAAATATCT 2991
Qy 2995 GTTATCCGGGTGTAATGCGGAAATTTTGAAGAAATTTAGAGGTGCGCATTTATCACCTGCA 3054
Db 2992 GTTATCCAGGTGTAATGCGGAAATTTTGAAGAAATTTAGAGGTGCGCATTTATCACCTGCA 3051
Qy 3055 ATCTCCCTATACGATGCGAGAAATCTCGTTAAAAAATGCGATTTTAATAATGGAATTAGCA 3114
Db 3052 ATCTCCCTATACGATGCGAGAAATCTCGTTAAAAAATGCGATTTTAATAATGGAATTAGCA 3111
Qy 3115 TGCTGGAATGTAAAAAGGCGATGTAGATGTACAAACAGAGCCATCACCGTTCGTCTCTTGT 3174
```

```
Db 3112 TGCTGGAATGTAAAAAGGCGATGTAGATGTACAAACAGAGCCATCACCGTTCGTCTCTTGT 3171
Qy 3175 ATCCAGATGCGAAGCAGAAAGTGTCAAGAGAGTTCCGCTCTGTCCGGGCGTGGCTAT 3234
Db 3172 ATCCAGATGCGAAGCAGAAAGTGTCAAGAGAGTTCCGCTCTGTCCGGGCGTGGCTAT 3231
Qy 3235 ATCTCCGTGTACAGCGTACAAAGAGGGATATGAGAGGGTGTGTGTAACGATCCATGAA 3294
Db 3232 ATCTCCGTGTACAGCGTACAAAGAGGGATATGAGAGGGTGTGTGTAACGATCCATGAA 3291
Qy 3295 ATCGAGAACATATACAGACGAACTAAAAATTTAAAAAATCTGTGAAGAGGAGTGTATCCA 3354
Db 3292 ATCGAGAACATATACAGACGAACTAAAAATTTAAAAAATCTGTGAAGAGGAGTGTATCCA 3351
Qy 3355 ACGGATACAGAAACGTGTAAATGATTAATCTGCACACCAAGGTACAGAGTATGTAATTC 3414
Db 3352 ACGGATACAGAAACGTGTAAATGATTAATCTGCACACCAAGGTACAGAGTATGTAATTC 3411
Qy 3415 CGTAATGCTGGATATGAGGATGCATATGAAGTTGATGATACAGCATCTGTTAATACAA 3474
Db 3412 CGTAATGCTGGATATGAGGATGCATATGAAGTTGATGATACAGCATCTGTTAATACAA 3471
Qy 3475 CCAGCTTTATCAAGAAAGAAACGTATACAGATGTACGAGAGATAATCATTTGTAATATGAC 3534
Db 3472 CCAGCTTTATCAAGAAAGAAACGTATACAGATGTACGAGAGATAATCATTTGTAATATGAC 3531
Qy 3535 AGAGGTATGTGAATTTATCCACCATCAGCTGGTTATATGACAAAGAAATTAGAATAC 3594
Db 3532 AGAGGTATGTGAATTTATCCACCATCAGCTGGTTATATGACAAAGAAATTAGAATAC 3591
Qy 3595 TTCCGAGAAACCGATAGGTATGAGTTGAGATTTGGAGAAACGGAAGGAGTTTATGTA 3654
Db 3592 TTCCGAGAAACCGATAGGTATGAGTTGAGATTTGGAGAAACGGAAGGAGTTTATGTA 3651
Qy 3655 GACAGCGTGAATTTACTCTTTATGGAGGAATAG 3687
Db 3652 GACAGCGTGAATTTACTCTTTATGGAGGAATAG 3684
```

RESULT 6
AR359400
LOCUS AR359400 3684 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 62 from patent US 6593293.
ACCESSION AR359400
VERSION AR359400.1 GI:33765710
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 3684)
AUTHORS Baum,J.A., Chu,C.-R., Donovan,W.P., Gilmer,A.J. and Rupar,M.J.
TITLE Lepidopteran-active Bacillus thuringiensis .delta.-endotoxin
compositions and methods of use
JOURNAL Patent: US 6593293-A 62-15-JUL-2003;
FEATURES Location/Qualifiers
source 1.3684
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 88.4%; Score 3260.2; DB 6; Length 3684;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 3445; Conservative 0; Mismatches 233; Indels 15; Gaps 3;

```
Qy 1 TTGACTTCAATAGGAAATGAGATGAATTAATTAATCTTATCGATTCCAGCTGTA 60
Db 1 TTGACTTCAATAGGAAATGAGATGAATTAATTAATCTTATCGATTCCAGCTGTA 60
Qy 61 TCGAATCATTTCCACACAAATGGATCTATCACAGATGCTCGTATTTGAGGATTTCTTGT 120
Db 61 TCGAATCATTTCCGACACAAATGAATCTATCAACCGATGCTCGTATTTGAGGATAGCTTGT 120
Qy 121 ATAGCCGAGGGGAATATATATCAATCCACTGTTGTTAGCGCATCAACAGTCCAAACGGGTATT 180
```


Db 121 ATAGCCGAGGGGAAACAATATATCGATCCATTTGTTAGCGCATCAACAGATCCCAACGGGTATT 180
 Qy 181 AACATAGCTGCTAGAACTACTAGGTGTTATAGGCGTACCGTTGCTGACAAATAGCTAGT 240
 Db 181 AACATAGCTGCTAGAACTACTAGGTGTTATAGGCGTACCGTTGCTGACAAATAGCTAGT 240
 Qy 241 TTTTATAGTTTTCTTTGTTGTTGTAATTTAGCCCGCGCGAGAGATCAGTGGGAAATTTTC 300
 Db 241 TTTTATAGTTTTCTTTGTTGTTGTAATTTAGCCCGCGCGAGAGATCCTTGGGAAATTTTC 300
 Qy 301 CTAGAACATGTGCAACAACTTTAATTAACAACAAATAACAGAAATGCTAGGAATACGGCA 360
 Db 301 CTAGAACATGTGCAACAACTTTAATTAACAACAAATAACAGAAATGCTAGGAATACGGCA 360
 Qy 361 CTTGCTCGATTAACAAGGTTTAGGAGATTCCTTTAGAGCCCTATCAACAGTCACTTTGAAGAT 420
 Db 361 CTTGCTCGATTAACAAGGTTTAGGAGATTCCTTTAGAGCCCTATCAACAGTCACTTTGAAGAT 420
 Qy 421 TGGCTAGAAACCGTGATGATGCAAGAAACGAGAGTGTCTTTATACCCCAATATATAGCC 480
 Db 421 TGGCTAGAAACCGTGATGATGCAAGAAACGAGAGTGTCTTTATACCCCAATATATAGCC 480
 Qy 481 TTAGAACTTGATTTCTTTAATGCGATGCGCGTTTTCGCAATAGAAACCAAGAGTTCCA 540
 Db 481 TTAGAACTTGATTTCTTTAATGCGATGCGCGTTTTCGCAATAGAAACCAAGAGTTCCA 540
 Qy 541 TTATTAAATGCTATGCTCAAGCTGCAAAATTTACACCTATATATTGAGAGATGCTCT 600
 Db 541 TTATTAAATGCTATGCTCAAGCTGCAAAATTTACACCTATATATTGAGAGATGCTCT 600
 Qy 601 CTTTTTGGTGTGAATTTGGGCTTTACATCGCAGAAATTCAAAGTTATTATGAGCGCAA 660
 Db 601 CTTTTTGGTGTGAATTTGGGCTTTACATCGCAGAAATTCAAAGTTATTATGAGCGCAA 660
 Qy 661 GTGGAAACAAACGAGAGATTTTCGACTATGCGTAGAATGGTATATATACAGTCTAAAT 720
 Db 661 GTGGAAACAAACGAGAGATTTTCGACTATGCGTAGAATGGTATATATACAGTCTAAAT 720
 Qy 721 AGCTTGAGGGGCAAAATGCGGAAGTTGGTGGTGTATATCAATTCCTGAGAGATCTA 780
 Db 721 AATTGAGAGGGGCAAAATGCGGAAGTTGGTGGTGTATATCAATTCCTGAGAGATCTA 780
 Qy 781 ACCTTGAGGGGTATTAGATCTAGTGGCACTATTCGCAAGCTATGACACTCTGCACTTATCCA 840
 Db 781 ACCTTGAGGGGTATTAGATCTAGTGGCACTATTCGCAAGCTATGACACTCTGCACTTATCCA 840
 Qy 841 ATAAATACGAGTGTCTAGTTAAACAGGGAAGTTTATACAGCGCAATGAGGCAACAGGG 900
 Db 841 ATGAATACCAAGTGTCTCAATTTAAACAGGGAAGTTTATACAGATCCAATTTGGGGAACAAAT 900
 Qy 901 GTAAAT-----ATGGCAAGTATGAATTTGGTATTAATAATATCAATTCCTGCTCGCT 954
 Db 901 GCACCTTCAGGATTTGCAAGTATGAATTTGGTATTAATAATATCAATTCCTGCTCGCT 954
 Qy 955 ATAGAGACTCGGGTTATCCGAAGCCCGCATCTACTTGATTTTCTAGAAACAACTTACAAT 1014
 Db 955 ATAGAGCTCGGGTTATCCGAAGCCCGCATCTACTTGATTTTCTAGAAACAACTTACAAT 1014
 Qy 1015 TTTAGCACTTCATCAAGATGCTAGTGTCTAGGCAATGATCTTCTGCGGGGGGACACA 1074
 Db 1021 TTCAGCGTATTAAGTTCGATGAGTAAATCTCAATATATGAATTTACTGGGTGGGACATAGA 1080
 Qy 1075 ATTCAATCTCGGCCAATAGAGGGGATTAATAACCTCAACGATGGTCTACCAATACT 1134
 Db 1081 CTTGAATCGGCAACAAATAAGGGGTCTAATAGTACCTGGACACACGGAATAACAATACT 1140
 Qy 1135 TCTATTAACTCTGTAAGATTATCATTTCTCTCGAGACGCTATATTGGACTGAATCATAT 1194
 Db 1141 TCTATTAACTCTGTAAGATTATCATTTCTCGAGACGCTTATAGAACAGAAATCATTT 1200
 Qy 1195 GCAGGAGTGTCTTATGGGAAATTTACCTTGAAACCTTATTCATGCTGCTTCTGTTAGA 1254

Db 1201 GCAGGATAAATAT-----ACTTCTAACTACTCTCTGTGAATGGAGTACCTTGGGCTAGA 1254
 Qy 1255 TTTTAAATTTAGGAACCTCTAGAACTACTTTTGAAGAGGTACTGCTAACTATAGTCAACCC 1314
 Db 1255 TTTTAAATTTAGGAATCCCCTGAATTTCTTT---AGAGTAGCCTTCTCTATATATAGG 1311
 Qy 1315 TATGAGTCACTCTGGGCTTCAATTTAAAGATTTCAGAACTGAAATTTACACAGAAACAA 1374
 Db 1312 TATACTGGAGTGGGACACAACCTATTGTTTCAGAACTGAAATTTACACAGAAACAA 1371
 Qy 1375 GAACGACCAAAATTTATGAATCATATAGTATAGGTTATCTCACATAGGGCTCATTTCA 1434
 Db 1372 GAACGACCAAAATTTATGAATCTTACAGTCAATGATTTCTAATATAGAACTAATATCAGGA 1431
 Qy 1435 TCTAGGCTCATGTCACAGTATATTCTTGAGCCACCGTAGTCAGATCGTACAAATACC 1494
 Db 1432 AACACTTTGAGACACAGTATATTCTTGAGCCACCGTAGTCAGATCGTACAAATACC 1491
 Qy 1495 ATTAGTTTCAGATAGCATAACACAATAACCAATTCGTAAATTCATTCAACCTTAATCAGGT 1554
 Db 1492 ATTAGTTTCAGATAGCATAACACAATAACCAATTCGTAAATTCATTCAACCTTAATCAGGT 1551
 Qy 1555 ACCTCTGTAGTCACTGGCCCGAGGATTTACAGAGGGGATATATCCGAACCTAAGTTAAT 1614
 Db 1552 ACCTCTGTAGTCACTGGCCCGAGGATTTACAGAGGGGATATATCCGAACCTAAGTTAAT 1611
 Qy 1615 GGTAGTGTACTAAGTATGGTCTTTAAATTTTAAATACATCAATTACAGCGGTATCGCGT 1674
 Db 1612 GGTAGTGTACTAAGTATGGTCTTTAAATTTTAAATACATCAATTACAGCGGTATCGCGT 1671
 Qy 1675 AGAGTTTCTGTTATGCTCTTCTCAACAATGGTCTCTGAGGGTAACTGTGCGAGGGAGTACT 1734
 Db 1672 AGAGTTTCTGTTATGCTCTTCTCAACAATGGTCTCTGAGGGTAACTGTGCGAGGGAGTACT 1731
 Qy 1735 ACTTTTGTCAAGGATTCCTTAGTACTATGAGTGCATAAGTGTCTTGACATCTCAATCA 1794
 Db 1732 ACTTTTGTCAAGGATTCCTTAGTACTATGAGTGCATAAGTGTCTTGACATCTCAATCA 1791
 Qy 1795 TTTAGATTTGCAAAATTTCTCTGTAGTATTAGTGCATCTGGCAGTCAAACTGCTGGAATA 1854
 Db 1792 TTTAGATTTGCAAAATTTCTCTGTAGTATTAGTGCATCTGGCAGTCAAACTGCTGGAATA 1851
 Qy 1855 AGTATAAGTAAATATGAGTGTAGCAAACTGTTTCACTTTGATATAAATTTGAATTCATTCCA 1914
 Db 1852 AGTATAAGTAAATATGAGTGTAGCAAACTGTTTCACTTTGATATAAATTTGAATTCATTCCA 1911
 Qy 1915 ATTTACTGCAACCTTCCAGAGCAATACGATTTAGAAAGGGCCGCAAGGGCGGTGAATGCT 1974
 Db 1912 ATTTACTGCAACCTTCCAGAGCAATACGATTTAGAAAGGGCCGCAAGGGCGGTGAATGCT 1971
 Qy 1975 CTGTTTACTAATACGAATCCAGAAATTTGAAACAGATGTGACAGATTCATATTTGAT 2034
 Db 1972 CTGTTTACTAATACGAATCCAGAAATTTGAAACAGATGTGACAGATTCATATTTGAT 2031
 Qy 2035 CAAGTATCCAAATTTAGTGGCGTCTTTATCGGATGAATTTCTGTTAGATGAAAGAGAGAA 2094
 Db 2032 GAAGTATCCAAATTTAGTGGCGTCTTTATCGGATGAATTTCTGTTGATGAAAGAGAGAA 2091
 Qy 2095 TTTACTTGAGAAAGTGAATATGCAAGCACTCAGTGTGATGAAAGAACTTACTTCCAGAT 2154
 Db 2092 TTTACTTGAGAAAGTGAATATGCAAGCACTCAGTGTGATGAAAGAACTTACTTCCAGAT 2151
 Qy 2155 CCAAACTTCACATCCATCAATAGCAACCAAGCTTCTATCTACTAATAGCAATCGAAT 2214
 Db 2152 CCAAACTTCACATCCATCAATAGCAACCAAGCTTCTATCTAATATAGCAATCGAAT 2211
 Qy 2215 TTCACATCTATCCATGAACCAATCTGAACATGGATGGTGGGAAAGTGAGAACATTACAATC 2274
 Db 2212 TTCACATCTATCCATGAACCAATCTGAACATGGATGGTGGGAAAGTGAGAACATTACAATC 2271
 Qy 2275 CAGGAAGGAATGACGTTATTAAGGAATAGTGCACACTACCGGGGACTTTTATGAG 2334
 Db 2272 CAGGAAGGAATGACGTTATTAAGGAATAGTGCACACTACCGGGGACTTTTATGAG 2331


```
QY 2335 TGTATCCGACGTATTTATATCAAAAAATAGGAGAGTCGGAATTTAAAGCTTATACCTGC 2394
DB 2332 TGTATCCGACGTATTTATATCAAAAAATAGGAGAGTCGGAATTTAAAGCTTATACCTGC 2391
QY 2395 TACCAATTAAGAGGGTATATTGAAGATAGTCAAGATTTAGAGATATATTGATTCGTTAT 2454
DB 2392 TACCAATTAAGTGGCTATATTGAAGATAGTCAAGATTTAGAGATATATTGATTCGTTAT 2451
QY 2455 AATCGAAACATGAACATTTGGATGTTTCCAGGTACCGAGTCCGATGCGCGCTTTTCAGTT 2514
DB 2452 AATCGAAACATGAACATTTGGATGTTTCCAGGTACCGAGTCCGATGCGCGCTTTTCAGTT 2511
QY 2515 GAAAGCCCAATCGAAGGTCGGAGAACCGAATCGATCGGCACACATTTTGAATGGAAT 2574
DB 2512 GAAAGCCCAATCGAAGGTCGGAGAACCGAATCGATCGGCACACATTTTGAATGGAAT 2571
QY 2575 CCTGATCTAGATGTTCTCGCAGAGATGGAGAAAAATGTGCGCATCATTTCCCATCATTTTC 2634
DB 2572 CCTGATCTAGATGTTCTCGCAGAGATGGAGAAAAATGTGCGCATCATTTCCCATCATTTTC 2631
QY 2635 TCTTTGATATTTGATTTGGATGCACAGACTTGCATGAGAATCTAGCGGTGTGGGTGTTA 2694
DB 2632 TCTTTGATATTTGATTTGGATGCATGAGACTTGCATGAGAATCTAGCGGTGTGGGTGTTA 2691
QY 2695 TTCAGATTAAGACGCGAAGGTCTAGTCAAGACTAGGGAATCTGGAATTTTATGAAGAG 2754
DB 2692 TTCAGATTAAGACGCGAAGGTCTAGTCAAGACTAGGGAATCTGGAATTTTATGAAGAG 2751
QY 2755 AAACCATTTATAGAGAGCACTGCTCTGTTGAGAGACAGAGAAAAATGGAGAGAC 2814
DB 2752 AAACCATTTATAGAGAGCACTGCTCTGTTGAGAGACAGAGAAAAATGGAGAGAC 2811
QY 2815 AAACGTGAAAACTTACATTTGAAAAACAAACGAGTATATACAGAGGCAAAAGAGCTGTG 2874
DB 2812 AAACGTGAAAACTTACATTTGAAAAACAAACGAGTATATACAGAGGCAAAAGAGCTGTG 2871
QY 2875 GATGCTTTATTTGATGATTTCAATATTAATAGATTACAAGCGGATACAAACATTTGGCATG 2934
DB 2872 GATGCTTTATTTGATGATTTCAATATTAATAGATTACAAGCGGATACAAACATTTGGCATG 2931
QY 2935 ATTCATCGCGCAGTAACTGTTTCATCGAATTCGAGAGCTTATCTGTCAGATATATCT 2994
DB 2932 ATTCATCGCGCAGTAACTGTTTCATCGAATTCGAGAGCGTATCTTTTTCAGAAATATCT 2991
QY 2995 GTTATCCCGGTGTAAATGCGGAAATTTTGAAGATTTAGAAGTCCGATTTATCACTGCA 3054
DB 2992 GTTATCCCGGTGTAAATGCGGAAATTTTGAAGATTTAGAAGTCCGATTTATCACTGCA 3051
QY 3055 ATCTCCCTATACGATCGAGAAATGTCGTTTAAAAATGGTGATTTTAAATAGGATTAGCA 3114
DB 3052 ATCTCCCTATACGATCGAGAAATGTCGTTTAAAAATGGTGATTTTAAATAGGATTAGCA 3111
QY 3115 TGCTGGAATGTAAAGGCGATAGATGTACACAGAGCCATCACCGTTCGTCTGCTTGT 3174
DB 3112 TGCTGGAATGTAAAGGCGATAGATGTACACAGAGCCATCACCGTTCGTCTGCTTGT 3171
QY 3175 ATCCAGAAATGGGAAGCAGAAAGTGTCAAGAGCTTCGCGTCTGTCGCGGCGGTGGCTAT 3234
DB 3172 ATCCAGAAATGGGAAGCAGAAAGTGTCAAGAGCTTCGCGTCTGTCGCGGCGGTGGCTAT 3231
QY 3235 ATCTCTCGTGTCAAGAGGATATGAGAGGGGTGTGTGTAACGATCCCATGAA 3294
DB 3232 ATCTCTCGTGTCAAGAGGATATGAGAGGGGTGTGTGTAACGATCCCATGAA 3291
QY 3295 ATCGAGAAATATCAGACGAATTAATAATTTAAATACTGTGAGAGAGGAGTGTATCCA 3354
DB 3292 ATCGAGAAATATCAGACGAATTAATAATTTAAATACTGTGAGAGAGGAGTGTATCCA 3351
QY 3355 ACGGATACGGAAGCTGTATGATTTATCTGCACACCAAGGTACAGAGTATGTATTC 3414
DB 3352 ACGGATACGGAAGCTGTATGATTTATCTGCACACCAAGGTACAGAGTATGTATTC 3411
```

```
QY 3415 CGTAATCTCGATATGAGGATGCATATGAAGTTGATACTACAGCATCTGTAAATTACAAA 3474
DB 3412 CGTAATCTCGATATGAGGATGCATATGAAGTTGATACTACAGCATCTGTAAATTACAAA 3471
QY 3475 CCGACTTATCAAGAAGAAACGTATACAGATGTACGAAGAGATAATCATTTGTGAATATGAC 3534
DB 3472 CCGACTTATCAAGAAGAAACGTATACAGATGTACGAAGAGATAATCATTTGTGAATATGAC 3531
QY 3535 AGAGGGTATGTGAATTTATCCACCTACAGCTGTTTATATGACAAAGAAATTAAGATATAC 3594
DB 3532 AGAGGGTATGTGAATTTATCCACAGTACCAAGTGTGTTTATATGACAAAGAAATTAAGATATAC 3591
QY 3595 TTCCCGAAGAACCCGATAGGATGATGATTCCTTATGGAGAAATAG 3654
DB 3592 TTCCCGAAGAACCCGATAGGATGATGATTCCTTATGGAGAAATAG 3651
QY 3655 GACAGCGTGAATTTACTCTTATGGAGAAATAG 3687
DB 3652 GACAGCGTGAATTTACTCTTATGGAGAAATAG 3684

RESULT 7
AX098692 LOCUS 3684 bp DNA linear PAT 02-APR-2001
DEFINITION Sequence 62 from Patent WO0119859.
ACCESSION AX098692
VERSION AX098692.1 GI:13537934
KEYWORDS Bacillus thuringiensis
SOURCE Bacillus thuringiensis
ORGANISM Bacillus thuringiensis
          Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE
  1 Baum, J. A., Chu, C. R., Donovan, W. P., Gilmer, A. J. and Rupar, M. J.
    Lepidopteran-active bacillus thuringiensis delta-endotoxin
    compositions and methods of use
    Patent: WO 0119859-A 62 22-MAR-2001;
    MONSANTO COMPANY (US)
    Location/Qualifiers
      source 1. 3684
      /organism="Bacillus thuringiensis"
      /mol_type="unassigned DNA"
      /db_xref="taxon:1428"

ORIGIN
Query Match 88.4%; Score 3260.2; DB 6; Length 3684;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 3445; Conservative 0; Mismatches 233; Indels 15; Gaps 3;

QY 1 TTGACTTCAAATAGGAAAAATGAGAAATGAAATTAATAATGCTTTATCGATTCCAGCTGTA 60
DB 1 TTGACTTCAAATAGGAAAAATGAGAAATGAAATTAATAATGCTTTATCGATTCCAGCTGTA 60
QY 61 TCGAATCATTTCCACACAAATGGATCTATCACAGATGCTCGTATTGAGGATCTTTTGT 120
DB 61 TCGAATCATTTCCGACAAATGAATCTATCAACCGATGCTCGTATTGAGGATAGCTTGT 120
QY 121 ATAGCGGAGGGGAATATATCAATCCACTTTGTAGCGCATCAACAGTCCAAAACGGGTATT 180
DB 121 ATAGCGGAGGGGAACAAATATCGATCCATTTGTAGCGCATCAACAGTCCAAAACGGGTATT 180
QY 181 AACATAGCTGTTAGAAATACATAGGTGTATTAGGGGTACCGTTTGTGACAAAATAGTAGT 240
DB 181 AACATAGCTGTTAGAAATACATAGGTGTATTAGGGGTACCGTTTGTGACAAAATAGTAGT 240
QY 241 TTTTATAGTTTTCTTGTGTGAATTTATGCGCCGCGGAGAGATCAGTGGGAAATTTTC 300
DB 241 TTTTATAGTTTTCTTGTGTGAATTTATGCGCCGCGGAGAGATCCTTGGGAAATTTTC 300
QY 301 CTAGAACATGTCGAACAACTTATTAATCAACAATTAACAATAATGCTAGGAAATACCGCA 360
DB 301 CTAGAACATGTCGAACAACTTATTAATCAACAATAATGCTAGGAAATACCGGATACCGGT 360
```

QY 361 CTTCCTCGATTAACAAGGTTAGGAGATTCCTTTAGAGCCTATCAACAGTCACCTTGGAAGAT 420
DB 361 CTTCCTCGATTAACAAGGTTAGGAGATTCCTTTAGAGCCTATCAACAGTCACCTTGGAAGAT 420
QY 421 TGGCTAGAAACCGTGATGATGCAAGAACGAGAGTGTTCTTTATACCCCAATATATAGCC 480
DB 421 TGGCTAGAAACCGTGATGATGCAAGAACGAGAGTGTTCTTTATACCCCAATATATAGCC 480
QY 481 TTAGAACTTCGATTTCTTAATGCGATGCCGCTTTTCGCAATTAGAAACCAAGAGTTCCA 540
DB 481 TTAGAACTTCGATTTCTTAATGCGATGCCGCTTTTCGCAATTAGAAACCAAGAGTTCCA 540
QY 541 TTATTAATGATATATGCTCAAGCTGCAAAATTTACACCTATTTATTTAGAGAGATGCCCTCT 600
DB 541 TTATTAATGATATATGCTCAAGCTGCAAAATTTACACCTATTTATTTAGAGAGATGCCCTCT 600
QY 601 CTTCCTGATGTAATTTGGGCTTTACATCGAGGAATTCGCTTTATTTATGAGCGCCAA 660
DB 601 CTTCCTGATGTAATTTGGGCTTTACATCGAGGAATTCGCTTTATTTATGAGCGCCAA 660
QY 661 GTGGAAACAAACGAGAGATTTTCGACTATTTGGGTAGAAATGGGTATATACAGGTCTAAAT 720
DB 661 GTGGAAACAAACGAGAGATTTTCGACTATTTGGGTAGAAATGGGTATATACAGGTCTAAAT 720
QY 721 AGCTTGAGAGGCAAAATGCGCAAGTTGGGTGCTTTATTAATCAATTCGCTGAGAGATCTTA 780
DB 721 AATTTGAGAGGCAAAATGCTGAAAGTTGGGTGCGATATTAATCAATTCGCTGAGAGATCTTA 780
QY 781 ACCTTAGGGGTATAGATCTAGTGGCACTATTCGAGCTATGACACTGCCACTTATCCA 840
DB 781 ACCTTAGGGGTATAGATCTAGTGGCACTATTCGAGCTATGACACTGCCACTTATCCA 840
QY 841 ATAAATACGAGTGCTCAGTTTAAACAGGGAAGTTTATACAGACGCAATTTGGAGCAACAGGG 900
DB 841 ATGAATACGAGTGCTCAATTTAAACAGAGAAATTTATACAGATCCAATTTGGGAGAACAAAT 900
QY 901 GTAAAT-----ATGGCAAGTATGAATTTGGTATTAATTAATGAATGACCTTCGTTTCGGT 954
DB 901 GCACCTTCAGGATTTGCAAGTACGAAATGGTTTAAATAATGAATGACCACTGGTTTCGTGCC 960
QY 955 ATAGAGACTCGGTTATCCGAAACCGCATCTACTTGATTTCTAGAACCACTTACAAAT 1014
DB 961 ATAGAGCTCGGTTATTTAGGCTTCGCACTCTACTTGATTTCCAGAACAGCTTACAAAT 1020
QY 1015 TTATGACACTTCATCAGCATGAGTGCTACTAGGCATATGACTTACTGGCGGGGCAACA 1074
DB 1021 TTACGCGTATTAAGTCATGAGTAATACTCAATATATGAATTAATCTGGGTGGGACATAGA 1080
QY 1075 ATTCATCTCGGCCAATPAGAGCGGATTAATACTCAACGCAATGGGTCTCACTACT 1134
DB 1081 CTTCGATTCGCAACAAATAGGGGCTCATTAAGTACCTGGACACACGGAATACCAATACT 1140
QY 1135 TCTATTAATCTGTAAGATTAATCTCTCTCGAGACGCTATATTTGGACTGATCATAT 1194
DB 1141 TCTATTAATCTGTAACATTAACAGTTTACATCTCGAGACGCTTTATAGAACAGAAATCAAT 1200
QY 1195 GCAGGAGTGCTTCTATGGGAAATTAACCTTGAACCTATTCATGCTGCTCCTACTGTTAGA 1254
DB 1201 GCAGGATTAATAT-----ACTTCTAATCTCTGCTGATGAGTACCTTGGGCTAGA 1254
QY 1255 TTTAATTTTAGGAACCTCAGAAATPACTTTTGAAGAGGTACTGCTAACTATAGTCAACCC 1314
DB 1255 TTTAATTTAGGAACCTCCCTGAATCTCTT---AGAGGTAGCCTTCTCTATCTATAGGG 1311
QY 1315 TATGAGTCACTGGGCTTCAATTAAGATTCGAACTGAATTTACCACAGAACAAACA 1374
DB 1312 TATCTGGAGTGGGACACAACTATTTGATTCAGAACTGAATTTACCACAGAACAAACA 1371
QY 1375 GAACGACCAAAATATGAATCATATAGTCATAGGTTATCTCACATAGGGCTCATTTTACAA 1434
DB 1372 GAACGACCAAAATATGAATCTTACATCATAGATTATCTAATATAGCAATATATCAGGA 1431
QY 1435 TCTAGGTCATGATVACCAATATATCTTTGGACGACCGTAGTCAGATCGTACAAATACC 1494

DB 1432 AACACTTTGAGACCAACAGTATATCTTGACCAACCGTAGTCAGATCGTACAAATACC 1491
QY 1495 ATTAGTTTCAGATAGCATAAACAAATACCAATTCGTTAAATCATTTCAACCTTAAATTCAGT 1554
DB 1492 ATTAGTTTCAGATAGCATAAACAAATACCAATTCGTTAAATCATTTCAACCTTAAATTCAGT 1551
QY 1555 ACCTCTGTAGTCAGTGGCCAGGATTTACAGGAGGGGATATAATCCGAACTAAACGTTAAT 1614
DB 1552 ACCTCTGTAGTCAGTGGCCAGGATTTACAGGAGGGGATATAATCCGAACTAAACGTTAAT 1611
QY 1615 GGTAGTGTACTAAGTATGGGTCTTAATTTTAATAATACATCATTTACAGCGGTATCGCGT 1674
DB 1612 GGTAGTGTACTAAGTATGGGTCTTAATTTTAATAATACATCATTTACAGCGGTATCGCGT 1671
QY 1675 AGATTTGCTTTATCTCTCTCAACAAATGCTCTGAGGGTAACTGTCTCGAGGGAGTACT 1734
DB 1672 AGATTTGCTTTATCTCTCTCAACAAATGCTCTGAGGGTAACTGTCTCGAGGGAGTACT 1731
QY 1735 ACTTTTGATCAAGGATTTCCCTAGTACTATGAGTGCAAATGAGTCTTTTGACATCTCAATCA 1794
DB 1732 ACTTTTGATCAAGGATTTCCCTAGTACTATGAGTGCAAATGAGTCTTTTGACATCTCAATCA 1791
QY 1795 TTTAGATTTGCAAAATTTCCCTGATAGTATTTAGTGCATCTGGCAGTCAAACTGCTGNAATA 1854
DB 1792 TTTAGATTTGCAAAATTTCCCTGATAGTATTTAGTGCATCTGGCAGTCAAACTGCTGNAATA 1851
QY 1855 AGTATAAGTAAATTAATGCAAGTACAAACGTTTTCATTTGATAAATTTGAATTTCAATCCA 1914
DB 1852 AGTATAAGTAAATTAATGCAAGTACAAACGTTTTCATTTGATAAATTTGAATTTCAATCCA 1911
QY 1915 ATTTACTGCAACCTTCGAAGCAGAAATACGATTTTGAAGGGCGCAAGGGCGGTGAATGCT 1974
DB 1912 ATTTACTGCAACCTTCGAAGCAGAAATATGATTTTGAAGAGCGCAAGGGCGGTGAATGCT 1971
QY 1975 CTGTTTACTAATACGAAATTCGAAGAAATGAAACAGATGTGACAGATTAATCATATTGAT 2034
DB 1972 CTGTTTACTAATACGAAATTCGAAGAAATGAAACAGATGTGACAGATTAATCATATTGAT 2031
QY 2035 CAAGTATCCAAATTTAGTGGCGTGTATCGATGAAATTTCTGTTAGATGAAAGAGAGAA 2094
DB 2032 GAAGTATCCAAATTTAGTGGCGTGTATCGATGAAATTTCTGCTTGGATGAAAGAGAGAA 2091
QY 2095 TTAATTTGAGAAAGTAAATATGCAACGACTCAGTGTGAAAGAACTTTACTCCTCAAGAT 2154
DB 2092 TTAATTTGAGAAAGTAAATATGCAACGACTCAGTGTGAAAGAACTTTACTCCTCAAGAT 2151
QY 2155 CCAAACTTCATCTCAATTAAGCAACCGACTTCAATTTCTAATTAATGAGCAATCGAAT 2214
DB 2152 CCAAACTTCATCTCAATTAAGCAACCGACTTCAATTTCTAATTAATGAGCAATCGAAT 2211
QY 2215 TTCACATCTATCCATCAATTAAGCAACCGACTTCAATTTCTAATTAATGAGCAATCGAAT 2274
DB 2212 TTCACATCTATCCATCAATTAAGCAACCGACTTCAATTTCTAATTAATGAGCAATCGAAT 2271
QY 2275 CAGGAAAGAAATCAGCTATTTAAAGAGAAATACGTCACACTACCGGGGACTTTTAAATGAG 2334
DB 2272 CAGGAAAGAAATCAGCTATTTAAAGAGAAATACGTCACACTACCGGGGACTTTTAAATGAG 2331
QY 2335 TGTATTCGAGCTATTTATTAATAAGAGAGTCCGAAATTAAGCTTATCTACTCGC 2394
DB 2332 TGTATTCGAGCTATTTATTAATAAGAGAGTCCGAAATTAAGCTTATCTACTCGC 2391
QY 2395 TACCAATTAAGAGGTATATTTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGTTAT 2454
DB 2392 TACCAATTAAGAGGTATATTTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGTTAT 2451
QY 2455 AATGCGAAACATGAACATTTGGATGTTTCCAGGTACCGAGTCCGCTGCGCTTTCAAGT 2514
DB 2452 AATGCGAAACATGAACATTTGGATGTTTCCAGGTACCGAGTCCGCTGCGCTTTCAAGT 2511
QY 2515 GAAGGCCAATCCGAGGTCCGAGACCGAATTCGATGCGCACCAATTTGATGGAAT 2574

2512 GAAAGCCCAATCGAAGGTCGGAGAACCGAATCGATCGGCACACATTTTGAATGGAAT 2571
 2575 CCTGATCTAGATGTTCTCTCAGAGATGAGAGAAAATGTGGCATCATTCCTCCATCATTT 2634
 2572 CCTGATCTAGATGTTCTCTCAGAGATGAGAGAAAATGTGGCATCATTCCTCCATCATTT 2631
 2635 TCCTTGGATATTGATTTGATGTCACAGACTTGGATGAGATCTAGCGGTGGTGGTGA 2694
 2632 TCCTTGGATATTGATTTGATGTCACAGACTTGGATGAGATCTAGCGGTGGTGGTGA 2691
 2695 TTCAAGATTAAAGACGCGAGGAGGTCATGCAAGACTAGCGAATCTGGAATTTATTGAAGAG 2754
 2692 TTCAAGATTAAAGACGCGAGGAGGTCATGCAAGACTAGCGAATCTGGAATTTATTGAAGAG 2751
 2755 AAACCAATTATTAGAGAGAACCTGTCTGTGTGAAGAGACAGAGAAAAAATGGAGAGAC 2814
 2752 AAACCAATTATTAGAGAGAACCTGTCTGTGTGAAGAGACAGAGAAAAAATGGAGAGAC 2811
 2815 AAACGTGAAAACCTACAAATTGGAACAAAACGAGTATATACAGAGGCAAAAGAGCTGTG 2874
 2812 AAACGTGAAAACCTACAAATTGGAACAAAACGAGTATATACAGAGGCAAAAGAGCTGTG 2871
 2875 GATGCTTTATTGTAGATTCTCAATATAATAGATTACAAGCGGATACAAACATTTGGCATG 2934
 2872 GATGCTTTATTGTAGATTCTCAATATAATAGATTACAAGCGGATACAAACATTTGGCATG 2931
 2935 ATTCAATCGGACAGATAAATCTGTTTCATGAAATTCAGAGGCTTATCTGTGAGAAATATCT 2994
 2932 ATTCAATCGGACAGATAAATCTGTTTCATGAAATTCAGAGGCTTATCTGTGAGAAATATCT 2991
 2995 GTTATCCCGGTGTAATGCGGAATTTTGAAGAAATTAGAAGTCCATATCACTGCA 3054
 2992 GTTATCCCGGTGTAATGCGGAATTTTGAAGAAATTAGAAGTCCATATCACTGCA 3051
 3055 ATCTCCCTATACAGATGCGAGAAATGTCGTTAAATAATGCTGATTTAATAATGATTAGCA 3114
 3052 ATCTCCCTATACAGATGCGAGAAATGTCGTTAAATAATGCTGATTTAATAATGATTAGCA 3111
 3115 TGCTGGAATGTAAAGGCGCATGTAGATGTACAAAGAGCCATCACCGTCTCTGCTCTGTT 3174
 3112 TGCTGGAATGTAAAGGCGCATGTAGATGTACAAAGAGCCATCACCGTCTCTGCTCTGTT 3171
 3175 ATCCAGAAATGGGAGAGAGAGTGTCAAGACAGTTCGCTGCTGTCGGGGCGTGGCTAT 3234
 3172 ATCCAGAAATGGGAGAGAGAGTGTCAAGACAGTTCGCTGCTGTCGGGGCGTGGCTAT 3231
 3235 ATCTCCGCTGTACAGAGTCAAGAGAGGATATGAGAGAGGTTGTTAAACGATCCATGAA 3294
 3232 ATCTCCGCTGTACAGAGTCAAGAGAGGATATGAGAGAGGTTGTTAAACGATCCATGAA 3291
 3295 ATCCAGAAACATACAGACGAATTTAAATAATTTAAACCTGTGAAGAGAGGAGTGTATCCA 3354
 3292 ATCCAGAAACATACAGACGAATTTAAATAATTTAAACCTGTGAAGAGAGGAGTGTATCCA 3351
 3355 ACGGATACAGAAAGTGTATGATATATCTGACACCAAGGATACAGAGTATGTAATCC 3414
 3352 ACGGATACAGAAAGTGTATGATATATCTGACACCAAGGATACAGAGTATGTAATCC 3411
 3415 CGTAACTCGATATGAGGATGATAGTGAAGTGTATGATGATGATGATGATGATGATGATGAT 3474
 3412 CGTAACTCGATATGAGGATGATAGTGAAGTGTATGATGATGATGATGATGATGATGATGAT 3471
 3475 CCGACTTATGAAGAGAGAAACCTATACAGATGTACGAGAGATATCATTTGTGAATATGAC 3534
 3472 CCGACTTATGAAGAGAGAAACCTATACAGATGTACGAGAGATATCATTTGTGAATATGAC 3531
 3535 AGAGGATATGTAATTTATCCACTACAGCTGGTGTATATGACAAAGAAATTAGAAATAC 3594
 3532 AGAGGATATGTAATTTATCCACTACAGCTGGTGTATATGACAAAGAAATTAGAAATAC 3591
 3595 TTCCAGAAACCGATAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3654
 3592 TTCCAGAAACCGATAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3651

Qy 3655 GACAGCGTGAATTAATCTCTTATGAGGAATAG 3687
 Db 3652 GACAGCGTGAATTAATCTCTTATGAGGAATAG 3684

RESULT 8

BTCRYA4

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. 3687

/organism="Bacillus thuringiensis"

/mol_type="genomic DNA"

/strain="HD-2"

/db_xref="taxon:1428"

1. 3687

/notes="unnamed protein product; delta-endotoxin (AA

1-1228)"

/codon_start=1

/transl_table=11

/protein_id="CAA29898.1"

/db_xref="GI:580949"

/db_xref="GOA:P05517"

/db_xref="UniProt/Swiss-Prot:P05517"

/translation="MTSNRKNENEIINAVNSHAQMDLPDARIEDSLCIAEAGNNIDP

FVSAATVQTGINIAGRIIVLGVFGAGLAFYFLVGLWPRGRDQWEIFLEHVEQL

INQITENARNTALRLQGLDSFRAYQOQSLDLENRDDARTSVLYTOYVIALELDF

LNAMPFLARNOEVLPLMYQAANLHLLRLDASLFGSEFGLTSQIORYYERQVER

TRYSYCVENYNTGLNSLGTNAASWRVNRQRRDLTLGLDLVALFPYDITPI

NTSAQUTREYVTDATGATGVNMAWMNNNAFSAIAEAAKSPHLLDFLEQITIF

SASSRNSNRHMTYWRGHTIQSRPIGGGLNTSTHGATNTINPVTLFASRDVYRTES

YAGVLLGIYLEPIHGVTFRFTNPQISDRGTANYSQPYSGIQLKDSLETLP

ETTERPNYSYSHRLSHIGIILQSRVNVVSWTHRSADRTNTIGPNRIQIIPMKVAS

ELPGCTTVRGPGTGDILRRNTGGGPIRVTVNGPLTQRYRIGRYASTVDPDFE

VSRGTTVNNFRFLRTHNSGDELKYGNFVRAATPTPTTQIIDIIRTSIQGLSGNE

YIDKLEIIPVTATFAEYDLERQAVNALFTNPRLUKTDITDTHIQVSNLVAC

LSDFCFLDEKRELLEKVKAKLSDERNLQDNFTSINKQDFISNQSNTSIHE

QSHGWGSENITQEGNDVFNKYVTLPGTFNECYPTLYIKGISELKAFTYQLR

GYLDSQDLIYLIRYNAXHETLDVPGTESLPLSPVESPIGRCEPNRCAHPFEPND

LDCSGDEKCAHSHHSLDIDVCTDLHNLGVWVFKIKTQEGHARLGNLFIE

KPLIGALSRLKRAEAKWRDKRKLQLETKRYVTEAKEAVDALFPVDSQYDLQADTNI

GTHADKLVRHIREAYLSLPLPGVNAEIFELEGHIIITSLISDARNVNRKNGDFN

NGITCNWGHVDVQSHHSLDVIPEWEAEVQAVRVCPCGVIIRVLTATKEGYGEG

CTVTHIENNTDELKFNREBEVYPTDGTCDNYTAHQGTAGCADCACNRNAGYEDA

YEYDITASVNYKTYBEETVTDVRRDNHCYDRGVNYPVPVAGYVTKLEYFPETDT

WVIEGTGKFKIVDSVELLMEE"

ORIGIN

Query Match 85.1%; Score 3136.8; DB 1; Length 3687;

Best Local Similarity 91.2%; Pred. No. 0;

Matches 3375; Conservative 0; Mismatches 297; Indels 30; Gaps 3;

Qy 1 TTGACTTCAATAGGAAAAATGAGATGAATTAATAATGCTTTATCGATTCAGCTGTGA 60

Db 1 |||||TTGACTTCAAAATAGGAAATGAGAAATGAAATATATAAAT-----GCTGTA 45
 Qy 61 TCGAATCATTTCCACACAAATGGATCTATACCAGATGCTCGTATGAGGATTTCTTTGTTG 120
 Db 46 TCGAATCATTTCCGACAAATGGATCTATACCAGATGCTCGTATGAGGATGCTTTGTTG 105
 Qy 121 ATAGCCGAGGGGAAATATATCAATCCACTTTGTTAGCGCATCAACAGTCCCAACGGGTATT 180
 Db 106 ATAGCCGAGGGGAAATATCGATCCATTTGTTAGCGCATCAACAGTCCCAACGGGTATT 165
 Qy 181 AACATAGCTGGTAGAATACATAGGTGATATAGGCGTACCGTTTGTCTGCAAAATAGCTAGT 240
 Db 166 AACATAGCTGGTAGAATACATAGGCGTATAGGCGTACCGTTTGTCTGCAAAATAGCTAGT 225
 Qy 241 TTTTATAGTTTTCTTTGTTGTTGTAATATGCGCGCGCGAGATCAGTGGGAAATTTTC 300
 Db 226 TTTTATAGTTTTCTTTGTTGTTGTAATATGCGCGCGCGAGATCAGTGGGAAATTTTC 285
 Qy 301 CTAGAACATGTCGAACAACTTATAAAATCAACAAATACAGAAATGCTAGGAATACGGCA 360
 Db 286 CTAGAACATGTCGAACAACTTATAAAATCAACAAATACAGAAATGCTAGGAATACGGCT 345
 Qy 361 CTGCTCGATTAACAAGTTTAGAGATTCCTTTAGAGCCTATCAACAGTCACTTGAAGAT 420
 Db 346 CTGCTCGATTAACAAGTTTAGAGATTCCTTTAGAGCCTATCAACAGTCACTTGAAGAT 405
 Qy 421 TGCTAGAAACCGTGATGATGAAGAACAGAGAGTCTCTTTATACCCCAATATATAGCC 480
 Db 406 TGGCTAGAAACCGTGATGATGAAGAACAGAGAGTCTCTTTATACCCCAATATATAGCT 465
 Qy 481 TTAGAACTTGATTTTCTTAATGCGATGCGCTTTTCGAAATAGAAACCAAGATTTCCA 540
 Db 466 TTAGAACTTGATTTTCTTAATGCGATGCGCTTTTCGAAATAGAAACCAAGATTTCCA 525
 Qy 541 TTATTAATGTTATGCTCAAGTGCAGAAATTTACACCTATTTATTTAGAGATGCTCT 600
 Db 526 TTATTAATGTTATGCTCAAGTGCAGAAATTTACACCTATTTATTTAGAGATGCTCT 585
 Qy 601 CTTTGTGTTAGTGAATTTGGGCTTACATCCGAGAAATTCACGTTTATTTAGCGCCAA 660
 Db 586 CTTTGTGTTAGTGAATTTGGGCTTACATCCGAGAAATTCACGTTTATTTAGCGCCAA 645
 Qy 661 GTGAAACAAACGAGAGATTTCCGACTATTTGGTGAATTTGGTATATACAGGTCTAAAT 720
 Db 646 GTGAAACAAACGAGAGATTTCCGACTATTTGGTGAATTTGGTATATACAGGTCTAAAT 705
 Qy 721 AGCTTGAGGGGACAAATGCGCAGTTGGTGGGTTATATCAATCCATCCGTAGATCTA 780
 Db 706 AGCTTGAGGGGACAAATGCGCAGTTGGTGGGTTATATCAATCCATCCGTAGATCTA 765
 Qy 781 ACGTTAGGGGTATTAGATCTAGTGGCACTATCCCAAGCTATGACCTCGCACTTATCCA 840
 Db 766 ACGTTAGGGGTATTAGATCTAGTGGCACTATCCCAAGCTATGACCTCGCACTTATCCA 825
 Qy 841 ATAAATACGAGTGTCTCAGTTTAAACAGGGAAGTTTATACAGACGCAATTTGAGCAACAGG 900
 Db 826 ATAAATACGAGTGTCTCAGTTTAAACAGGGAAGTTTATACAGACGCAATTTGAGCAACAGG 885
 Qy 901 GTAATATGCAAGTATGAATTTGGTATTAATAATATGCACTTCCTGTTTCCGCTATAGAG 960
 Db 886 GTAATATGCAAGTATGAATTTGGTATTAATAATATGCACTTCCTGTTTCCGCTATAGAG 945
 Qy 961 ACTGCGGTATCCGAAGCCGCACTCTACTTTGATTTTCTAGAACAACTTACAAATTTTTC 1020
 Db 946 GCTGCGGTATCCGAAGCCGCACTCTACTTTGATTTTCTAGAACAACTTACAAATTTTTC 1005
 Qy 1021 ACTTCATCAGATGGAGTGTCTAGGCAATATGATTTACTGGGGGGGACAAATTTCAA 1080
 Db 1006 GCTTCATCAGATGGAGTGTCTAGGCAATATGATTTACTGGGGGGGACAAATTTCAA 1065
 Qy 1081 TCTCGGCCAATAGGAGCGGAATTAATACCTCAACGATGGGCTACCAATCTCTATT 1140

Db 1066 TCTCGGCCAATAGGAGCGGATTAATACTCAACGATGGGGCTACCAATCTCTTATT 1125
 Qy 1141 AATCCTGTAAGATTATCATTTCTCTCGAGAGCTATATTGGACTGAATCATATGACGGA 1200
 Db 1126 AATCCTGTAACATTACGTTCCGATCTCGAGAGCTTTTAGGACTGAATCATATGACGGA 1185
 Qy 1201 GTCTTTCTATGGGGAATTTACCTTTGAACCTTATTCATGGTGTCCCTACTGTTAGATTAA 1260
 Db 1186 GTCTTTCTATGGGGAATTTACCTTTGAACCTTATTCATGGTGTCCCTACTGTTAGATTAA 1245
 Qy 1261 TTTAGGAACCTTCAGAAATACCTTTTGAAGAGGTACTGCTTAACCTATATAGTCAACCTATGAG 1320
 Db 1246 TTTAGGAACCTTCAGAAATATTTCTGATAGAGTACCGCTAACTATATAGTCAACCTATGAG 1305
 Qy 1321 TCACCTGGGCTTCAATTTAAAGATTCAGAAATTCAGAAATTCACACAGAAACAAACAGAACGA 1380
 Db 1306 TCACCTGGGCTTCAATTTAAAGATTCAGAAATTCAGAAATTCACACAGAAACAAACAGAACGA 1365
 Qy 1381 CCAAAATATGAATCATATATAGTCTATAGTTCATCATAGGGCTCATTTTCACAATCTTAGG 1440
 Db 1366 CCAAAATATGAATCTTTACAGTCAAGTTCATCATATAGGTATATTTTACAAATCCAGG 1425
 Qy 1441 GTGCATGTACCAGTATATTTCTTGGACGCAACCGTAGTGCAGATCGTACAAATACCATTAGT 1500
 Db 1426 GTGAATGTACCGGTATATTTCTTGGACGCAACCGTAGTGCAGATCGTACAAATACCATTAGG 1485
 Qy 1501 TCAGATAGCATAAACAAATACCAATTTGGTAAATCATTTCAACCTTAATTCAGGTACTCT 1560
 Db 1486 CCAAAATAGAAATCAACCAATCCCAATTTGGTAAAGCATTCGAATTTCTCAAGTACCACT 1545
 Qy 1561 GTAGTCAGTGGCCAGGATTTACAGAGGGGATATTAATCCGAACCTAAACGTTAATGGTAGT 1620
 Db 1546 GTTGTGTAGAGGACAGGATTTACTGTTGGGATATTTCTTCGAAGAACGAATATCTGGTGA 1605
 Qy 1621 GTACTAAGTATGGTCTTAAATTTTAAATATACATCATTTACAGCGGTATCCGCTGAGATT 1680
 Db 1606 TTTGGACCGAATAGAGTAACTGTAAACGACCACTAAACAAAGATATCGTATAGGATTC 1665
 Qy 1681 CGTTATGCTGCTTCTCAACAAATGGTCTCGAGGGTAACTGTTCGAGGGAGTACTACTTTT 1740
 Db 1666 CGCTATGCTTCACTGTAGATTTTGATTTCTTTGTATCAGTGGAGGTACTACTGTAAAT 1725
 Qy 1741 GATCAAGGATTCCTTAGTACTATGATGCAAAATGAGTCTTTTGACATCTCAATCATTTAGA 1800
 Db 1726 AATTTTAGATTTCTAGCTCAATGAAACAGTGGAGAGCACTAAATACGGAATTTTGTG 1785
 Qy 1801 TTTTGCAAAATTTCTGTAGGTATTTAGTGCATCTGGCAGTCAA--ACTGCTGGAATAAGT 1857
 Db 1786 AGACGTGCTTTTACTACACCTTTTACTTTTACACAAATTCAGATATATTCGAACGTCT 1845
 Qy 1858 ATAAGTAAATAATGCAGGTAGACAAACGTTTCACTTTGATAAAATTTGAAATTCATTTCAAAT 1917
 Db 1846 ATTCAGAGCCTTAGTGGAAATGGGGAAGTCTATATAGATAAAATTTGAAATTTTCCAGTT 1905
 Qy 1918 ACTGCAACCTTTCGAAGCAATACGATTTAGAAAGGGCGCAAGGGCGGTGAATGCTCTG 1977
 Db 1906 ACTGCAACCTTTCGAAGCAATATGATTTAGAAAGAGCGCAAGGGCGGTGAATGCTCTG 1965
 Qy 1978 TTTTACTAATACGAATCCAGAGAGATTTGAAACAGATGTCACAGATTTATCATTTGATCAA 2037
 Db 1966 TTTTACTAATACGAATCCAGAGAGATTTGAAACAGATGTCACAGATTTATCATTTGATCAA 2025
 Qy 2038 GTATCCAAATTTAGTGGCTGTTTATCGGATGAATTTCTGCTTAGATGAAAGAGAGAAATTA 2097
 Db 2026 GTATCCAAATTTAGTGGCTGTTTATCGGATGAATTTCTGCTTGGATGAAAGAGAGAAATTA 2085
 Qy 2098 CTTGAGAAATGTAATATGCGAAACGACTCAGTGTGAAGAAACTTACTCCAGATCCA 2157
 Db 2086 CTTGAGAAATGTAATATGCGAAACGACTCAGTGTGAAGAAACTTACTCCAGATCCA 2145
 Qy 2158 AACTTCACATCCATCAATAGGCAACGACTTTCATATCTACTAATGAGCAATCGAATTTTC 2217
 Db 2146 AACTTCACATCCATCAATAGGCAACGACTTTCATATCTACTAATGAGCAATCGAATTTTC 2205

VYIDKRIIPVATFEAYDILERAQEAVALFTNPNRLKTDVTDHYHQVSNLVC
 LSDEFCLDEKLEKYAKRLSDERNLLQDPNPTFSINKOPDPFISNEOSNFTSIE
 QSEHGWSENIITQEDNVFKNVYTLPGTFNESCPTLYXOKIGESSELKAYFYQLR
 GYIEDSODLEIYLRYNAKHETLDVPGTESLWPLSVESPIGRCEPNNRCAPIHFWNPD
 LDCSRDEKCAKSHHPSLSDIDVGCOTDLHENLVWVWFVKIKTOBEHARIGNLEFIBE
 KPLLEALSRVAKKWRDKREKLOLETRVYTEAKEAVDALFVDSQYDLQADNTI
 GMIHAADKLVRHIREALVSELPVPGVNAEIPFEELGHIITATISLYDARNVKNQDFN
 NGLTCMNKGVHDVQOQSHHSDLVIPWEAEVSOAVRCPGCVILRVATVKEGYGBG
 CVTLENNDELKFKNRREERYPTDTGTCDNYTAHQGTAGCADAENRAGYEDA
 YEVDTTASVNYKPYESETYDVRDNHCEYDRGYVNPVPPVAGVYVTKELIYFPEIT
 VWIEIGETEGKFIVDSEVLLLEE"

ORIGIN

Query Match 85.0%; Score 3135.2; DB 1; Length 3687;
 Best Local Similarity 91.1%; Pred. No. 0;
 Matches 3374; Conservative 0; Mismatches 298; Indels 30; Gaps 3;

Qy	1	TTGACTTCAATAGAGAAAATGAGAATGAAATTAATAATGCTTTATCGATTTCCAGCTGTGA	60
Db	1	TTGACTTCAATAGAGAAAATGAGAATGAAATTAATAATGCTTTATCGATTTCCAGCTGTGA	45
Qy	61	TCGAATCATCCACACAAATGGATCTATACACGATGCTCGTATTGAGGATCTTTGTGT	120
Db	46	TCGAATCATTCGGCACAAATGGATCTATACACGATGCTCGTATTGAGGATGCTTGTGT	105
Qy	121	ATAGCCGAGGGGAATAATCAATCCACTTGTGTAGCGCATCAACAGTCCAAACGGGTATT	180
Db	106	ATAGCCGAGGGGAACATATCGATCCATTTGTGTAGCGCATCAACAGTCCAAACGGGTATT	165
Qy	181	AACATAGCTGTAGAATACTAGGTGTATTAGCGCTACCGTTTGTGTGACAAAATAGCTAGT	240
Db	166	AACATAGCTGTAGAATACTAGCGGTATTGGCGGTACCGTTTGTGTGACAACTAGCTAGT	225
Qy	241	TTTTATAGTTTTCTTTGTGTGAATATTGCGCGCGCGAGATCAGTGGGAAATTTTC	300
Db	226	TTTTATAGTTTTCTTTGTGTGAATATTGCGCGCGCGAGATCAGTGGGAAATTTTC	285
Qy	301	CTAGAACATGTGAAACAACTTATAAATCAACAAATAACAGAAAATGCTAGGAATACGGCA	360
Db	286	CTAGAACATGTGAAACAACTTATAAATCAACAAATAACAGAAAATGCTAGGAATACGGCT	345
Qy	361	CTTGCTCGATTACAGGTTTAGGAGATTCCTTTAGAGCCTATCAACAGTCACTTGAAGAT	420
Db	346	CTTGCTCGATTACAGGTTTAGGAGATTCCTTTAGAGCCTATCAACAGTCACTTGAAGAT	405
Qy	421	TGGCTAGAAAACCTGTATGATGCAAGAACAGAGATGCTTTTATATCCCAATATATAGCC	480
Db	406	TGGCTAGAAAACCTGTATGATGCAAGAACAGAGATGCTTTTATATCCCAATATATAGCT	465
Qy	481	TTAGAACTTGATTTTCTTAATGCGATCGCGCTTTTCGCAATTAGAAAACCAAGAGTTCCA	540
Db	466	TTAGAACTTGATTTTCTTAATGCGATCGCGCTTTTCGCAATTAGAAAACCAAGAGTTCCA	525
Qy	541	TTATTATGTTATATGCTCAAGCTGCAAAATTTACACCTATTATTATTGAGAGATGCTCT	600
Db	526	TTATTATGTTATATGCTCAAGCTGCAAAATTTACACCTATTATTATTGAGAGATGCTCT	585
Qy	601	CTTTTGTGTAGTGAATTTGGGCTTTACATCGCAGAAATTCACGTTATTATTAGAGCGCAA	660
Db	586	CTTTTGTGTAGTGAATTTGGGCTTTACATCGCAGAAATTCACGTTATTATTAGAGCGCAA	645
Qy	661	GTGGAAACAAACGAGAGATTATTCGACTATTTCGGTAGAATGGTATATAACAGCTCTAAAT	720
Db	646	GTGGAAACAAACGAGAGATTATTCGACTATTTCGGTAGAATGGTATATAACAGCTCTAAAT	705
Qy	721	AGCTTGAGAGGACAAATGCGCAAGTTGGTGGCTTATTAATCAATTCGATAGATCTTA	780
Db	706	AGCTTGAGAGGACAAATGCGCAAGTTGGTGGCTTATTAATCAATTCGATAGATCTTA	765
Qy	781	ACGTTAGGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGACACTCGCACTTATCCA	840
Db	766	ACGTTAGGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGACACTCGCACTTATCCA	825

Qy	841	ATAAATACGAGTGTCTCAGTTTAAACAGGGAAGTTTATACAGACGCAATTTGAGCAACAGGG	900
Db	826	ATAAATACGAGTGTCTCAGTTTAAACAGGGAAGTTTATACAGACGCAATTTGAGCAACAGGG	885
Qy	901	GTAATAATGCAAGTATGAATGGTATTAATAATGCAACCTTCGTTTTCGGCTATAGAG	960
Db	886	GTAATAATGCAAGTATGAATGGTATTAATAATGCAACCTTCGTTTTCGGCTATAGAG	945
Qy	961	ACTGCGGTATTCGAGAGCCCGCATCTACTTGAATTTCTAGAAACAACTTAAATTTTATG	1020
Db	946	GCTGCGGCTATTCGAGAGCCCGCATCTACTTGAATTTCTAGAAACAACTTAAATTTTATG	1005
Qy	1021	ACTTTCATCAGATGAGTGTCTACTAGCATATGACTTACTTGGCGGGGCGACAAATTTCAA	1080
Db	1006	GCTTTCATCAGATGAGTGTCTACTAGCATATGACTTACTTGGCGGGGCGCGCAATTTCAA	1065
Qy	1081	TCTCGGCAATAGGAGCGGATTAATACCTCAACGCATGGGTCTACCAATATCTTCTATT	1140
Db	1066	TCTCGGCAATAGGAGCGGATTAATACCTCAACGCATGGGTCTACCAATATCTTCTATT	1125
Qy	1141	AATCCTGTAGATTAATCTTCTCTCGAGAGCTATATTGGACTGAATCATATGACGGA	1200
Db	1126	AATCCTGTAACTTACCGTTTCGATCTCGAGAGCTTTATAGGACTGAATCATATGACGGA	1185
Qy	1201	GTGCTTCTATGGGGAATTTTACCTTGAACCTTATTCTCATGGTGTCCCTACTGTAGATTAA	1260
Db	1186	GTGCTTCTATGGGGAATTTTACCTTGAACCTTATTCTCATGGTGTCCCTACTGTAGATTAA	1245
Qy	1261	TTTAGGAACCTCTCAGAAATCTTTTGAAGAGGTATCTGTAACTATATAGTCAACCTATGAG	1320
Db	1246	TTTAGGAACCTCTCAGAAATCTTTCTGTATAGAGGTACCGCTAACTATATAGTCAACCTATGAG	1305
Qy	1321	TCACCTGGGCTTCAATTTAAAGATTCAGAACTTCAAGAACTTACCACAGAAACAAACAGAACGA	1380
Db	1306	TCACCTGGGCTTCAATTTAAAGATTCAGAACTTCAAGAACTTACCACAGAAACAAACAGAACGA	1365
Qy	1381	CCAAATTTATGAATCATATATAGTTCATAGGTTTATCTACATAGGGCTCAATTTCACAATCTAGG	1440
Db	1366	CCAAATTTATGAATCTTTACAGTCAACAGTTTATCTCATATAGGTATTAATTTTACAACTCCAGG	1425
Qy	1441	GTGCATGTACAGTATATTTCTTGGAGCGACCGTAGTGCAGATCGTACAAATACCATTAGT	1500
Db	1426	GTGAATGTACCGGTATATTTCTTGGAGCGATCGTAGTGCAGATCGTACGAATACCATTTGA	1485
Qy	1501	TCAGATAGCATACAAATAACCATTTGTTAAATCAATCAACCTTAAATTTTCAAGTACCTCT	1560
Db	1486	CCAAATAGAAATCACCAATCCCAATGGTAAAGCATCGAACTTCTCCTCAAGTACCACT	1545
Qy	1561	GTAGTCAGTGGCCAGGATTTTACAGAGGGGATATTAATCCGAACTAACCGTTAATGGTAGT	1620
Db	1546	GTGTGTAGAGGACCAAGATTTTACTGGTGGGATATTTCTCGAAGAACGAATACCTGGTGA	1605
Qy	1621	GTACTAAGTATGGTCTTAAATTTTAAATATACATCATTAACAGCGGTATCGGTGAGAGTT	1680
Db	1606	TTTGGACCGATAAGAGTAACTGTTTAACCGGACCAATTAACACAAAGATATCGTATAGGATTC	1665
Qy	1681	CGTTATGCTTCTTCAACAAATGGTCTCGAGGTAACCTGTCGGAGGGAGTACTACTTTT	1740
Db	1666	CGCTATGCTTCAACTGTAGATTTTGAATTTCTTTGTATACGTGGAGGTACTACTGTAAT	1725
Qy	1741	GATCAAGGATTTCCCTAGTACTATGATGCAAAATGAGTCTTTGACAFCTCAATCAATTTAGA	1800
Db	1726	AAATTTTAGATTTCTACGTACAAATGAACAGTGGAGACGAATTAATAACGAAATTTTGTG	1785
Qy	1801	TTTGCAGAAATTTCTGTAGGTATTAGTGCATCTGGCAGTCAA---ACTGCTGGAATAAGT	1857
Db	1786	AGACGTGCTTTTACTACACTTTTACTTTTACAAATTTCAAGATATAATTCGAACGTCT	1845
Qy	1858	ATAAGTAATAATGCAAGGTAGACAAACGTTTCTTGTATAAAATTTGAAATTCATTTCAAAT	1917
Db	1846	ATTCAAGGCTTTAGTGGAAATGGGGAAGTGTATATAGATATAAATTTGAATTTTCCAGTT	1905
Qy	1918	ACTGCAACCTTCGAAGCAGAAATACGATTTTAGAAAGGGCGCAAGCGGTGAATGCTCTG	1977

1906 ACTGCAACCTTCGAGCAGAAATGATTTAGAAAGCGCAGAGCGGTGAATGCTCTG 1965
1978 TTTTACTAATACGAATCCAGAAGATTGAAACAGATGTGACAGATTATCATATTGATCAA 2037
1966 TTTTACTAATACGAATCCAGAAGATTGAAACAGATGTGACAGATTATCATATTGATCAA 2025
2038 GTATCCAAATTTAGTGGCGTGTATTCGGATGAATTCCTGCTTAGATGAAAGAGAGAAATTA 2097
2026 GTATCCAAATTTAGTGGCGTGTATTCGGATGAATTCCTGCTTAGATGAAAGAGAGAAATTA 2085
2098 CTTGAGAAAGTGAATATCGAAACGACTCAGTGAATGAAGAACTTACTCCAGATCCA 2157
2086 CTTGAGAAAGTGAATATCGAAACGACTCAGTGAATGAAGAACTTACTCCAGATCCA 2145
2158 AACTTCACATCCATCAATTAAGCAACCAAGCTTCATATCTACTAATGAGCAATCGAATTTTC 2217
2146 AACTTCACATCCATCAATTAAGCAACCAAGCTTCATATCTACTAATGAGCAATCGAATTTTC 2205
2218 ACATCTATCCATGAACAACTCTGAACATGGATGGTGGGAAAGTGAGAACATTAACAATCCAG 2277
2206 ACATCTATCCATGAACAACTCTGAACATGGATGGTGGGAAAGTGAGAACATTAACAATCCAG 2265
2278 GAAGGAATACGCTATTTAAGAGAAATTAAGTACACTACCGGGACTTTAATGAGTGT 2337
2266 GAAGGAATACGCTATTTAAGAGAAATTAAGTACACTACCGGGACTTTAATGAGTGT 2325
2338 TATCCGACGCTATTTATATCAAAAATAGGAGAGTCGGAATTTAAAGCTTATATCTCGCTAC 2397
2326 TATCCGACGCTATTTATATCAAAAATAGGAGAGTCGGAATTTAAAGCTTATATCTCGCTAC 2385
2398 CAATTAAGAGGCTATATTTGAAGATGATCAAGATTTAGAGATATATTTGATTCGTTATAAT 2457
2386 CAATTAAGAGGCTATATTTGAAGATGATCAAGATTTAGAGATATATTTGATTCGTTATAAT 2445
2458 GCGNAACATGAACATTTGGATGTTCCAGGTACCGAGTCCGTTATGGCCGCTTTCAGTTGAA 2517
2446 GCGNAACATGAACATTTGGATGTTCCAGGTACCGAGTCCGTTATGGCCGCTTTCAGTTGAA 2505
2518 AGCCCAATCGGAAGTCCGGAAGACCGAATCGATGCGCACACATTTTGAATGGAATCCCT 2577
2506 AGCCCAATCGGAAGTCCGGAAGACCGAATCGATGCGCACACATTTTGAATGGAATCCCT 2565
2578 GATCTAGATTTTCTCAGAGATGGAAGAAAATGTCGCGATCATTTCCCATCAITTTCTCT 2637
2566 GATCTAGATTTTCTCAGAGATGGAAGAAAATGTCGCGATCATTTCCCATCAITTTCTCT 2625
2638 TTGATATTTGATTTGATGACAGACTTGCATGAGAAATCTAGCGGTGCTGGTGGTATTC 2697
2626 TTGATATTTGATTTGATGACAGACTTGCATGAGAAATCTAGCGGTGCTGGTGGTATTC 2685
2698 AAGATTAAGACGCAAGGATCTGCAAGACTAGGGAATCTGGAATTTATTTGAAGAGAAA 2757
2686 AAGATTAAGACGCAAGGATCTGCAAGACTAGGGAATCTGGAATTTATTTGAAGAGAAA 2745
2758 CCATTTATTAGGAGAACACTGCTCTGCTGTAAGAGAGCAGAGAGAAAATGGAGACAAA 2817
2746 CCATTTATTAGGAGAACACTGCTCTGCTGTAAGAGGCGCAGAGAAAATGGAGACAAA 2805
2818 CGTGAAAACCTAATTTGGAACAAACGAGTATATACAGGGCAAAAGAGCTGTGGAT 2877
2806 CGTGAAAACCTAATTTGGAACAAACGAGTATATACAGGGCAAAAGAGCTGTGGAT 2865
2878 GCCTTTATTGTAGATTTCTCAATATAATAGATTACAAGCGGATACAAACATTTGGCATGATT 2937
2866 GCCTTTATTGTAGATTTCTCAATATAATAGATTACAAGCGGATACAAACATCGGCATGATT 2925
2938 CATCGGCAGATAAATCTGTTTCATCGAATTCGAGAGGCTTATCTGTGAGAAATTTATCTGTT 2997
2926 CATCGGCAGATAAATCTGTTTCATCGAATTCGAGAGGCTTATCTTTCAGAAATTTACCTGTT 2985
2998 ATCCCGGCTGTAATGCGGAAATTTTGAAGAAATTAAGAGTCCCATTTATCAGTGAATC 3057

2986 ATCCAGGTGTAATGCGGAAATTTTGAAGAAATTAGAAAGTACATTATCATCTGCAATC 3045
3058 TCCTTATACGATCGAGAAATGCTGTTAAAAATGGTGATTTTAAATATGATGATGATGTC 3117
3046 TCCTTATACGATCGAGAAATGCTGTTAAAAATGGTGATTTTAAATATGATGATGATGTC 3105
3118 TGGAAATGTAAGAGGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3177
3106 TGGAAATGTAAGAGGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3165
3178 CCAGAAATGGGAAGCAGAAAGTGTCAAGCAGTTCGCGTCTGTCCGGGCGTGGCTATATC 3237
3166 CCAGAAATGGGAAGCAGAAAGTGTCAAGCAGTTCGCGTCTGTCCGGGCGTGGCTATATC 3225
3238 CTCCTGTCTCACAGCGTCAAAAGAGGGATATGGAAGAGGTTGTGTAAACGATCCATGAAATC 3297
3226 CTTTCGTGTACAGCGTACAAAGAGGGATATGGAAGAGGCTGCGTAAACGATCCATGAAATC 3285
3298 GAGAACATACAGACGAACTTAAATTTTAAAACTGTGAAGAGGAAAGTGTATCCAAACG 3357
3286 GAGAACATACAGACGAACTTAAATTTTAAAACTGTGAAGAGGAAAGTGTATCCAAACG 3345
3358 GATACAGGAACGCTGTAATGATTTACTGACACCAAGGTATACAGC-----AGTA 3405
3346 GATACAGGAACGCTGTAATGATTTACTGACACCAAGGTATACAGC-----AGTA 3405
3406 TGTAAATTCCTGATGCTGATATGAGGATGATGATGATGATGATGATGATGATGATGATGATG 3465
3406 TGTAAATTCCTGATGCTGATATGAGGATGATGATGATGATGATGATGATGATGATGATGATG 3465
3466 AATTACAAACCGCTTATGGAAGAAACGATATACAGATGTAAGAGAGAGATAATCATTTGT 3525
3466 AATTACAAACCGCTTATGGAAGAAACGATATACAGATGTAAGAGAGAGATAATCATTTGT 3525
3526 GAATATGACAGAGGCTGTAATTTACCACTACCACTACCACTGTTTATATGACAAAAAGAA 3585
3526 GAATATGACAGAGGCTGTAATTTACCACTACCACTACCACTGTTTATATGACAAAAAGAA 3585
3586 TTAGAATATCTTCCAGAAACCGATTAAGGATGATGATGATGATGATGATGATGATGATGATGATG 3645
3586 TTAGAATATCTTCCAGAAACCGATTAAGGATGATGATGATGATGATGATGATGATGATGATGATG 3645
3646 TTTTATTGTACAGCGCTGGAATTTACTCTTATGGAAGAAATAG 3687
3646 TTTTATTGTACAGCGCTGGAATTTACTCTTATGGAAGAAATAG 3687

RESULT 10

BTCRY1BA2
LOCUS B.thuringiensis cry1Ba2 gene.
DEFINITION X95704
ACCESSION X95704.1 GI:1200001
VERSION cry1Ba2 gene.
KEYWORDS Bacillus thuringiensis
SOURCE Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
ORGANISM
REFERENCE 1
AUTHORS Soetaert, P.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 4074)
AUTHORS Soetaert, P.
TITLE Direct Submission
JOURNAL Submitted (15-FEB-1996) P. Soetaert, Plant Genetic Systems, R&D, J. Plateauststraat 22, Gent, B 9000, Belgium
FEATURES
source
1. 4074
/organism="Bacillus thuringiensis"
/mol_type="genomic DNA"
/strain="HD-110"
/variety="entomocidus"
/db_xref="taxon:1428"

BTCRY1BA2 4074 bp DNA linear BCT 21-FEB-1996


```

RBS      174. .177
gene      186. .3872
          /gene="cry1Ba2"
CDS       186. .3872
          /gene="cry1Ba2"
          /codon_start=1
          /transl_table=11
          /protein_id="CAA65003.1"
          /db_xref="GI:1200002"
          /db_xref="GOA:P05517"
          /db_xref="UniProt/Swiss-Prot:P05517"
          /translation="MTSNRNKENIINAVSNHSAQMDLLPDARTEDSLCIAEGRNIDP
FVSASTQGTGINAGRIQLVGLVFPAGQASFYSLVGLWPRGRDQWEIFLEHVEQL
INQOITNARNALRLQGLDSFRAYQOQSLDLENDKRDARTSRVSHIOVIALELDF
LNAMPFAIRNOEVLPLVYAOAANHLILLRLDASLFGSBEFLTSQIRYVEROVER
TRDYSVCVEVNTGLSLGCTNAASWVUNQPERDLTGLVLDLVALPPSYDRTYFI
NTSAQLREVYTDALGATGVNMAWNNNAPSFALEAAHNSPHLLDFLEOLITF
SASGRNTRMTWRIGHTQSRPIGGLNTSTHGATNTSINPVLRFASRDVYRTES
YAGVLLWGIYLEPIHGVTVPFNFTNPQNTSDRGATANYSPQYESPGQLKDSLETLP
ETTERPNYESYSHRLSHIGIILQSRVNVVSVWTHRSADRTNIGPNRIQIIPWVKAS
ELPOGTTVVRPGFTGDIILRRTVGGFPIRVTVNGPLTQRVRIQPRYASTVDPDFP
VSRGTTVNNFRPLRTWNSGDELKYGNFVRAFTPTFTQIODIISTSLQGLSGNGE
VYIDKIELIPWTAFEAEDLERAEAVNALFTNINPRRLKTDVTDVHIDQVSNLVA
LSDFCDERKELLEKVKIARGLSDERNLLQDPNFTSINKQDPFISINEOSNFTSIHE
QSEHWGSENIITIQEGNVFKNYVTLPGTFNECYPTIYQKIGESLKYATRYQR
GYIEDSDLEIYLRYNKHEHETLDVPGTESLWPLSVESPIRCQEPNRCARLPHFENPD
LDCSRDEKCAHSHHFLSIDVGCETDLHENLGVWVFKIKTQEBGHRNGLNLEFIE
KPLLEALSRLVRKAEKWRDKREKLOLETKRVVTEAKEAVDALEFVDSQYDRLOADINI
GMHAADKLVHRLEAYLSELVPIPGVNAEIPFELECHIITLSLDARNVKNQGNPN
NGLTCWNKGVHDVQQSHHRSDLVLPWEAEVSOAVRVCPCGGTILKRVATYKRGYGG
CYVDTHLENNITDELKFNREBEETVDVRDNHCEYDRGVNYPVPAGYVTKLEYFPETDT
VWIEIGTEGKFIIVDSVELLMEE"
          3958. .3981
          terminator
          ORIGIN

Query Match      85.0%; Score 3133.6; DB 1; Length 4074;
Best Local Similarity 91.1%; Pred. No. 0;
Matches 3373; Conservative 0; Mismatches 299; Indels 30; Gaps 3;

QY      1  TTGACTTCAATAGAAAATAGCAATGAATTAATTAATGCTTTATCGATTCCAGCTGTA 60
DB      186 TTGACTTCAATAGAAAATAGCAATGAATTAATTAATGCTTTATCGATTCCAGCTGTA 230

QY      61  TCGAATCATTCACACAAATGGATCTATCACAGATGCTCGTATGTAGGAGTCTTCTGTGT 120
DB      231 TCGAATCATTCACACAAATGGATCTATCACAGATGCTCGTATGTAGGAGTCTTCTGTGT 290

QY      121 ATAGCCGAGGGGATATATCAATCCACTGTTAGCGCATCAACAGTCCAAACGGGTATT 180
DB      291 ATAGCCGAGGGGAAACAATAATGATCCCAATTTGTTAGCGCATCAACAGTCCAAACGGGTATT 350

QY      181 AACATAGCTGTAGAACTACTAGGTGTATTAGCGGTACCGTTTGTGTCGACAAATAGCTAGT 240
DB      351 AACATAGCTGTAGAACTACTAGGTGTATTAGCGGTACCGTTTGTGTCGACAACTAGCTAGT 410

QY      241 TTTTATAGTTTCTGTGTGTGTAATTATGCCCCGGCGGAGAGATCAGTCGGGAAATTTTC 300
DB      411 TTTTATAGTTTCTGTGTGTGTAATTATGCCCCGGCGGAGAGATCAGTCGGGAAATTTTC 470

QY      301 CTAGAACATGTCGACAACTTATAATCAACAATAACAGAAAATGCTAGGATACGGCA 360
DB      471 CTAGAACATGTCGACAACTTATAATCAACAATAACAGAAAATGCTAGGATACGGCT 530

QY      361 CTGTGCTCGATTACAAGGTTTAGGAGATTCCTTTAGAGCCCTATCAACAGTCACTTGAAGAT 420
DB      531 CTGTGCTCGATTACAAGGTTTAGGAGATTCCTTTAGAGCCCTATCAACAGTCACTTGAAGAT 590

QY      421 TGGCTAGAAAACCGTGATGATGCAAGAACGAGAAAGTGTCTTTATATCCCAATATATAGCC 480
DB      591 TGGCTAGAAAACCGTGATGATGCAAGAACGAGAAAGTGTCTTTATATCCCAATATATAGCT 650

QY      481 TTAGAACTTGATTTCTTAAATGCGATGCCCTTTTCGCAATTAGAACCAAGAGTTCCA 540

```

```

DB      651 TTAGAACTTGATTTCTTAAATGCGATGCCCGCTTTTCGCAATTAGAACCAAGAGTTCCA 710
QY      541 TTATTAATGTATATGCTCAAGCTGCAAAATTTACACCTATTATTTATGAGAGATGCTCTCT 600
DB      711 TTATTAATGTATATGCTCAAGCTGCAAAATTTACACCTATTATTTATGAGAGATGCTCTCT 770
QY      601 CTTTGTGGTAGTGAATTTGGGCTTACATCGCAGGAATTCAGGTTATTTATGAGCGCAA 660
DB      771 CTTTGTGGTAGTGAATTTGGGCTTACATCGCAGGAATTCAGGTTATTTATGAGCGCAA 830
QY      661 GTGGAACAAACGAGAGATTTATTCGCACTATTGCGTGAAGTGTATATAACAGGTCTAAAT 720
DB      831 GTGGAACGAACGAGAGATTTATTCGCACTATTGCGTGAAGTGTATATAACAGGTCTAAAT 890
QY      721 AGCTTGAGAGGGAACAATGCGCGAAGTTGGGTGCGTTTAAATCAATTCCTGAGATCTA 780
DB      891 AGCTTGAGAGGGAACAATGCGCGAAGTTGGGTGCGTTTAAATCAATTCCTGAGATCTA 950
QY      781 ACCTTAGGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGACACTCGCAGCTTATCCA 840
DB      951 ACCTTAGGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGACACTCGCAGCTTATCCA 1010
QY      841 ATAAATACGAGTCTCAGTTAAACAGGGAAGTTTATACAGACGCAATTTGAGCAACAGGG 900
DB      1011 ATAAATACGAGTCTCAGTTAAACAGGGAAGTTTATACAGACGCAATTTGAGCAACAGGG 1070
QY      901 GTAAATATGCAAGTATGAATTTGGTATATAATAATGCACTTCGTTTCCGCTATAGAG 960
DB      1071 GTAAATATGCAAGTATGAATTTGGTATATAATAATGCACTTCGTTTCCGCTATAGAG 1130
QY      961 ACTGCGGTTATCCGAAGCCGCACTTACTTGATTTCTTGAACAACTTACAAATTTTATAGC 1020
DB      1131 GCTGCGGCTATCCGAAGCCGCACTTACTTGATTTCTTGAACAACTTACAAATTTTATAGC 1190
QY      1021 ACTTCATACGATGAGTGTCTACTAGGCATATGACTTCTGCGGGGGGACACAAATTCAA 1080
DB      1191 GCTTCATACGATGAGTGTCTACTAGGCATATGACTTCTGCGGGGGGACACAAATTCAA 1250
QY      1081 TCTCGGCCCAATAGGAGCGGATTAATACCTCAACGATGGGTCTACCAATCTTCTATT 1140
DB      1251 TCTCGGCCCAATAGGAGCGGATTAATACCTCAACGATGGGTCTACCAATCTTCTATT 1310
QY      1141 AATCCTGTGAAGTATTACTTCTCTCGAGAGCTATATTGGAAGTCAATCATATGAGGAG 1200
DB      1311 AATCCTGTGAAGTATTACTTCTCGAGAGCTTATGAGGACTGAATCATATGAGGAG 1370
QY      1201 GTGCTTCTATGGGAATTTTACCTTGAACCTTATGATGTTGTCCTACTGTTAGATTTAAT 1260
DB      1371 GTGCTTCTATGGGAATTTTACCTTGAACCTTATGATGTTGTCCTACTGTTAGATTTAAT 1430
QY      1261 TTTAGGAACCTTCAGAAATACTTTTGAAGAGGTACTGCTAACTATATAGTCAACCTATGAG 1320
DB      1431 TTTAGGAACCTTCAGAAATACTTTGATAGAGGTACTGCTAACTATATAGTCAACCTATGAG 1490
QY      1321 TCACCTGGGCTTCAATTAAGAAAGATTGAGAAATGAAATACCAACAGAAACAAACAGAACGA 1380
DB      1491 TCACCTGGGCTTCAATTAAGAAAGATTGAGAAATGAAATACCAACAGAAACAAACAGAACGA 1550
QY      1381 CCAAATTTGAATCATATATAGTCAATAGGTTTATCTACATATAGGCTCATTTTCAATCTAG 1440
DB      1551 CCAAATTTGAATCATATATAGTCAATAGGTTTATCTATATAGGTTATTTTCAATCTAG 1610
QY      1441 GTGCAATGACAGTATATTTCTTGGAGCGCACTGAGTGAAGTCTGCTACCAATACCAATAGT 1500
DB      1611 GTGCAATGACAGTATATTTCTTGGAGCGCACTGAGTGAAGTCTGCTACCAATACCAATAGT 1670
QY      1501 TCAGATAGCAATACCAAAATCAATGTTGTTAAATCATTCACCTTAAATTCAGGTACCTCT 1560
DB      1671 CCAAATAGAAATCACCCAAATCCCAATGGTAAAGATCCGAACCTTCTCCTCAAGGTACCACT 1730
QY      1561 GTAGTCAGTGGCCCGAGGATTTACAGGAGGAGTATATCCGAACTAACCTTATGTTAGT 1620

```


Db 1731 GTTCTTAGAGCAGGATTTACTGTTGGGATATTCTTCAAGAAACGAATACCTGTTGGA 1790
 Qy 1621 GTACTAAGTAGTGGTCTTAATTTTAAATAATACATCATTTACAGCGGTATPCGCGTGAGAGTT 1680
 Db 1791 TTTTGGACCGGTAAGAGTAACCTGTTTAAACCGACCAATTAACACAAAGATATCGTATAGGATTC 1850
 Qy 1681 CGTTATGCTGCTTCTCAAAACAACTGCTCTGAGGGTAACTGTCGAGGAGGTACTACTTTT 1740
 Db 1851 CGTATGCTTCACTGTAGATTTTGAATTTCTTTGTATCAGCTGGAGGTACTACTGTAAAT 1910
 Qy 1741 GATCAAGGATTCCTTAGTACTATGAGTGCATAATGAGTCTTTTGACATCTCAATCAATTTAGA 1800
 Db 1911 AATTTTAGATTCCTACGTACATGACAGTGCAGACGAACTAAATAACGGAAATTTTGTG 1970
 Qy 1801 TTTTGCAGAAATTTCTGTAGGTATTTAGTGCATCTGGCAGTCAA---ACTGCTGGAATAAGT 1857
 Db 1971 AGACGTGCTTTTACTACACCTTTTACTTTTACACAAATTCAGATATAAATTCGAACGCTCT 2030
 Qy 1858 ATAAGTAAATGACAGTACAGAAACGTTTCACTTTTGATTAATAATTTGAATTCATTCCTCAAT 1917
 Db 2031 ATTCAGGCTTGTAGTGAATTTGGGAAGTGTATATGATATAAATTTGAATTTATTTCCAGTT 2090
 Qy 1918 ACTGCAACCTTTCGAAGCAGAAATCGATTTAGAAAAGGCGCAAGAGCGGTGAATGCTCTG 1977
 Db 2091 ACTGCAACCTTTCGAAGCAGAAATCGATTTAGAAAAGGCGCAAGAGCGGTGAATGCTCTG 2150
 Qy 1978 TTTTACTAATACGAATCCAAAGAAATTTGAAACAGATGTGACAGATTTATCATATTTGATCAA 2037
 Db 2151 TTTTACTAATACGAATCCAAAGAAATTTGAAACAGATGTGACAGATTTATCATATTTGATCAA 2210
 Qy 2038 GTATCCAAATTTAGTGGGCTGTTTATCGGATGAATTTCTGTTAGTGAATAAGAGAGAAATTA 2097
 Db 2211 GTATCCAAATTTAGTGGGCTGTTTATCGGATGAATTTCTGTTAGTGAATAAGAGAGAAATTA 2270
 Qy 2098 CTTGAGAAAGTGAATATCGAAACGACTCAGTGAATGAAGAACTTACTCCAGATCCA 2157
 Db 2271 CTTGAGAAAGTGAATATCGAAACGACTCAGTGAATGAAGAACTTACTCCAGATCCA 2330
 Qy 2158 AACTTCACATCCATCAATTAAGAAACACGACTTCAATCTACTAATGAGCAATCGAATTTTC 2217
 Db 2331 AACTTCACATCCATCAATTAAGAAACACGACTTCAATCTACTAATGAGCAATCGAATTTTC 2390
 Qy 2218 ACATCTATCATGAACATCTGAACATGATGGTGGGGAAGTGAAGACATTTACAAATCCAG 2277
 Db 2391 ACATCTATCATGAACATCTGAACATGATGGTGGGGAAGTGAAGACATTTACCAATCCAG 2450
 Qy 2278 GAAGGAATACGCTATTTAAGAAATTTAGTCACTACCTACCGGACTTTTATGAGTGT 2337
 Db 2451 GAAGGAATACGCTATTTAAGAAATTTAGTCACTACCTACCGGACTTTTATGAGTGT 2510
 Qy 2338 TATCCGACGCTATTTATCAAAAATAGGAGAGTCCGAAATTTAAAGCTTATACCTCGCTAC 2397
 Db 2511 TATCCGACGCTATTTATCAAAAATAGGAGAGTCCGAAATTTAAAGCTTATACCTCGCTAC 2570
 Qy 2398 CAATTAAGAGGTATATTGAAGATGATCAAGATTTAGAGATATATTGATTCGTTATPAT 2457
 Db 2571 CAATTAAGAGGTATATTGAAGATGATCAAGATTTAGAGATATATTGATTCGTTATPAT 2630
 Qy 2458 GCGAAACATGAACATTTGATTTTCCAGGTACCGAGTCCGATGGCCGCTTTCACTGTTGAA 2517
 Db 2631 GCGAAACATGAACATTTGATTTTCCAGGTACCGAGTCCGATGGCCGCTTTCACTGTTGAA 2690
 Qy 2518 AGCCCAATCGGAAGTCCGAGAACCGAATTCGATGCGCACACCAATTTTGAATGGAATCCCT 2577
 Db 2691 AGCCCAATCGGAAGTCCGAGAACCGAATTCGATGCGCACACCAATTTTGAATGGAATCCCT 2750
 Qy 2578 GATCTAGATTTTCTCTGACAGATGAGAAAAATGTGCGCATCATTTCCCATCATTTTCTCT 2637
 Db 2751 GATCTAGATTTTCTCTGACAGATGAGAAAAATGTGCGCATCATTTCCCATCATTTTCTCT 2810
 Qy 2638 TTGATATTTGATTTGGAATGACAGACTTGTGATGAGAAATCTAGCGGTGGGTGTTATTC 2697
 Db 2811 TTGATATTTGATTTGGAATGACAGACTTGTGATGAGAAATCTAGCGGTGGGTGTTATTC 2870

Qy 2698 AAGATTAAAGCAGAGGAAGGTCTATGCAAGACTAGGGAATCTGGAATTTATTGAAGAGAAA 2757
 Db 2871 AAGATTAAAGCAGAGGAAGGTCTATGCAAGACTAGGGAATCTGGAATTTATTGAAGAGAAA 2930
 Qy 2758 CCATTATTAGGAGAAACGACATGCTCTGCTGCTGAAGAGACAGAGAAAAAATGGAGAGACAAA 2817
 Db 2931 CCATTATTAGGAGAAACGACATGCTCTGCTGCTGAAGAGGCGAGAAAAAATGGAGAGACAAA 2990
 Qy 2818 CGTGAATAAATCAATTTGGAACAAAACGAGTATATACAGAGGCAAAAGAGCTGTGGAT 2877
 Db 2991 CGTGAATAAATCAATTTGGAACAAAACGAGTATATACAGAGGCAAAAGAGCTGTGGAT 3050
 Qy 2878 GCTTTATTGTAGATTTCTCAATATATATAGATTTACAGCGGATACAAACATTTGGCATGATT 2937
 Db 3051 GCTTTATTGTAGATTTCTCAATATATATAGATTTACAGCGGATACAAACATCGCATGATT 3110
 Qy 2938 CATGCGGACAGATAAATCTGTTTCAATTTGGAAGGCTTATCTGTCAGAAATTTATCTGTT 2997
 Db 3111 CATGCGGACAGATAAATCTGTTTCAATTTGGAAGGCTTATCTTTTCAAGATTTACCTGTT 3170
 Qy 2998 ATCCCGGCTGTAATGCGGAAATTTTGAAGAAATTTAGAAAGTTCGCAATTTACCTGCAATC 3057
 Db 3171 ATCCAGGTGTAATGCGGAAATTTTGAAGAAATTTAGAAAGTTCGCAATTTACCTGCAATC 3230
 Qy 3058 TCCTTATACGATGCGGAAATGTCGTTTAAATAATGGTGAATTTTAAATAGATTTAGCATGC 3117
 Db 3231 TCCTTATACGATGCGGAAATGTCGTTTAAATAATGGTGAATTTTAAATAGATTTAATCATGT 3290
 Qy 3118 TGGAAATGTAAGAGGCAATGTAGATGTACACAGAGCCATCACGTTTCTGCTTGTATTATC 3177
 Db 3291 TGGAAATGTAAGAGGCAATGTAGATGTACACAGAGCCATCATCGTTCTGACCTTTGTTATC 3350
 Qy 3178 CCAGATGGGAAGCAGAAAGTGTCAAGCAGTTTCCGCTCTGTCGCGGCGGTGGCTATATC 3237
 Db 3351 CCAGATGGGAAGCAGAAAGTGTCAAGCAGTTTCCGCTCTGTCGCGGCGGTGGCTATATC 3410
 Qy 3238 CTCCTGTCTACAGCGTACAAAGAGGATTTGAGAGGGTGTGTGTAAACGATCCCATGAAATC 3297
 Db 3411 CTCCTGTCTACAGCGTACAAAGAGGATTTGAGAGGGTGTGTGTAAACGATCCCATGAAATC 3470
 Qy 3298 GAGAACATACAGACGAACTTAAATTTTAAACCTGTGAAGAGGAAAGTGTATCCAAAG 3357
 Db 3471 GAGAACATACAGACGAACTTAAATTTTAAACCTGTGAAGAGGAAAGTGTATCCAAAG 3530
 Qy 3358 GATACAGGAACGTTGAATGATTTATCTGACACCAAGGTACAGC-----AGTA 3405
 Db 3531 GATACAGGAACGTTGAATGATTTATCTGACACCAAGGTACAGCTGGATGGCGAGATGCA 3590
 Qy 3406 TGTAAATTTCCCGTAAATGCTGGATATGAGGATGCAATGAAAGTTGATACACGATCTGTT 3465
 Db 3591 TGTAAATTTCCCGTAAATGCTGGATATGAGGATGCAATGAAAGTTGATACACGATCTGTT 3650
 Qy 3466 AATTACAAACCGATTTATGAAGAAAGAAACGATATACAGATGTACAGAGATTAATCATTTGT 3525
 Db 3651 AATTACAAACCGATTTATGAAGAAAGAAACGATATACAGATGTAAAGAGAGATTAATCATTTGT 3710
 Qy 3526 GAATATACAGAGGGTATGTAATTTATCCACCTACCAAGCTGTTTATATGACAAAAAGAA 3585
 Db 3711 GAATATACAGAGGGTATGTAATTTATCCACCTACCAAGCTGTTTATGTAACAAAAAGAA 3770
 Qy 3586 TTAGAATATCTTCCAGAAACCGATTAAGGATTTGAGATTTGAGATTTGAGAAACCGAGGGAAG 3645
 Db 3771 TTAGAATATCTTCCAGAAACCGATTAAGGATTTGAGATTTGAGATTTGAGAAACCGAGGGAAG 3830
 Qy 3646 TTTTATTGTAGACGCTGGAATTTACTCTTTATCGAGGAATAG 3687
 Db 3831 TTTTATTGTAGACGCTGGAATTTACTCTCTCATGGAAGATAG 3872

RESULT 11
 142103
 LOCUS

4074 bp DNA linear PAT 07-OCT-1997

DEFINITION Sequence 1 from patent US 5628995.

ACCESSION I42103

VERSION I42103.1 GI:2467598

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 4074)

AUTHORS Peferoen, M., Jansens, S. and Denolf, P.

TITLE Control of Ostrinia

JOURNAL Patent: US 5628995-A 13-MAY-1997;

FEATURES Location/Qualifiers

source 1..4074

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match 85.0%; Score 3133.6; DB 6; Length 4074;

Best Local Similarity 91.1%; Pred. No. 0;

Matches 3373; Conservative 0; Mismatches 299; Indels 30; Gaps 3;

QY	1	TTGACTTCAATAGGAAATGGAATGAATGAAATATATAAATGCTTTATCGATTCCAGCTGTA	60
DB	186	TTGACTTCAATAGGAAATGGAATGAATGAAATATATAAATGCTTTATCGATTCCAGCTGTA	230
QY	61	TGCAATCATTCACACAAATGGATCTATCACAGATGCTCGTATTGAGGATTTCTTTGTGT	120
DB	231	TGCAATCATTCGACAAATGGATCTATTAACAGATGCTCGTATTGAGGATAGCTTTGTGT	290
QY	121	ATAGCGAGGGGAATATATCAATCCACTTTGTTAGCGCATCAACAGTCCAAACGGGTATT	180
DB	291	ATAGCGAGGGGAATATATGATCCACTTTGTTAGCGCATCAACAGTCCAAACGGGTATT	350
QY	181	AACATAGCTGTAGATACCTATGATGATAGGATAGGCGTACCGTTTCTGACAAATAGCTAGT	240
DB	351	AACATAGCTGTAGATACCTATGATGATAGGCGTACCGTTTCTGACAAATAGCTAGT	410
QY	241	TTTTATAGTTTTCTTTGTTGTAATATGCGCGCGGAGAGATCAGTGGGAAATTTTC	300
DB	411	TTTTATAGTTTTCTTTGTTGTAATATGCGCGCGGAGAGATCAGTGGGAAATTTTC	470
QY	301	CTAGAACATGTGAAACAACTTATAATCAACAAATAACAGAAATGCTAGGAATACGGCA	360
DB	471	CTAGAACATGTGAAACAACTTATAATCAACAAATAACAGAAATGCTAGGAATACGGCT	530
QY	361	CTTGCTCGATTCAAGTTTATAGGATTTCTTTAGAGCTTATCAACAGTCACTTGAGAT	420
DB	531	CTTGCTCGATTCAAGTTTATAGGATTTCTTTAGAGCTTATCAACAGTCACTTGAGAT	590
QY	421	TGGCTAGAAAACCGTGATGATGCAAGAACGAGAGTGTCTTTATATCCCAATATATAGCC	480
DB	591	TGGCTAGAAAACCGTGATGATGCAAGAACGAGAGTGTCTTTATATCCCAATATATAGCT	650
QY	481	TTAGAACTTGATTTTCTTAATGCGATCCGCTTTTTCGCAATTAAGAAACCAAGAGTTCCA	540
DB	651	TTAGAACTTGATTTTCTTAATGCGATCCGCTTTTTCGCAATTAAGAAACCAAGAGTTCCA	710
QY	541	TTATTATGTTATGCTTCAAGTGCATAATTTACACCTATATATTATGAGAGTGCCTCT	600
DB	711	TTATTATGTTATGCTTCAAGTGCATAATTTATACACCTATATTATTATGAGAGTGCCTCT	770
QY	601	CTTTTTCGTAGTGAATTTGGCTTTACATCGCAGGAAATTCACCGTATTATTATGAGCGCAA	660
DB	771	CTTTTTCGTAGTGAATTTGGCTTTACATCGCAGGAAATTCACCGTATTATTATGAGCGCAA	830
QY	661	GTGGAACAAACGAGAGATTTATCCGACTATGCGTAGAATGGTATATAACAGTCTAAAT	720
DB	831	GTGGAACAAACGAGAGATTTATCCGACTATGCGTAGAATGGTATATAACAGTCTAAAT	890
QY	721	AGCTTGAGGGGCAAAATGCGCAAGTTGGGTGCTTATTAATCAATCCGTAGAGATCTA	780
DB	891	AGCTTGAGGGGCAAAATGCGCAAGTTGGGTGCTTATTAATCAATCCGTAGAGATCTA	950

QY	781	ACGTTAGGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGACACTCGCACTTATCCA	840
DB	951	ACGTTAGGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGACACTCGCACTTATCCA	1010
QY	841	ATAAATACGAGTCTCAGTTAAACAAGGAGTTTATACAGACCGCAATTTGAGCAACAGGG	900
DB	1011	ATAAATACGAGTCTCAGTTAAACAAGGAGTTTATACAGACCGCAATTTGAGCAACAGGG	1070
QY	901	GTAATATGCAAGTATGAATGCTTATATAATAATGCACTTTCGTTTTCGCTATATAGAG	960
DB	1071	GTAATATGCAAGTATGAATGCTTATATAATAATGCACTTTCGTTTTCGCTATATAGAG	1130
QY	961	ACTGCGGTTATCCGAAGCCGCACTACTCTTGTATTTCTAGAAACAATTTATTTTATG	1020
DB	1131	GCTGCGGTTATCCGAAGCCGCACTACTCTTGTATTTCTAGAAACAATTTATTTTATG	1190
QY	1021	ACTTCATCAGATGGAGTGTACTAGGCATATGACTTACTTGGCGGGGCAACAATTTCAA	1080
DB	1191	GCTTCATCAGATGGAGTGTACTAGGCATATGACTTATTTGGCGGGGCAACAATTTCAA	1250
QY	1081	TCTCGGCCAATAGGAGCGGATTAATACCTCAACGCATGGGTCTACCAATATCTTCTATT	1140
DB	1251	TCTCGGCCAATAGGAGCGGATTAATACCTCAACGCATGGGTCTACCAATATCTTCTATT	1310
QY	1141	AATCCTGTAAAGTATTATCTTTCTCTCGAGACGTATATTTGGACTGAATCATATGACGGA	1200
DB	1311	AATCCTGTAAATTAACGTTTCGCATCTCGAGACGTTTATAGGACTGAATCATATGACGGA	1370
QY	1201	GTGCTTCTATGGGGAATTTTACCTTGAACCTTATTCATGGTGTCCCTACTGTTAGTTTAA	1260
DB	1371	GTGCTTCTATGGGGAATTTTACCTTGAACCTTATTCATGGTGTCCCTACTGTTAGTTTAA	1430
QY	1261	TTTAGGAACCTCTCAGAAATCTTTTGAAGAGGTACTGTCTAACTATATAGTCAACCTATGAG	1320
DB	1431	TTTAGGAACCTCTCAGAAATCTTTTGAAGAGGTACTGTCTAACTATATAGTCAACCTATGAG	1490
QY	1321	TCACCTGGGCTTCAATTTAAAGATTCAGAAATCGAAATTTACCAACAGAAACAACAGAACGA	1380
DB	1491	TCACCTGGGCTTCAATTTAAAGATTCAGAAATCGAAATTTACCAACAGAAACAACAGAACGA	1550
QY	1381	CCAAATTTGAATCATATAGTATAGTATCTCATATAGGCTTCTTTCACATCTTAGG	1440
DB	1551	CCAAATTTGAATCTTACAGTCAAGTTATCTCATATAGGTTATTTTACAAATCCAGG	1610
QY	1441	GTGCATGTACAGTATATCTTTCGAGCGACCGTAGTGCAGATCGTACAAATACCATTAGT	1500
DB	1611	GTGAATGTACCGGTATATCTTTCGAGCGATCGTGTAGTGCAGATCGTACAGATACGATTGGA	1670
QY	1501	TCAGATAGCAATAACAATAACCAATTCGTTGTTAAATCAATTCACCTTAAATTCAGGTACCTCT	1560
DB	1671	CCAAATAGAAATCACCAATCCCAATCCCAATGGTAAAGCATCCGAATTCCTCAAGGTACCACT	1730
QY	1561	GTAGTCAAGTGGCCAGGATTTACAGGAGGGATATTAATCCGAATCAAGTAACTAGTGTAGT	1620
DB	1731	GTGTTTAGAGGACAGGATTTACTGTGGGGATTTCTTCCGAAGAACGAATACCTGGTGGGA	1790
QY	1621	GTACTAAGTATGGTCTTAAATTTTAAATATATATATATATATATATATATATATATATAT	1680
DB	1791	TTTGACCGGATATAGATTAATCTTAAACGACCAATTAACAAGATATCGTATAGGATTC	1850
QY	1681	CGTTATGCTGCTTTCTCAACAATGGTCTCGAGGGTAACTGTGCGAGGGAGTACTACTTTT	1740
DB	1851	CGCTATGCTTCAACTGTAGATTTTGAATTTCTTTGTATCAGTGGAGGTACTACTGTAAAT	1910
QY	1741	GATCAAGGATTCCTTAGTACTATAGTGCATAATGATGCTTTTGTATCTCAATCATTTTGA	1800
DB	1911	AAATTTTAGATTTCTTACGTAATGAACAGTGGAGACGAATCAAAATACGGAATTTTGTG	1970
QY	1801	TTTGCAAAATTTCTGTAGGTATTAGTGCATCTGGCAGTCAA---ACTGCTGGAATTAAGT	1857
DB	1971	AGAGGTGCTTTTACTACACCTTTTACTTTTACACAATTTCAAGATATAATTCGAACGCTCT	2030
QY	1858	ATAAGTAATAATGCAGGTAGACAAACGTTTTCATCTTTGTATATAATTTGAATTCATTTCCAAT	1917

Db	2031	ATTCAAGGCCCTTAGTGGAAATGGGGAAAGTGATATAGATAAAATTGAAATTTATTTCCAGTT	2090
Qy	1918	ACTGCAACCTTCGAAGCAGAATA CGATTTAGAAAAGCGCGCAAGAGCGGTGAATGCTCTCG	1977
Db	2091	ACTGCAACCTTCGAAGCAGAATA TGATTTAGAAAAGCGCGCAAGAGCGGTGAATGCTCTCG	2150
Qy	1978	TTTACTAATACGAATCCAAGAAGATTGAAAA CAGATGTGACAGATTATCATATTTGATCAA	2037
Db	2151	TTTACTAATACGAATCCAAGAAGATTGAAAA CAGATGTGACAGATTATCATATTTGATCAA	2210
Qy	2038	GTATCCAAATTTAGTGGCGTGTTTATCGGATGCAATTTCTGCTTTAGATGAAAAGAGAGAAATTA	2097
Db	2211	GTATCCAAATTTAGTGGCGTGTTTATCGGATGCAATTTCTGCTTTGAGTGAAGAAGAGAGAAATTA	2270
Qy	2098	CTTCAGAAAAGTGAATATGCGAAAACGACTCAGTGCATGAAAAGAACTTTACTCCAGATGCCA	2157
Db	2271	CTTCAGAAAAGTGAATATGCGAAAACGACTCAGTGCATGAAAAGAACTTTACTCCAGATGCCA	2330
Qy	2158	AACTTCACATCCATCAATAAGCAACCCAGACTTCATATCTACTAATGAGCAATCGAAATTC	2217
Db	2331	AACTTCACATCCATCAATAAGCAACCCAGACTTCATATCTACTAATGAGCAATCGAAATTC	2390
Qy	2218	ACATCTATCCATGAAACAATCTGAAACATGGATGGTGGGGAAGTGAGAACATTCACATCCAG	2277
Db	2391	ACATCTATCCATGAAACAATCTGAAACATGGATGGTGGGGAAGTGAGAACATTCACATCCAG	2450
Qy	2278	GAAGGAAATGACGTATTTTAAAGAGAAATTCGTGCACACTACCGGGGACCTTTTAAATGAGTGT	2337
Db	2451	GAAGGAAATGACGTATTTTAAAGAGAAATTCGTGCACACTACCGGGGACCTTTTAAATGAGTGT	2510
Qy	2338	TATCCGACGTATTTTATATCAAAAAATAGGAGAGTCGGAATTTAAAGCTTATACTCGCTAC	2397
Db	2511	TATCCGACGTATTTTATATCAAAAAATAGGAGAGTCGGAATTTAAAGCTTATACTCGCTAC	2570
Qy	2398	CAATTAAGAGGTTATTTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGTTATAAT	2457
Db	2571	CAATTAAGAGGTTATTTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGTTATAAT	2630
Qy	2458	GCGAAAACATGAAACATTTGGATGTTTCCAGGTACCCGAGTCGCTATGGCCGCTTTTCAGTTGAA	2517
Db	2631	GCGAAAACATGAAACATTTGGATGTTTCCAGGTACCCGAGTCGCTATGGCCGCTTTTCAGTTGAA	2690
Qy	2518	AGCCCAATCGGAAGGTGCGGAGAACCGAATCGATGCGCACCA CATTTTGAATGGAATCCCT	2577
Db	2691	AGCCCAATCGGAAGGTGCGGAGAACCGAATCGATGCGCACCA CATTTTGAATGGAATCCCT	2750
Qy	2578	GATCTAGATTTTCTCGAGAGATGGAGAGAAAAATGTCCGATCATTTCCCATCATTTCTCT	2637
Db	2751	GATCTAGATTTTCTCGAGAGATGGAGAGAAAAATGTCCGATCATTTCCCATCATTTCTCT	2810
Qy	2638	TTGGATATTGATTTGGATGCACAGACTTCGATCAGAAATCTAGCGGTGTGGGTGTTATTC	2697
Db	2811	TTGGATATTGATTTGGATGCACAGACTTCGATCAGAAATCTAGCGGTGTGGGTGTTATTC	2870
Qy	2698	AAGATTAAAGACGCAAGGAAGTTCATGCAAGACTAGGGAATCTGGAATTTTATTTGAAGAGAAA	2757
Db	2871	AAGATTAAAGACGCAAGGAAGTTCATGCAAGACTAGGGAATCTGGAATTTTATTTGAAGAGAAA	2930
Qy	2758	CCATTAATTAGGAGAGCACTGTCTCGTGTGAAGAGACGACAGAAAAAATCGAGAGACAAA	2817
Db	2931	CCATTAATTAGGAGAGCACTGTCTCGTGTGAAGAGACGACAGAAAAAATCGAGAGACAAA	2990
Qy	2818	CGTGAAAACTACAAATTTGAAAACAAACGAGTATATACAGAGGCAAAAGAGCTGTGGAT	2877
Db	2991	CGTGAAAACTACAAATTTGAAAACAAACGAGTATATACAGAGGCAAAAGAGCTGTGGAT	3050
Qy	2878	GCCTTATTTGTAGATTTCTCAATATAATAGATTTACAAGCGGATACAAACATTTGGCATGATT	2937
Db	3051	GCCTTATTTGTAGATTTCTCAATATGATAGATTTACAGCGGATACAAACATTCGGCATGATT	3110
Qy	2938	CATCGCGCAGATAAATCTGTTTCATTCGAAATTCGAGAGGCTTATCTGTGCAGAAATATCTGTT	2997

Db	3111	CATGCGGCAGATAAACCTGTGTTCTTACGAAATTCGAGAGCGGTATCTTTTCAGAAATTCACCTGTT	3117
Qy	2998	ATCCGGGTGTAATATGCGGAAATTTTTTGAAGAATTAAGAAGTCGCAATTATCATCTGCAATC	3057
Db	3171	ATCCAGGTGTAATGCGGAAATTTTTTGAAGAATTAAGAAGTCACATTATCATCTGCATC	3230
Qy	3058	TCCTTATACGATCGAGAAATGTCGTTTAAAAATGGTGATTTTAAATATGGAATAGCATGC	3117
Db	3231	TCCTTATACGATCGAGAAATGTCGTTTAAAAATGGTGATTTTAAATATGGAATTAACATGT	3290
Qy	3118	TGGAAATGTAAGGGGCAATGTAGATGTACAACAGAGCCATCACCGTTCGTCTCTTGTATTTC	3177
Db	3291	TGGAAATGTAAGGGGCAATGTAGATGTACAACAGAGCCATCATCTGTTCTGACCTTGTATTTC	3350
Qy	3178	CCAGAATGGGAAGCAGAAAGTGTCAACAGCAGTTTCGGGTCTGTCCGGGGCGTGCTATATC	3237
Db	3351	CCAGAATGGGAAGCAGAAAGTGTCAACAGCAGTTTCGGGTCTGTCCGGGGGTGCGCTATATC	3410
Qy	3238	CTCCGTGTCTACAGCGTACAAAGAGGATATGGAGAGGGTTGTGTAAACGATCCCATGAAATC	3297
Db	3411	CTTCGTGTCTACAGCGTACAAAGAGGATATGGAGAGGGCTGCGTAAACGATCCCATGAAATC	3470
Qy	3298	GAGAACATATCAGACGAACTTAAATTTTAAAACTGTGAAGAACAGGAAGTGATCCAAAG	3357
Db	3471	GAGAACATATCAGACGAACTTAAATTTTAAAACTGTGAAGAACAGGAAGTGATCCAAAG	3530
Qy	3358	GATACAGGAACGTGTAATGATTAATCTGCACACCAAGGTACAGC-----AGTA	3405
Db	3531	GATACAGGAACGTGTAATGATTAATCTGCACACCAAGGTACAGCTGGATGCGCAGATGCA	3590
Qy	3406	TGTAATTTCCGTAAATGCTGGATATGAGGATGCATATGAAGTTGATACTACAGCATCTGTT	3465
Db	3591	TGTAATTTCCGTAAATGCTGGATATGAGGATGCATATGAAGTTGATACTACAGCATCTGTT	3650
Qy	3466	AATTACAAACCGACTTATGAAGAAGAAAAGTATACAGATGTACAGAGAGATATCATTTGT	3525
Db	3651	AATTACAAACCGACTTATGAAGAAGAAAAGTATACAGATGTATGAAGAGAGATATCATTTGT	3710
Qy	3526	GAATATGACAGAGGGTATGTAATTAATCCACACTACACAGCTCGTTTATATGACAAAGAA	3585
Db	3711	GAATATGACAGAGGGTATGTAATTAATCCACAGTACCAGCTGGTTATGTGACAAAGAA	3770
Qy	3586	TTAGAATACTTCCAGAAAACCGATAAGAGTATGGATTGAGATTGGAGAAAACGGAAGGAAG	3645
Db	3771	TTAGAATACTTCCAGAAAACAGATACAGTATGGATTGAGATTGGAGAAAACGGAAGGAAG	3830
Qy	3646	TTTATTTGTAGACAGCGTGGAAATTACTCTTTATGGAGGAATAG	3687
Db	3831	TTTATTTGTAGTAGCGTGGAAATTACTCTCTCATCGGAAGAATAG	3872

RESULT 12

AF363025

LOCUS

DEFINITION

ACCESSION

ACCESSION
VERSION

KEYWORDS

SOURCE

ORGANIS

REFERENCE

AUTHORS

TITLE

CONTENTS

REFERENCE

AUTHORS

TITLE

FEATURES

source Location/Qualifiers
 1..4798 /organism="Bacillus thuringiensis serovar entomocidus"
 /mol_type="genomic DNA"
 /strain="HD-9"
 /sub_species="entomocidus"
 /db_xref="taxon:1436"
 193..231
 promoter /note="BtII promoter"
 215..243
 promoter /note="BtI promoter"
 406..4107
 gene /gene="cry1Ba2"
 406..415
 RBS /gene="cry1Ba2"
 /note="putative"
 421..4107
 CDS /gene="cry1Ba2"
 /codon_start=1
 /transl_table=11
 /product="delta-endotoxin Cry1Ba2"
 /protein_id="AAK51084.1"
 /db_xref="GI:13959051"
 /translation="MISNRKNEHII NAVNSHAQMDLLPDIARIEDSLCTAEGNDDP
 FVSASTVQTGINAGRI LGLVGFPAQLASFYFLVGLWLPGRDQWELFLEHVQL
 INQITENARNTALRLQGLGDSFRAYQQSLEDLENRDDARTSVLHTQYIALELDF
 LNAPLFAIRNQSVPLLMVYQAANLHLRLDASLFGSEFGLTSQBIQRYIEROVER
 TRDYSVCVWYNTGLNSLRTNAAASWVRNQFRDLTLGLDLVALFSPYDRTYPI
 NTSQDLTREYVTAIGATGVNMAWNNNAFSAIEAAIRSPHILDFLEQLIF
 SASRWNTHMYTWRGHTIQSRPIGGLNTSHGATNINPVLRFASRDYRTES
 YAGVLLWGLYELHGVPTFRFPNIPQNSDRGTANYSQPYSPGLQKDSLELPP
 ETLERNPYESYHRLSHIGIILQSRVNVPIVSWTHRSADRTNIGPNRIQIPMKVAS
 ELPOGTVTVNFRFLRTMNSDELKYGNEVRAFTTPTPTQIOIIRTSQGLSGNGE
 VSRGHTVWVNFRLRTMNSDELKYGNEVRAFTTPTPTQIOIIRTSQGLSGNGE
 VYDKIEIIPVATPEAYDLERAQAVNALPNTNPRRLKTDVTDYHIDQVSNLVC
 LSDFCLDEKRELLKVKAKRUSDERNLQDPNFTSINKQPDFISTNEOSNFTSHE
 QSHGWGSENIITQGNDFKENVYTLPGTFNECYTLYIQKIGSELKAYTRYQLR
 GYTESDLEIYIIRNAKHETIDVPGTESLWPLSVESPIRCGEPNRCAPHPEWNP
 LDSCRDGEKAAHSHFSLDIDVGTDLHENLGVWVFKIKTQEGHARLGNLEPDE
 KPLGLBSALVRKAEKWRDKREKLOLETKRVVTEAKEAVDALFVDSOYDRLQADNI
 GMHAADKLVHRIAREALSELPLVPGVNAEIPFELSGHIIITALSIDARNVNGDN
 NGLTWNVGHVDVQSHHRSDLVPEWEAEVSQVRVCPGCGYILURVYAKGSGEG
 CVTHIEINNTDELKPNREBEVYPTDGTCDNYTAHQGTAGCADCASNRNAGYBDA
 YEVDTHTSVNYKPYEEETVDVDRDNHCEYDRGVNYPVPVAGYVTKLEYPPETDT
 VWIEIGTEGKFDVDSVELLLMBE"
 repeat_region 4200..4238
 /rpt_type=inverted
 ORIGIN
 Query Match 85.0%; Score 3133.6; DB 1; Length 4798;
 Best Local Similarity 91.1%; Pred. No. 0;
 Matches 3373; Conservative 0; Mismatches 299; Indels 30; Gaps 3;
 QY 1 TTGACTTCAATAGGAAATGAGATGAATTAATAATGCTTATCGATTCAGCTGTA 60
 DB 421 TTGACTTCAATAGGAAATGAGATGAATTAATAATGCTTATCGATTCAGCTGTA 465
 QY 61 TCGAATCATTTCCACAAATGATCTATCACAGATGCTCGTATTGAGGATCTTTGTGT 120
 DB 466 TCGAATCATTTCCGACAAATGATCTATTAACAGATGCTCGTATTGAGGATAGCTTGTGT 525
 QY 121 ATAGCCGAGGGGAATAATCAATCCACTTTGTTAGCGCATCAACAGTCCAAACGGGTATT 180
 DB 526 ATAGCCGAGGGGAATAATTTGATCCATTTGTTAGCGCATCAACAGTCCAAACGGGTATT 585
 QY 181 AACATAGCTGTAGATCTAGTGTATTTAGCGTACCGTTTGTGTCGACAAATAGCTAGT 240
 DB 586 AACATAGCTGTAGATCTAGTGTATTTAGCGTACCGTTTGTGTCGACAAATAGCTAGT 645
 QY 241 TTTTATAGTTTTCTTTGTTGTAATTTATGCCCCGGCGGAGAGATCAGTGGGAAATTTTC 300
 DB 646 TTTTATAGTTTTCTTTGTTGTAATTTATGCCCCGGCGGAGAGATCAGTGGGAAATTTTC 705

QY 301 CTAGAACATGTGCAACAACTTATAAATCAACAAATTAACAGAAATGCTAGAAATACGGCA 360
 DB 706 CTAGAACATGTGCAACAACTTATAAATCAACAAATTAACAGAAATGCTAGAAATACGGCT 765
 QY 361 CTTGCTCGATTACAAGGTTTAGGAGATTCCTTTTAGAGCCTATCAACAGTCACATGAGAT 420
 DB 766 CTTGCTCGATTACAAGGTTTAGGAGATTCCTTTAGAGCCTATCAACAGTCACATGAGAT 825
 QY 421 TGGCTAGAAAACCGTGATGATGCAAGAACGAGAAAGTGTCTTTTATATATATATATAGCC 480
 DB 826 TGGCTAGAAAACCGTGATGATGCAAGAACGAGAAAGTGTCTTTTATATATATATATAGCT 885
 QY 481 TTAGAACTTGATTTTCTTAATGCGATGCCGCTTTTCGCAATTAGAAACCAAGAGTTCCA 540
 DB 886 TTAGAACTTGATTTTCTTAATGCGATGCCGCTTTTCGCAATTAGAAACCAAGAGTTCCA 945
 QY 541 TTATTAATGATGATGCTCAAGCTGCAAAATTTACACTATTTATTTAGAGATGCTCTCT 600
 DB 946 TTATTAATGATGATGCTCAAGCTGCAAAATTTACACTATTTATTTAGAGATGCTCTCT 1005
 QY 601 CTTTGTGAGTGAATTTGGGCTTACATCGCAGGAAATTCACGCTTATTTAGAGCGCAA 660
 DB 1006 CTTTGTGAGTGAATTTGGGCTTACATCGCAGGAAATTCACGCTTATTTAGAGCGCAA 1065
 QY 661 GTGGAACAAACGAGAGATTTATTCGACTATTTCGCTAGATGCTTATTAATACAGCTTAAT 720
 DB 1066 GTGGAACAAACGAGAGATTTATTCGACTATTTCGCTAGATGCTTATTAATACAGCTTAAT 1125
 QY 721 AGCTTGAGGGGCAAAATCGCGAAGTGGTGGTGTATTAATCAATTCGCTAGAGATCTA 780
 DB 1126 AGCTTGAGGGGCAAAATCGCGAAGTGGTGGTGTATTAATCAATTCGCTAGAGATCTA 1185
 QY 781 ACCTTGAGGGGATATTAGATCTAGTGGCACTATTTCCCAAGCTATGACACTCCGACTTATCCA 840
 DB 1186 ACCTTGAGGGATATTAGATCTAGTGGCACTATTTCCCAAGCTATGACACTCCGACTTATCCA 1245
 QY 841 ATAAATACGAGTCTCAGTTAAACAAGGAAGTTTATACAGACGCAATGGAGCAACAGGG 900
 DB 1246 ATAAATACGAGTCTCAGTTAAACAAGGAAGTTTATACAGACGCAATGGAGCAACAGGG 1305
 QY 901 GTAAATACGCAAGTATGAATTCGTATATAATAATGCACTTCGTTTCCTGCTATAGAG 960
 DB 1306 GTAAATACGCAAGTATGAATTCGTATATAATAATGCACTTCGTTTCCTGCTATAGAG 1365
 QY 961 ACTGCGGTTATCCGAAGCCGCACTCTACTTGATTTTCTAGAACAACTTACAAATTTTATGC 1020
 DB 1366 GCTGCGGCTATCCGAAGCCGCACTCTACTTGATTTTCTAGAACAACTTACAAATTTTATGC 1425
 QY 1021 ACTTCATCAGATGGAGTGTCTAGGCATATGACTTACTGGCGGGGGCACAAATTCAA 1080
 DB 1426 GCTTCATCAGATGGAGTGTCTAGGCATATGACTTACTGGCGGGGGCACAAATTCAA 1485
 QY 1081 TCTCGGCCAATAGGAGCGGATTAATAATACCTCAACGATGGGTCTACCAATATCTTCTATT 1140
 DB 1486 TCTCGGCCAATAGGAGCGGATTAATAATACCTCAACGATGGGTCTACCAATATCTTCTATT 1545
 QY 1141 AATCCTGTGAAGATTATCATTTCTTCTCGAGACGATATATTGGAATCATATGACGGA 1200
 DB 1546 AATCCTGTGAAGATTATCATTTCTTCTCGAGACGATATATTGGAATCATATGACGGA 1605
 QY 1201 GTGCTTCTATGGGAAATTTACCTTGAACCTTATTCATGGGTGCTCCCTACTGTAGATTTAAT 1260
 DB 1606 GTGCTTCTATGGGAAATTTACCTTGAACCTTATTCATGGGTGCTCCCTACTGTAGATTTAAT 1665
 QY 1261 TTTTAGGAACCTCAGAAATCTTTTGAAGAGGTACTGTAACTATAGTCAACCTATGAG 1320
 DB 1666 TTTTAGGAACCTCAGAAATCTTTTGAAGAGGTACTGTAACTATAGTCAACCTATGAG 1725
 QY 1321 TCACCTGGGCTTCAATTTAAAGATTTCAGAAATTCAGAAATTCAGAAACCAACAGAACGA 1380
 DB 1726 TCACCTGGGCTTCAATTTAAAGATTTCAGAAATTCAGAAATTCAGAAACCAACAGAACGA 1785
 QY 1381 CCAATTTAGAACATCATATAGTCTATGATGTTATCTCACATAGGGCTCATTTTCAATCTAGG 1440

Db 1786 CCAAAATATGAATCTTACAGTACAGGTTATCTCATATAGGTATAATTTTACAAATCCAGG 1845
 Qy 1441 GTGCATGTACAGTATATCTTGTGACGACCGTAGTCAGATCGTACAAATACCAATAGT 1500
 Db 1846 GTGAATGTACCGGTATATCTTGTGACGATCGTAGTCAGATCGTACGAATACGAATTGA 1905
 Qy 1501 TCAGATAGCATACACAAATACCAATTCGGTAAATCATCTCAACCTTAATTCAGGTACTCT 1560
 Db 1906 CCAATAGAAATCACCAAAATCCCAATGGTAAAGCATCCGAATCTTCCCTCAAGGTACCAC 1965
 Qy 1561 GTAGTCAGTGGCCAGGATTTACAGGAGGGGATATAATCCGAATACGTTAATGGTAGT 1620
 Db 1966 GTTGTAGAGGACCGAGATTCTCTGGTGGGATATCTTCCGAAGACGAATACTGGTGA 2025
 Qy 1621 GTACTAAGTATGGTCTTAATTTTAAATAATACATCATTTACAGCGGTATCGGTGAGAGTT 1680
 Db 2026 TTTGGACCGATAGAGTAACTGTGTAAACCGACATTAACACAAAGATATCGTATAGGATTC 2085
 Qy 1681 CGTATCTGCTTCTCAAAACAAATGGTCTCGAGGTAACTGTGAGGGAGTACTACTTTT 1740
 Db 2086 CGCTATGCTTCAACTGTAGATTTTGAATTTCTTTGTATCACGTGAGGTACTACTGTAAAT 2145
 Qy 1741 GATCAAGGATTCCTAGTATCATAGTGCATAATGAGTCTTTTGACATCTCAATCATTTAGA 1800
 Db 2146 AATTTTAGATTCCTACGTCAATGAACAGTGGAGACGAACCTTAAATACGGAAATTTTGTG 2205
 Qy 1801 TTTGCGAAATTTCTGTAGGTATTAGTGCATCTGGAGTCAA --- ACTGCTGGAATAAGT 1857
 Db 2206 AGAGTGTCTTTACTACACCTTTTACTTTTACACAAATTCAGATATAATTCGAAATCT 2265
 Qy 1858 ATAGTAAATATGACAGGTAGACAAACGTTTCACTTTGATAAATTTGAATTCATTTCCAATT 1917
 Db 2266 ATTCAGGCTTACTGGAATGGGAGTGTATATAGATAAAATTTGAATTTTCCAGTT 2325
 Qy 1918 ACTGCAACCTTGAAGCAGATACGATTTAGAAAGGGCGCAAGGCGGTGAATGCTCTG 1977
 Db 2326 ACTGCAACCTTGAAGCAGATATGATTTAGAAAGAGCGCAAGGCGGTGAATGCTCTG 2385
 Qy 1978 TTTTACTAATACGAATCCAAAGAAATTCGAACAGATGTGACAGATTTATCATATTTGATCAA 2037
 Db 2386 TTTTACTAATACGAATCCAAAGAAATTCGAACAGATGTGACAGATTTATCATATTTGATCAA 2445
 Qy 2038 GTATCCAAATTTAGTGGCGTGTATCGGATGAATTTCTGCTAGATGAAAGAGAGAAATTA 2097
 Db 2446 GTATCCAAATTTAGTGGCGTGTATCGGATGAATTTCTGCTTGGATGAAAGAGAGAAATTA 2505
 Qy 2098 CTTGAGAAAGTGAATATGCGAAACGACTCAGTGATGAAAGAACTTTACTCCAAAGATCCA 2157
 Db 2506 CTTGAGAAAGTGAATATGCGAAACGACTCAGTGATGAAAGAACTTTACTCCAAAGATCCA 2565
 Qy 2158 AACTTCACATCCATTAAGCAACAGACTTCAATCTCTAATGAGCAATCGAATTTTC 2217
 Db 2566 AACTTCACATCCATTAAGCAACAGACTTCAATCTCTAATGAGCAATCGAATTTTC 2625
 Qy 2218 ACATCTATCCATGAACAACTTGAACATGAGTGTGGGGAAGTGAAGACATTAACAATCCAG 2277
 Db 2626 ACATCTATCCATGAACAACTTGAACATGAGTGTGGGGAAGTGAAGACATTAACAATCCAG 2685
 Qy 2278 GAAGGAAATGACGTTTAAAGAGAAATTAACGTCACTACCGGGGACTTTTAAATGAGTGT 2337
 Db 2686 GAAGGAAATGACGTTTAAAGAGAAATTAACGTCACTACCGGGGACTTTTAAATGAGTGT 2745
 Qy 2338 TATCCGAGCTATTTATCAAAAATAGGAGAGTCCGGAATTAAGCTTATCTACGCTAC 2397
 Db 2746 TATCCGAGCTATTTATCAAAAATAGGAGAGTCCGGAATTTAAAGCTTATCTACGCTAC 2805
 Qy 2398 CAATTAAGAGGTATTTGAAGTAGTCAAGATTTAGAGATATATTTGATTTGTTATAAT 2457
 Db 2806 CAATTAAGAGGTATTTGAAGTAGTCAAGATTTAGAGATATATTTGATTTGTTATAAT 2865
 Qy 2458 GCGAAACATGAACATTTGATGTTTCCAGGTACCGGATCCGCTATGCGCGCTTTTCAGTTGAA 2517

Db 2866 GCGAAACATGAACATTTGGATGTTTCCAGGTACCGAGTCCCTATGCGCGCTTTTCAGTTGAA 2925
 Qy 2518 AGCCCAATCGGAAGGTGCGGAGAACCGAATCGATGCGCACCAATTTTGAATGGAATCCT 2577
 Db 2926 AGCCCAATCGGAAGGTGCGGAGAACCGAATCGATGCGCACCAATTTTGAATGGAATCCT 2985
 Qy 2578 GATCTAGATTTGTTCTCTCAGAGATGGAGAAAAATGTGGCATCATTTCCCATCATTTCTCT 2637
 Db 2986 GATCTAGATTTGTTCTCTCAGAGATGGAGAAAAATGTGGCATCATTTCCCATCATTTCTCT 3045
 Qy 2638 TTGATATTTGATATTTGGATGACACAGCTTGCATCAGAAATCTAGCGGTGTGGGTGTATTC 2697
 Db 3046 TTGATATTTGATATTTGGATGACACAGCTTGCATCAGAAATCTAGCGGTGTGGGTGTATTC 3105
 Qy 2698 AAGATTAAAGCGCAGGAAGGTCTATGCAAGACTAGGGAATCTGGAATTTATTTAAAGAGAAA 2757
 Db 3106 AAGATTAAAGCGCAGGAAGGTCTATGCAAGACTAGGGAATCTGGAATTTATTTAAAGAGAAA 3165
 Qy 2758 CCATTTATAGGAGAGACACTGTCTGTTGTGAGAGAGCAGAGAAAAAATTTGAGAGACAAA 2817
 Db 3166 CCATTTATAGGAGAGACACTGTCTGTTGTGAGAGAGGCGCAGAGAAAAAATTTGAGAGACAAA 3225
 Qy 2818 CGTGAAAACTACAAATTTGGAACAAAAACGAGTATATACAGAGGCAAAAGAGCTGTGAT 2877
 Db 3226 CGTGAAAACTACAAATTTGGAACAAAAACGAGTATATACAGAGGCAAAAGAGCTGTGAT 3285
 Qy 2878 GCCTTTATTTCTAGATTTCTCAATATAATAGATTAACAAGCGGATACAAACATTTGGCATGAT 2937
 Db 3286 GCCTTTATTTCTAGATTTCTCAATATAGATTAACAAGCGGATACAAACATTTGGCATGAT 3345
 Qy 2938 CATGCGCAGATAAACTTTGTTTCTCAATTTGAGAGGCTTATCTGTGAGAAATTTCTGTT 2997
 Db 3346 CATGCGCAGATAAACTTTGTTTCTCAATTTGAGAGGCTTATCTTTCAGAAATTTACTGTT 3405
 Qy 2998 ATCCGCGTGAATTCGCGAAATTTTGAAGAAATTTAGAGCTGCATATACATGCAATC 3057
 Db 3406 ATCCGCGTGAATTCGCGAAATTTTGAAGAAATTTAGAGCTGCATATACATGCAATC 3465
 Qy 3058 TCCCTATACCATGCGAGAAATGCTGTTAAATAATGCTGATTTAATAATGGAATTTAGCATGC 3117
 Db 3466 TCCTTATACCATGCGAGAAATGCTGTTAAATAATGCTGATTTAATAATGGAATTTAGCATGC 3525
 Qy 3118 TGAATGTAAAGGCGATGTAGATGTACACAGAGCCATCACCGTTCTGCTGTTTATC 3177
 Db 3526 TGAATGTAAAGGCGATGTAGATGTACACAGAGCCATCATCTGTTCTGACCTGTTATC 3585
 Qy 3178 CCAGATGGAAGCAGAGGTGTACAGAGCTGCGCTGCTGCGGCGGTGGCTATATC 3237
 Db 3586 CCAGATGGAAGCAGAGGTGTACAGAGCTGCGCTGCTGCGGCGGTGGCTATATC 3645
 Qy 3238 CTCGCTGTCAGCGTACAAAGAGGGATATGGAGAGGTTGTGTAAACGATCCATGAAATC 3297
 Db 3646 CTTGCTGTCAGCGTACAAAGAGGGATATGGAGAGGCTGCGTAAACGATCCATGAAATC 3705
 Qy 3298 GAGAACAAATACAGCGAACTTAAATTTTAAACCTGTGAAGAGAGGAGTGTATCCAAAG 3357
 Db 3706 GAGAACAAATACAGCGAACTTAAATTTTAAACCTGTGAAGAGAGGAGTGTATCCAAAG 3765
 Qy 3358 GATACAGGAACGTGTATGATTTATCTGCAACCAAGGTACAGC-----AGTA 3405
 Db 3766 GATACAGGAACGTGTATGATTTATCTGCAACCAAGGTACAGC-----AGTA 3825
 Qy 3406 TGTAAATCCCGTAAATGCTGGATGAGGATGATCATGAGTTGATCTACAGCATCTGTT 3465
 Db 3826 TGTAAATCCCGTAAATGCTGGATGAGGATGATCATGAGTTGATCTACAGCATCTGTT 3885
 Qy 3466 AATTTACAAACCGACTTATGAAGAGAAACGTTATACAGATGTGACGAGAGATAATCATTTG 3525
 Db 3886 AATTTACAAACCGACTTATGAAGAGAAACGTTATACAGATGTGACGAGAGATAATCATTTG 3945
 Qy 3526 GAATATGACAGAGGTATGGAATTTATCCACCACTACAGCTGTTTATATGACAAAGAA 3585
 Db 3946 GAATATGACAGAGGTATGTCAAATTTATCCACCACTACAGCTGTTTATATGACAAAGAA 4005

QY 3586 TTAGAAATCTCCAGAAACCGATAAGTATGAGTTCAGATTGAGATTGAGAAACGGAAGGGAAG 3645
 Db 4006 TTAGAAATCTCCAGAAACCGATAAGTATGAGTTCAGATTGAGATTGAGAAACGGAAGGGAAG 4065
 QY 3646 TTTATTGTAGACAGCGTGGAAATCTCTCTTATGGAGGAATAG 3687
 Db 4066 TTTATTGTAGATAGCGTGGAAATCTCTCTCTATGGAAGAATAG 4107

RESULT 13
 LOCUS BACCRIE 3934 bp DNA linear BCT 25-APR-1994
 DEFINITION Bacillus thuringiensis crystal protein (cryI ET5) gene, complete cds.
 ACCESSION L32020
 VERSION L32020.1 GI:474893
 KEYWORDS crystal protein.
 SOURCE Bacillus thuringiensis
 ORGANISM Bacillus thuringiensis
 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
 REFERENCE 1 (bases 1 to 3934)
 AUTHORS Donovan, W.P.
 JOURNAL Unpublished (1994)
 COMMENT Original source text: Bacillus thuringiensis (strain EG 5847) DNA.
 FEATURES
 Location/Qualifiers
 1..3934
 /organism="Bacillus thuringiensis"
 /mol_type="genomic DNA"
 /strain="EG 5847"
 /db_xref="taxon:1428"
 67..3756
 /gene="cryI ET5"
 67..3756
 /gene="cryI ET5"
 /function="insect toxin"
 /codon_start=1
 /transl_table=11
 /product="crystal protein"
 /protein_id="AA022344.1"
 /db_xref="GI:474894"

translation="MTSNRNKNEINIALSIPTVSNPSTQNLSPDARIBDSLCVAV
 NNIDPFVASTVGTQINIAIRILGVLGVPAGLAFSPFLVGLWPSGRDPWEIE
 LEQLDITAIPLFRIRNEEVPLMVYAQAANLHLLRLDASLFGSEWMASSDVNOYV
 EQIRYEEYNHCQWYNTGLNLRGNAESWLRNQFRDLILGLVDLVALFSPDY
 RTYPINTSAQLTREIYDPIGRNAPGFASTNWFNNAPFSAIEAIAIFRPPLHDF
 PEQUTYSASSRWSSTQHMNYWVGHRLNFRPIGTLTSTQGLNNTSINPVLQFS
 RDVYTESNAGTINILFTVPVGPWFARFNPINQNIYERGATTYSQPYQGVGLQFDS
 ETLPPTETPRPNVSYSHRLSHGLIIGNTLRAPVSWTHRSADRNTIGPNRIQI
 PLKALNLHSGVTVGGPGTGGDILRRNTGTGDIRLNINPLSORVVRVRYAST
 TDLOFFTRNGTVNGFNRGMNLEIRYRSTAGFSTPNFLNAQSTFTLGAQS
 FSNQEVYDRVEVPVPAEYFEAYDLERAQKAVNALFTSNPRLLKTDVTDYHDQVS
 NMVACLSDEFLEKELPEKRYAKLSLDERNLQDNFTFISGLQSFASIDQSNF
 PSNLSLSEHWGMSANVTIOEGNDVFNENYVILPFTNECYPNLYKIGESILKAT
 RYOLGVYEDSODLEIVLIRYNAKHETLDVPGTDSLWPLSVESPIGRGEPNRCAPH
 EWNPDLCSDCDEGRCAHSHFTLDIDVCGTDLHENLGVYVFKIKTOEGYARLGNL
 EFTLEKPLIGALSRLVKRAEKKWRDKRKLQETKRYVTEAKEAVDALFVDSQDLQ
 ADTNIGMHAADKLHVRIRAYLSLPLVPVNAIEFEELEGHIITAMSLYDARNVVK
 NGDFNGLTCKWYGVDDVQSHRSDLVIPWEAEVSQARVPCPGRGYLLRVATYKE
 GYEGECVTIHEINNTDELKNCBEEVYPTDTGTCDNYTAHQGTAAACNSRNVGED
 AYEVDTTAVNYKPTVEEYTDVRDNRHCEYDRGVYVYPPVAGYVTKLEYFPETD
 TWVIEIGETSGKFIIVDSVELLMEE"

ORIGIN
 Query Match 72.9%; Score 2687.2; DB 1; Length 3934;
 Best Local Similarity 83.5%; Pred. No. 0;
 Matches 3088; Conservative 0; Mismatches 593; Indels 15; Gaps 3;

QY 1 TTGACTTCAATAGGAATGAGAAATGAAATATTAATGCTTTATCGATTCAGCTGTA 60
 Db 67 TTGACTTCAATAGGAATGAGAAATGAAATATTAATGCTTTATCGATTCAGCTGTA 126

QY 61 TCGAATCAATCCACACAAATGGATCTATCACCAGATGCTCCTATTTAGGATTTCTTTGT 120
 Db 127 TCGAATCCTTCCACGCAATGAATCTATCACCAGATGCTCCTATTTAGGATTTCTTTGT 186
 QY 121 ATAGCCGAGGGGAATATATCAATCCACTTTGTAGCGCATCAACAGTCCAAACGGGTATT 180
 Db 187 GTAGCCGAGGTGAACAATATTTGATCCATTTGTTAGCGCATCAACAGTCCAAACGGGTATA 246
 QY 181 AACATAGCTGTAGATACTAGGTGTATTAGGCGTACCGTTTGTGACAAATAGTAGT 240
 Db 247 AACATAGCTGTAGATAATTTGGCGGTATTAGGTGTGCGGTTTGTGACAACTAGTAGT 306
 QY 241 TTTTATAGTTTTCTTTGTTGTTGAATTTATGCCCCTGCGGCGAGAGATCAGTGGGAAATTTTC 300
 Db 307 TTTTATAGTTTTCTTTGTTGGGAATTTATGSCCTAGTGGCAGAGATCCATGGGAAATTTTC 366
 QY 301 CTAGAACATGTCGAACAACTTATAATCAACAATAACAGAAATGCTAGGAATACGGCA 360
 Db 367 CTGGAACATGTAGAACAACTTATAAGAACAAAGTAAACAGAAATATCTAGGAATACGGCT 426
 QY 361 CTGTGCTGATTCAAGGTTTATAGGAGATTCCTTTAGAGCCTATCAACAGTCACTTTGAAGAT 420
 Db 427 ATTGCTCGATTAGAGGTCTAGGAAGAGGTATAGATCTTACCAGAGGCTCTTGAACCT 486
 QY 421 TGGCTAGAAACCGTGTATGATGCAAGAACGAGAGTGTTCTTTATACCCCAATATATAGCC 480
 Db 487 TGGTTAGATAACCGAAATGATGCAAGATCAAGAGCATTTATCTTGGAGCGCTATGTTGCT 546
 QY 481 TTAGAACTTGATTTCTTAATGCGATGCGCTTTTGCATTTAGAAACCAAGAAAGTTCCA 540
 Db 547 TTAGAACTTGATTTCTTAATGCGATGCGCTTTTGCATTTAGAAACCAAGAAAGTTCCA 606
 QY 541 TTATTAATGTTATGCTCAAGCTGCAAAATTTACACCTTATTTATTATGAGAGATGCTCT 600
 Db 607 TTATTAATGTTATGCTCAAGCTGCAAAATTTACACCTTATTTATTATGAGAGATGCTCT 666
 QY 601 CTTTGTGTAGTGAATTTGGGCTTTACATCGCAGGAAATTCACGTTTATTATGAGCGCAA 660
 Db 667 CTTTGTGTAGTGAATTTGGGCTTTACATCGCAGGATGCGCATCTTCCGATGTTAAACCAATATACCAAGAACAA 726
 QY 661 GTGGAACAAACGAGAGATTTATTCGACTATTCGTTAGTAAATGGTATATATACAGTCTTAAT 720
 Db 727 ATCAGATATATACAGAGGAATTTCTTAACATTTGCTGCTACATTTGGTATATATACAGGCTTAAT 786
 QY 721 AGCTTGAGAGGGAACAATGCGCAAGTTGGTGGCTTATTAATCAATTCCTGAGAGACTA 780
 Db 787 AACTTGAAGGGGAACAATGCTGAAGTTGGTGGCTTATTAATCAATTCCTGAGAGACTA 846
 QY 781 ACCTTAGGGGTATTAGATCTTAGTGGCACTATTTCCCAAGCTATGACACTCGACCTTATCCA 840
 Db 847 ACCTTAGGGGTATTAGATTTAGTAGCCCTATTTCCCAAGCTATGATATACTCGACCTTATCCA 906
 QY 841 ATAAATACAGTGTCTAGTTTAAACAGGAAGTTTATACAGACGCAATTTGAGACNACAGG 900
 Db 907 ATCAATACAGTGTCTAGTTTAAACAGGAAGTTTATACAGATCCATTTGGGAGAGAAAT 966
 QY 901 GTAAT-----ATGCAAGTATGAATTTGTTGTTAAATAATTAATGACCTTCGTTTCCGCT 954
 Db 967 GCACCTTCAGATTTGCAAGTAGAATTTGTTTAAATTAATTAATGACCATGTTTCTGCTGCC 1026
 QY 955 ATAGAGACTCGGGTTATTCGGAAGCCGCACTCTACTTGAATTTCTTAGAACCAACTTACAAT 1014
 Db 1027 ATAGAGCTCCCAATTTTCAGGCTCCGCACTCTACTTGAATTTTCAGAACCAACTTACAAT 1086
 QY 1015 TTTAGCACTTCATCAGATGAGTGTCTACTAGGCATATGACTTACTGGCGGGGACACA 1074
 Db 1087 TACAGTGTCAATCAAGCGCTTGGAGTAGCACTCAACATATGAATTTATGGTGGGACATAGG 1146
 QY 1075 ATTCAATCTCGGCAATAGGAGCGGATTAATACCTCAACGATGGGTCTTACCA---AT 1131
 Db 1147 CTTAACTTCGCGCCATAGGAGGAGCATTAATACCTCAACAGGACTTACTTAAT 1206

QY 1132 ACTTCTAATTAATCTGTGAAGATTATCAATCTTCTCTCGAGACGTATATTGGACGTGAATCA 1191
DB 1207 ACTTCAATTAATCTGTGAACATTTACAGTCTCTCGAGACGTATATTAGAACAAGATCA 1266
QY 1192 TATGACGAGTCTTCTATGGGGAATTTACTCTGAACCTTATCTATGATGTCCTTACTGTT 1251
DB 1267 AATGACGGGCAAAATAT-----ACTAATTTACTACTCTCTGTAATGGAGTACCTTGGGCT 1320
QY 1252 AGATTTAATTTTATAGGAACCTCTGAAATPACTTTTGAAGAGGTACTGCTAACTATAGTCAA 1311
DB 1321 AGATTTAATTTTATAAACCCTCAGAAATATTATGAAGAGGCGCCACTACTACAGTCAA 1380
QY 1312 CCCTATGAGTCACTTGGGCTTCAATTTAAAGATTTCAGAACTGAATTTACCACAGAAACA 1371
DB 1381 CCGTATCAGGAGTGGGATTTCAATTTTGAATTTTCAAGAACTGAATTTACCACAGAAACA 1440
QY 1372 ACAGAACGCAAAATTAATGAATCATATAGTCAATAGTTCATAGGTTTCTCACATAGGCTCATTTCA 1431
DB 1441 ACAGAACGCAAAATTAATGAATCATATAGTCAATAGTTCATATAGGACTTAATCATTA 1500
QY 1432 CAATCTAGGCTGCATGTPACCAGTATATTCTTGGACGCAACCGTAGTGAGATCGTACAAAT 1491
DB 1501 GGAACACTTTGAGAGCACCCAGTCTATTCTTGGACGCACTGCTAGTGAGATCGTACGAAT 1560
QY 1492 ACCATTAAGTTCAGATAGCATTAACAAATACCAATTTGGTAAATCATTTCAACCTTAATCA 1551
DB 1561 ACGATTTGGACCAAAATAGAAATTAACAAATACCAATTTGGTAAAGCACTGAATCTTCATTCA 1620
QY 1552 GGTACCTCTGTCAGTGCAGGCGCCAGGATTTACAGGAGGGATATAATCCGAACTAAGCTT 1611
DB 1621 GGTGTTACTGTTTGGAGGCGCCAGGATTTACAGGTTGGGATATCTCTCGTAGAACAAAT 1680
QY 1612 AATGGTAGTGTACTAAGTATGGGTCTTAAATTTTAAATAATACATTAACAGCGGTATCGC 1671
DB 1681 ACGGTACATTTGGAGATATACGATTAATTAATTAATGTCGCCATTTATCCCAAGATATCG 1740
QY 1672 GTGAGAGTTCGTTATGCTGCTTCTCAACAAATGGTCTGAGGGTAACTGCGGAGGAGT 1731
DB 1741 GTAAGGATTCGTTATGCTTCTACTACAGATTTACAATTTTTCACGAAATTAATGGAACC 1800
QY 1732 ACTACTTTTGCATCAAGATTTCCCTAGTACTATGATGCAATGCTTTTGCATCTCAA 1791
DB 1801 ACTGTTAATATTTGGTAAATTTCTCAAGAACTATGAATAGGGGGATTAATTTAGAAATAGA 1860
QY 1792 TCATTTAGATTTGCAGAAATTTCTGTAGGTATTAGTGCACTGCGCAGTCAAACTGCTGGA 1851
DB 1861 AGTTTTAGAACTGCAGATTTAGTACTCTCTTTTAAATTTTAAATGCCCAAGCACATTC 1920
QY 1852 ATAAGTATAAGTAAATATGCAAGGTAGACAAACGTTTTCATTTGATAAATTTGAATTCAT 1911
DB 1921 ACATGGGCTCTCAGAGTTTTTCAATCAGGAAGTTTATATAGATAGAGTCGAATTTGTT 1980
QY 1912 CCAATTTACTGCAACCTTCGAAGCAGAAATACGATTTAGAAAGGGCGCAAGAGCGGTGAAT 1971
DB 1981 CCAGCAGAGTAACTTTGAGGAGATATGATTTAGAAAGAGCACAAAGGGCGGTGAAT 2040
QY 1972 GCTCTGTTTACTAATACGAATCCAAGAGATTTGAAACAGATGTGACAGATTTATCATATT 2031
DB 2041 GCTCTGTTTACTTCTACAAATCCAAGAGATTTGAAACAGATGTGACAGATTTATCATATT 2100
QY 2032 GATCAAGTATCCAAATTTAGTGGGCTGTTTATCGGATGAATTTCTGCTTAGATGAAAGAGA 2091
DB 2101 GACCAAGTGTCCAATATGTTGGCATGTTTATCAGATGAATTTTGTGATGAGAGCGA 2160
QY 2092 GAATTTACTGAGAAAGTGAATATGCGAAACGACTCAGTGAATGAAGAACTTACTCCAA 2151
DB 2161 GAATTTATTTGAGAAAGTGAATATGCGAAGCGACTCAGTGAATGAAGAACTTACTCCAA 2220
QY 2152 GATCCAACTTCACATCCATCAATACGCAACCGACTTTCATCTATCTAATAGGCAATCG 2211
DB 2221 GATCCAACTTCACATTCATCAGTGGGCAATTAAGTTTCGCATCCATCGATGACATCA 2280
QY 2212 AATTTTCACATCTATCCATGAACAACTCTGAACATGGATGGTGGGAGAGTGAGAACATTTACA 2271

DB 2281 AACTTCCCTCTATTAATAGCTATCTGAACATGGATGGTGGGGAAGTGCGAATTTACC 2340
QY 2272 ATCCAGGAAGGAATGACGTATTTAAAGAAATTAACGTCACTACCTACCGGAGACTTTTAAT 2331
DB 2341 ATTCAGGAAGGAATGACGTATTTAAAGAAATTAACGTCACTACCTACCGGACTTTTAAT 2400
QY 2332 GAGTGTATCCGACGTATTTATATCAAAAAATAGGAGAGTCGGAATTTAAAGCTTATACT 2391
DB 2401 GAGTGTATCCAAATTTATATCAAAAAATAGGAGAGTCGGAATTTAAAGCTTATACG 2460
QY 2392 CGCTACCAATTAAGAGGATATTTGAAGATAGTCAAGATTTAGAGATATATTGATTCGT 2451
DB 2461 CGCTATCAATTAAGAGGATATTTGAAGATAGTCAAGATCTAGAGATTTATTTAAATTCGT 2520
QY 2452 TATAATGCGAAACATGAACATTTGGATGTTCCAGGTACCGAGTCCGTATGCGCGCTTTCA 2511
DB 2521 TACAAATGCAAGCATGAAACATTTGGATGTTCCAGGTACCGATTTCCCTATGCGCGCTTTCA 2580
QY 2512 GTTGAAGGCCAATCGGAAGGTGCGGAGAACCGAATCGATCGCACCAATTTTGAATGG 2571
DB 2581 GTTGAAGGCCAATCGGAAGGTGCGGAGAACCGAATCGATCGCACCAATTTTGAATGG 2640
QY 2572 AATCCTGATCTAGATTTGTTCTCGAGAGATGGAAGAAATGTTGGGATCATTTCCCATCAT 2631
DB 2641 AATCCTGATCTAGATTTGTTCTCGAGAGATGGAAGAAATGTTGGGATCATTTCCCATCAT 2700
QY 2632 TTCTCTTTGGATATTCATATTGGATGACACAGACTTGCATGAGAACTCTAGGCGTGTGGGTG 2691
DB 2701 TTCACTTTGGATATTCATATTGGTGGTGACACAGACTTGCATGAGAACTCTAGGCGTGTGGGTG 2760
QY 2692 GTATTCAAGATTAAAGACGCGAAGGTCTATGCAAGACTTAGGGAATCTGGAATTTATTGAA 2751
DB 2761 GTATTCAAGATTAAAGACGCGAAGGTCTATGCAAGACTTAGGGAATCTGGAATTTATTGAA 2820
QY 2752 GAGAAACCATTTATGAGAGAGCACTGTCTGCTGTGAGAGAGCAGAGAGAGAGAGAGAGAG 2811
DB 2821 GAGAAACCATTTATTTGAGAGAGCACTGTCTGCTGTGAGAGAGCAGAGAGAGAGAGAGAG 2880
QY 2812 GACAAACGTTGAAACCTACAAATTTGAAACCAAAACGAGTATATACAGAGGCAAAAGAGCT 2871
DB 2881 GACAAACGTTGAAACCTACAAATTTGAAACCAAAACGAGTATATACAGAGGCAAAAGAGCT 2940
QY 2872 GTGGATGCTTTATTTGTTAGATTTCTCAATATAATAGATTACAAGCGGATACAAACATTTGGC 2931
DB 2941 GTGGATGCTTTATTTGTTAGATTTCTCAATATGATCAATTACAAGCGGATACAAACATTTGGC 3000
QY 2932 ATGATTCATGCGGACAGATAAACTTTGTTTCATCGAATTCGAGAGGCTTATCTGTGAGAAATTA 2991
DB 3001 ATGATTCATGCGGACAGATAAACTTTGTTTCATCGAATTCGAGAGGCTTATCTTTGAGAAATTA 3060
QY 2992 TCTGTTATCCCGGCTGTAATGCGGAATTTTGAAGAAATTTAGAGGTCGCTATTCACAT 3051
DB 3061 CCGTGTATCCCGGCTGTAATGCGGAATTTTGAAGAAATTTAGAGGTCGCTATTCACAT 3120
QY 3052 GCAATCTCCCTATACCATGCGAGAAATGCTGTTAAATAATGCTGATTTTAATAATGGAATTA 3111
DB 3121 GCAATGCTTTATACGATGCGAGAAATGCTGTTAAATAATGCTGATTTTAATAATGGAATTA 3180
QY 3112 GCAATGCTGGAATTTAAAGGCAATGTAGATGTACAAAGAGGCTTGTGTAAACGATCCAT 3171
DB 3181 ACATGTTGGAATTTAAAGGCAATGTAGATGTACAAAGAGGCTTGTGTAAACGATCCAT 3240
QY 3172 GTTATCCAGATGCGAAGAGGCTGTCACAGAGTTCGCGCTGCTGCGGCGCGTGGC 3231
DB 3241 GTTATCCAGATGCGAAGAGGCTGTCACAGAGTTCGCGCTGCTGCGGCGCGTGGC 3300
QY 3232 TATATCTCTGCTCACAGGTCACAAAGAGGATATGAGAGGCTTGTGTAAACGATCCAT 3291
DB 3301 TATATCTCTGCTCACAGGTCACAAAGAGGATATGAGAGGCTTGTGTAAACGATCCAT 3360
QY 3292 GAAATCGAGAACAAATACAGACGAATTTTAAATAATGCTGTGAGAGAGGAGTGTAT 3351

Qy	1432	CAATCTAGGTCATGACCAAGTATATCTTTGGACGACCGTAGTCAGATCGTACAAAT	1491
Db	1501	GGAAACACTTTTGAGAGCACCAGTCTATCTTTGGACGCATCGTAGTCAGATCGTACGAAT	1560
Qy	1492	ACCATTAGTTCAGATAGCATACCAATACCAATTTGTTAAATCATTTCAACCTTAATTC	1551
Db	1561	ACGATTGGACCAATAGAAATACCAATACCAATTTGTTAAAGCAGTGAATCTTCATTCA	1620
Qy	1552	GGTACCTCTGTAGTCAGTGGCCAGGATTTACAGGAGGGATATAATCCGAACCTAAACGTT	1611
Db	1621	GGTGTTACTGTGTTGGAGGCCAGGATTTACAGTGGGGATATCTTCGTAGAACAAAT	1680
Qy	1512	AATGGTAGTGTACAAAGTGGTCTTAATTTTAAATATATCAATTTACAGCGGTATCGC	1671
Db	1681	ACGGGTACATTTGGAGATATACGATTAAATTAATGTGCCATTTATCCCAAGATATCGC	1740
Qy	1672	GTGAGAGTTCGTTATGCTGCTCTCAACAAATGCTCTGAGGGTAACTGTGCGGGAGT	1731
Db	1741	GTAAGGATTCGTTATGCTCTTACTACAGATTTACAATTTTTCAGAGAAATTAATGGAACC	1800
Qy	1732	ACTACTTTTGATCAAGGATTCCTTAGTACTATGAGTCAAAATGAGTCTTTGACATCTCAA	1791
Db	1801	ACTGTTAATTTGTAATTTCTCAAGAACTATGAAATAGGGGGATTAATTTAGATATAGA	1860
Qy	1792	TCATTTAGATTTGAGAAATTTCTGTAGGTATTTAGTGCATCTGGCAGTCAAACTGTGGA	1851
Db	1861	AGTTTTAGAACTGCAGGATTTAGTACTCTTTTAAATTTTAAATGCCAAAGCACATTC	1920
Qy	1852	ATAAGTATAGTAAATATGAGGTAGACAAACGTTTCACTTTGATATAAATTTGAATTCAT	1911
Db	1921	ACATTTGGTCTCAGAGTTTTTCAATCAGGAATTTTATAGATAGATCGAAATTTGTT	1980
Qy	1912	CCAATTTACTGCAACTTCGAAGCAGAAATACGATTTAGAAAGGGCGCAAGGGCGTGAAT	1971
Db	1981	CCAGCAGAGTACATTTTGAGGCAGAAATATGATTTAGAAAGCACAAGAGGGCGGTGAAT	2040
Qy	1972	GCTCTGTTTACTAATACGAATTCGAAGAGATTTGAAACAGATGTGACAGATTTATCATATT	2031
Db	2041	GCTCTGTTTACTTCTACAAATCCAAAGAAATTTGAAACAGATGTGACAGATTTATCATATT	2100
Qy	2032	GATCAAGTATCCAAATTTAGTGGCGTGTATTCGATGAATTTCTGTTAGATGAAAGAGA	2091
Db	2101	GACCAAGTGTCCAAATTTGGTGGCATGTTTATCAGATGAATTTTCTTGGATGAGAAGCGA	2160
Qy	2092	GAATTTACTTCAGAAAGTGAATATGCGAAACGACTCAGTGTGATGAAAGAACTTACTCCAA	2151
Db	2161	GAATTTTGGAAAGTGAATATGCGAAGGACTCAGTGTGATGAAAGAACTTACTCCAA	2220
Qy	2152	GATCCAACTTCATCCATCAATTAAGCAACCAAGACTTCATATCTACTAATGAGCAATCG	2211
Db	2221	GATCCAACTTCATCCATCAATTCAGTGGCAATTAAGTTTTCGATCCATCGATGGACAATCA	2280
Qy	2212	AATTTACATCTATCTATGAACAATCTGAACATGGATGGTGGGAGTGAAGACATTTACA	2271
Db	2281	AACCTCCCTCTAATTAATGAGTATCTGAACATGGATGGTGGGAGTGGCAATTTGTTACC	2340
Qy	2272	ATCCAGGAAGAAATGACGTATTTAAAGAGAAATTTACGTCACTTACCGGGGACTTTTAAAT	2331
Db	2341	ATTCCAGGAAGGAATGACGTATTTAAAGAGAAATTTACGTCACTTACCGGGTACTTTTAAAT	2400
Qy	2332	GAGTGTATCCGAGTATTTATCAAAAAATAGGAGAGTCCGAATTTAAAGCTTATPACT	2391
Db	2401	GAGTGTATCCAAATTTATATCAAAAAATAGGAGAGTCCGAATTTAAAGCTTATPACG	2460
Qy	2392	CGGTACCAATTAAGAGGTATTTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGT	2451
Db	2461	CGGTATCAATTAAGAGGTATTTGAAGATAGTCAAGATTTAGAGATTTATTTAAATTCGT	2520
Qy	2452	TATTAATCGGAAACATGAACATTTGGATGTTCCAGTACCGAGTCCGTTATCGCGCTTCA	2511
Db	2521	TACAAATCAAGCATGAACATTTGGATGTTCCAGGTACCGATTCCTTATGGCGCGCTTCA	2580

Qy	2512	GTTGAAGCCCAATCGAAGTGGGAGAACCGAATCGATCGGCACACATTTTGAATGG	2571
Db	2581	GTTGAAGCCCAATCGAAGTGGGAGAACCGAATCGATCGGCACACATTTTGAATGG	2640
Qy	2572	AATCCTGATCTAGATTTCTTCAGAGATGGAGAAAAATGTGCGCATCATTTCCCATCAT	2631
Db	2641	AATCCTGATCTAGATTTCTTCAGAGATGGAGAAAAATGTGCGCATCATTTCCCATCAT	2700
Qy	2632	TTCTCTTTGGATTTGATTTGGATGCACAGACTTGCATGAGAAATCTAGCGTGTGGGTG	2691
Db	2701	TTCACTTTGGATTTGATTTGGATGCACAGACTTGCATGAGAACTTAGCGTGTGGGTG	2760
Qy	2692	GTATTTCAAGATTTAAGACGAGGAAGTCTCAAGACTAGGATCTGGAATTTTATTTGAA	2751
Db	2761	GTATTTCAAGATTTAAGACGAGGAAGTCTCAAGATTTAGGAAATCTGGAATTTTATCGAA	2820
Qy	2752	GAGAAACCATTTATAGGAGAACGACTGTCTCGTGTGAAGAGAGCAGAGAAAAAATGAGA	2811
Db	2821	GAGAAACCATTTATTTGGAGAACGACTGTCTCGTGTGAAGAGAGCGGAAAAAATGAGA	2880
Qy	2812	GACAAACGTCGAAAAAATCTCAATTTGAAAAAAGAGTATATACAGAGGCAAAAGAAAGCT	2871
Db	2881	GACAAACGTCGAAAAAATCTCAATTTGAAAAAAGAGTATATACAGAGGCAAAAGAAAGCT	2940
Qy	2872	GTGGATGCTTTATTTGTAGATTTCTCAATATAATAGATTAACAAGCGGATACAACATTTGGC	2931
Db	2941	GTGGATGCTTTATTTGTAGATTTCTCAATATAATAGATTAACAAGCGGATACAACATTTGGC	3000
Qy	2932	ATGATTCATCGCGCAGATAAATCTGTTCAATCGAATTCGAGAGGCTTATCTGTCAGAAATTA	2991
Db	3001	ATGATTCATCGCGCAGATAAATCTGTTCAATCGAATTCGAGAGGCTTATCTGTCAGAAATTA	3060
Qy	2992	TCGTGTTATCCCGGTGTAAATTCGGAATTTTGTGAAAGAAATAGAAAGTCCCATTTATCACT	3051
Db	3061	CTGTGTTATCCCGGTGTAAATTCGGAATTTTGTGAAAGAAATAGAAAGTCCCATTTATCACT	3120
Qy	3052	GCAATCTCCCTATACGATGCGAGAAATGTCTGTTAAAAATGGTGATTTTAAATAGAAATTA	3111
Db	3121	GCAATGCTCTTATACGATGCGAGAAATGTCTGTTAAAAATGGTGATTTTAAATAGAAATTA	3180
Qy	3112	GCAATCTCGAATTTAAAGGCGATGTAGATGTACAACAGAGCCATCACCGTCTGTCCTT	3171
Db	3181	ACATGTTGGAATGTAAAGGCGATGTAGATGTACAACAGAGCCATCATCGTCTGACCTT	3240
Qy	3172	GTTATCCCAAGATGGGAAGCAGAAAGTGTCAACAAGCAGTTCGCGTCTGTCGCGGCGTGGC	3231
Db	3241	GTTATCCCAAGATGGGAAGCAGAAAGTGTCAACAAGCAGTTCGCGTCTGTCGCGGCGTGGC	3300
Qy	3232	TATATCTCTCGTGTCAAGGCTACAAAGAGGGATATGGAGAGGGTGTGTAAACGATCCAT	3291
Db	3301	TATATCTCTCGTGTCAAGGCTACAAAGAGGGATATGGAGAGGGTGTGTAAACGATCCAT	3360
Qy	3292	GAAATCGAGAACCAATACAGACGAACTAAAATTTAAAACTGTGAAGAGAGGAGTGTAT	3351
Db	3361	GAAATCGAGAACCAATACAGACGAACTAAAATTTAAAACTGTGAAGAGAGGAGTGTAT	3420
Qy	3352	CCAACGGATACAGGAACTGTGATTAATTAATGATTAATGATTAATGATTAATGATTAAT	3411
Db	3421	CCAACGGATACAGGAACTGTGATTAATTAATGATTAATGATTAATGATTAATGATTAAT	3480
Qy	3412	TCCCGTAAATGCTGGATATGAGGATGCAATGAAAGTGTGATTAATGATTAATGATTAAT	3471
Db	3481	TCCCGTAAATGCTGGATATGAGGATGCAATGAAAGTGTGATTAATGATTAATGATTAAT	3540
Qy	3472	AAACCGACTTTTCAAGAGAAACGTTATACAGATGTACGAGAGATTAATCTGTCGATAT	3531
Db	3541	AAACCGACTTTTCAAGAGAGAAACGTTATACAGATGTACGAGAGATTAATCTGTCGATAT	3600
Qy	3532	GACAGAGGGTATGTTGAATTTATCCCACTACAGCTGGTGTATATGACAAAGAAATTAGAA	3591
Db	3601	GACAGAGGGTATGTTGAATTTATCCCACTACAGCTGGTGTATATGACAAAGAAATTAGAA	3660
Qy	3592	TACTTCCAGAAACCGATTAAGGTATGATTTGAGATTTGGAGAAACGGAAAGGAAATTTATT	3651

Db 1741 GTAAAGGATTCGTTAATGCTTCTACTACAGATTACAATTTTTCACGAAATTAATGGAACC 1800
Qy 1732 ACTACTTTTGGATCAAGGATTCCTCTAGTACTATGAGTGCATAATGAGTCTTTTGACATCTCAA 1791
Db 1801 ACTGTTAATATGCTAATTTCTCAAGAACTATGAATAGGGGGGATTAATTTAGATATAGA 1860
Qy 1792 TCAATTTAGATTTGAGAAATTTCTGTAGGTATTTAGTGCATCTGGCAGTCAAACTGCTGGA 1851
Db 1861 AGTTTTAGAACTGCGAGATTTAGTACTCTCTTTAAATTTTTTAAATGCCCAAGCAATTC 1920
Qy 1852 ATAAGTATAGTAAATATGCGAGGTAGACAAACGTTTCACATTTGATAAAATTTGAATTCAT 1911
Db 1921 ACATGGGTCTCAGAGTTTTCCAAATCAGGAAGTTTATAGATAGTCGAATTTGTT 1980
Qy 1912 CCAATTAATCTCAACCTTCGAAGCAGAAATACGATTTAGAAAAGGCGCAAGAGGCGGTGAAT 1971
Db 1981 CCAGCAGAGTAACTTTGAGGAGAGATATGATTTAGAAAGAGACAAAGGCGGTGAAT 2040
Qy 1972 GCTCTGTTTACTAATACGAATCCAAAGAGATTTGAAAACAGATGTGACAGATTAATCATATT 2031
Db 2041 GCTCTGTTTACTTCTACAAATCCAAAGAGATTTGAAAACAGATGTGACAGATTAATCATATT 2100
Qy 2032 GATCAAGTATCCAAATTTAGTGGCGTGTATCCGATCAATTTCTGTAGATGAAGAGA 2091
Db 2101 GACCAAGTGTCCAAATATGGTGGCATGTTTATCAGATGAATTTTCTTGGATGAGAGCGA 2160
Qy 2092 GAATTAATCTCAGAAAAGTGAATATGCGAAACGACTCAGTCAATCAAGAAACTTTACTCCAA 2151
Db 2161 GAATTAATCTCAGAAAAGTGAATATGCGAAACGACTCAGTCAATCAAGAAACTTTACTCCAA 2220
Qy 2152 GATCCAAATCTCATCATCAATTAAGCAACAGAGACTTCATATCTACTAATAGCAATCG 2211
Db 2221 GATCCAAATCTCATCATCAATTAAGCAACAGAGACTTCATATCTACTAATAGCAATCG 2280
Qy 2212 AATTTACATCTATCCATGAACATCTGAACATGGATGGTGGGAGTGAACATTAACA 2271
Db 2281 AATTTCCCTCTATTAATGAGCTATCTGAACATGGATGGTGGGAGTGAACATTAACA 2340
Qy 2272 ATCCAGGAAGCAATGACGTATTTAAAGAGAAATTAAGTCACTACCGGGGACTTTTAAT 2331
Db 2341 ATTCAGGAAGCAATGACGTATTTAAAGAGAAATTAAGTCACTACCGGGGACTTTTAAT 2400
Qy 2332 GAGTGTATCCGAGCTATTTATCAAAAAATAGGAGAGTCCGAATTTAAAGCTTATACT 2391
Db 2401 GAGTGTATCCAAATTTATATCAAAAAATAGGAGAGTCCGAATTTAAAGCTTATACG 2460
Qy 2392 CGCTACCAATTAAGAGGTATATTAAGATAGTCAAGATTTAGAGATATATTTGATTCGT 2451
Db 2461 CGCTATCAATTAAGAGGTATATTAAGATAGTCAAGATTTAGAGATATATTTAATTCGT 2520
Qy 2452 TATAATGCGAAACATGAACATTTGGATGTTCCAGGTACCGAGTCCGATATGCGCGCTTTCA 2511
Db 2521 TACAAATGCAAGCATGAACATTTGGATGTTCCAGGTACCGATTTCCCTATGCGCGCTTTCA 2580
Qy 2512 GTTGAAGCCCAATCGGAAGGTGCGGAGAACCGAATCGATCGCACCAATTTTGAATGG 2571
Db 2581 GTTGAAGCCCAATCGGAAGGTGCGGAGAACCAAAATCGATCGCACCAATTTTGAATGG 2640
Qy 2572 AATCCTGATCTAGATTTGCTCGAGAGATGGAGAAAATGTCGGCATCATTTCCCATCAT 2631
Db 2641 AATCCTGATCTAGATTTGCTCGAGAGATGGAGAAAATGTCGGCATCATTTCCCATCAT 2700
Qy 2632 TTCTCTTTGATATGATATTTGATGTCACAGACTTGCATCAGAACTTAGCGGTGTCGGTG 2691
Db 2701 TTCACTTTGATATTTGATTTGGGTGTCACAGACTTGCATCAGAACTTAGCGGTGTCGGTG 2760
Qy 2692 GTATTCAGATTAAGACGCGAGAGGTCTATCGAAGCTAGCGAATCTGGAATTTATTGAA 2751
Db 2761 GTATTCAGATTAAGACGCGAGAGGTATGTCAGATTTAGGAATCTGGAATTTATCGAA 2820
Qy 2752 GAGAAACCATTTATAGGAGAGCACTGCTCTGTTGAAGAGAGAGAGAGAGAGAGAGAGAG 2811

Db 2821 GAGAAACCATTAATTTGAGAGACACTGCTCTGTTGAGAGAGCGGAGAGAGAGAGAGAGAG 2880
Qy 2812 GACAAACGTGAAACACTCAATTTGAAACAAACAGATATATACAGAGGCAAAAGAGCT 2871
Db 2881 GACAAACGCGGAGAGAGACTCAATTTGAAACAAACAGAGATATATACAGAGGCAAAAGAGCT 2940
Qy 2872 GTGGATGCTTTTATTTAGATTTCTCAATTAATAGATTACAAGCGGATACAACATTTGGC 2931
Db 2941 GTGGATGCTTTTATTTCTAGATTTCTCAATATGATCAATTTACAAGCGGATACAACATTTGGC 3000
Qy 2932 ATGATTCATGCGGCAGATAAACCTTTGATCGAAATTCGAGAGCTTATCTGTGAGAAATTA 2991
Db 3001 ATGATTCATGCGGCAGATAAACCTTTGATCGAAATTCGAGAGCGGTATCTTTGAGAAATTA 3060
Qy 2992 TCTGTTATCCCGGTGTAATGCGGAAATTTTTGAGAAATTTAGAAAGTGCATATATCACT 3051
Db 3061 CCTGTTATCCAGGTGTAATGCGGAAATTTTTGAGAAATTTAGAAAGTGCATATATCACT 3120
Qy 3052 GCATCTCCCTATACGATCGGAGAAATGCTGTTAAAAATGGTGATTTTAATTAATGGAATTA 3111
Db 3121 GCAATGCTCTTATACGATCGGAGAAATGCTGTTAAAAATGGTGATTTTAATTAATGGAATTA 3180
Qy 3112 GCATGCTGGAATGTAAGAGGCAATGTAGATGTACAACAGAGCCATCACCGTCTGTCTCT 3171
Db 3181 ACATGTTGGAATGTAAGAGGCAATGTAGATGTACAACAGAGCCATCATCTGTTCTGACCTT 3240
Qy 3172 GTTATCCAGAAATGGAAGCAGAAAGTGTCAAAAGCAGTTCGCGTCTGTCCGGGCGGTGGC 3231
Db 3241 GTTATCCAGAAATGGAAGCAGAAAGTGTCAAAAGCAGTTCGCGTCTGTCCGGGCGGTGGC 3300
Qy 3232 TATATCTCTGTTGTCACAGGTCACAAAGAGGATTTGGAGAGGTTGTGTAAACATTCAT 3291
Db 3301 TATATCTCTGTTGTCACAGGTCACAAAGAGGATTTGGAGAGGTTGTGTAAACATTCAT 3360
Qy 3292 GAAATCGAGAAACATACAGAGCAATCTAAATTTAAAACTGTCAAGAGAGGAGTGTAT 3351
Db 3361 GAAATCGAGAAACATACAGAGCAATCTAAATTTAAAACTGTCAAGAGAGGAGTGTAT 3420
Qy 3352 CCAACGGATACAGAAACGTGTATGATTTACTGCAACCAAGGTACAGCAGATGTGTAAT 3411
Db 3421 CCAACGGATACAGAAACGTGTATGATTTACTGCAACCAAGGTACAGCAGATGTGTAAT 3480
Qy 3412 TCCCGTAATGCTGGATATGAGGATGATATGAAGTTGATCTACAGATCTGTTAATTAC 3471
Db 3481 TCCCGTAATGCTGGATATGAGGATGATATGAAGTTGATCTACAGATCTGTTAATTAC 3540
Qy 3472 AAACCCACTTATGAAGAGAAACGTATACAGATGTACAGAGATTAATCATTTGTAATAT 3531
Db 3541 AAACCCACTTATGAAGAGAAACGTATACAGATGTACAGAGATTAATCATTTGTAATAT 3600
Qy 3532 GACAGAGGTTATGTAATTTATCCACCACTACCAAGCTGGTTATATGACAAAGAAATTAGAA 3591
Db 3601 GACAGAGGTTATGTAATTTATCCACCACTACCAAGCTGGTTATGACAAAGAAATTAGAA 3660
Qy 3592 TACTTCCGAGAAACCGATTAAGGATGATTTGAGATTGGAGAGAAACCGAGAGGAGTTTATT 3651
Db 3661 TACTTCCGAGAAACCGATTAAGGATGATTTGAGATTGGAGAGAAACCGAGAGGAGTTTATT 3720
Qy 3652 GTAGACAGCGTGAATTTACTCTCTTATGGAGGAATAG 3687
Db 3721 GTAGATAGCGTGAATTTACTCTCTCATGGAGGAATAG 3756

Search completed: April 21, 2005, 00:32:35
Job time : 15279. secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 20, 2005, 16:05:50 ; Search time 1752 Seconds
(without alignments)
12457.812 Million cell updates/sec

Title: US-10-614-524-1
Perfect score: 3687
Sequence: 1 ttgactcaaatggagaaaa.....tactcttatggaggagaatag 3687

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	3687	100.0	3687	AAH28240	Aah28240 Nucleotid
2	3666.2	99.4	4173	AAH28240	Aa02482 B. thurin
3	3266.6	88.6	3684	AAV15222	Aav15222 Bacillus
4	3266.6	88.6	3684	AAH89221	Aa89221 Bacillus
5	3260.2	88.4	3684	AAH89221	Aa02489 B. thurin
6	3132	84.9	4074	AAQ56804	Aaq56804 Bacillus
7	2687.2	72.9	3932	AAQ64112	Aaq64112 cryET5 ge
8	2687.2	72.9	3932	AAQ64112	Aa09160 B. thurin
9	2687.2	72.9	3934	AAAT95051	Aat95051 DNA encod
10	2687.2	72.9	3934	AAAT95051	Aat68434 CryET5 ge
11	2687.2	72.9	3934	AAV83927	Aav83927 DNA encod
12	2684.2	72.8	3687	ADK98478	Adk98478 B thuring
13	2630.2	71.3	3627	AAQ54854	Aa04854 Bacillus
14	2544.2	69.0	3663	AAAS00422	Aa00422 B. thurin
15	2541.2	68.9	3663	AAAS00421	Aa00421 B. thurin
16	2394.2	64.7	3624	AAAS04853	Aa04853 Bacillus
17	2004.8	54.4	3651	AAAS04852	Aa04852 Bacillus
18	1793.4	48.6	3522	AAAT16558	Aat16558 B.t. toxi
19	1791.8	48.6	3522	AAQ06830	Aaq06830 Sequence
20	1791.8	48.6	3522	AAAT49592	Aat49592 Bacillus

21	1790.2	48.6	3522	2	AAQ26928	Aaq26928 DNA encod
22	1662	45.1	4106	2	AAV16214	Aav16214 DNA encod
23	1662	45.1	4106	2	AAV09318	Aav09318 Bacillus
24	1581.6	42.9	3558	2	AAQ60619	Aaq60619 Polynucle
25	1501	40.7	3766	2	AAQ77858	Aaq77858 Crystal p
26	1438.6	39.0	8854	2	AAZ20086	Aaz20086 DNA encod
27	1432.4	38.9	3713	2	AAQ64111	Aaq64111 cryET4 ge
28	1432.4	38.9	3713	2	AAAT95050	Aat95050 DNA encod
29	1432.4	38.9	3713	2	AAAT68435	Aat68435 CryET4 ge
30	1432.4	38.9	3713	2	AAV83926	Aav83926 DNA encod
31	1432.4	38.9	3713	2	AAZ09159	Aaz09159 B. thurin
32	1411.4	38.3	4020	2	AAQ14648	Aaq14648 cryLF gen
33	1408.4	38.2	3522	2	AAQ10182	Aaq10182 Lepidopte
34	1408.4	38.2	3522	2	AAQ47291	Aaq47291 Delta end
35	1408.4	38.2	3522	2	AAV62081	Aav62081 Plasmid p
36	1408.4	38.2	3522	2	AAQ60606	Aaq60606 wild-type
37	1408.4	38.2	3522	4	AAAS00565	Aas00565 B. thurin
38	1406.8	38.2	3522	2	AAAT18722	Aat18722 Codon-rew
39	1405.2	38.1	3522	2	AAAT05270	Aat05270 CryIF tox
40	1402.2	38.0	5170	12	ADK98488	Adk98488 B thuring
41	1402.2	38.0	5600	12	ADK98490	Adk98490 B thuring
42	1402.2	38.0	6600	12	ADK98482	Adk98482 B thuring
43	1402.2	38.0	7000	12	ADK98485	Adk98485 B thuring
44	1402	38.0	3534	2	AAV31162	Aav31162 Bacillus
45	1402	38.0	3534	6	ABK11833	Abk11833 DNA encod

ALIGNMENTS

RESULT 1

AAH28240
ID AAH28240 standard; DNA; 3687 BP.

XX AC AAH28240;

XX DT 05-SEP-2001 (first entry)

XX DE Nucleotide sequence of a CryIbF insecticidal protein.

XX KW CryIbF; insecticidal protein; CryIbF; Cry9Fa; lepidoptera; coleoptera;
XX KW insect pest; transgenic plant; ss.

XX OS Bacillus thuringiensis.

XX FH Key Location/Qualifiers
XX FT CDS 1..3687

XX FT /*tag= a
XX FT /product= "CryIbF insecticidal protein"

XX PN WO200147952-A2.

XX PD 05-JUL-2001.

XX PF 19-DEC-2000; 2000WO-EP013184.

XX PR 28-DEC-1999; 99US-0173387P.

XX PA (AVET) AVENTIS CROPS SCIENCE NV.

XX XX Arnaut G, Boets A, Damme N, Mathieu E, Vanneste S, Van Rie J;

XX WPI; 2001-425619/45.

XX P-PSDB; AAB84628.

XX PT Novel insecticidal proteins CryIbF, Cry9Fa and CryIbF, derived from
XX PT Bacillus thuringiensis, useful for controlling insects in plants.

XX PS Claim 5; Page 30-36; 65pp; English.

XX CC The present sequence encodes CryIbF, an insecticidal protein derived from
XX CC Bacillus thuringiensis. The specification also describes CryIbF and
XX CC Cry9Fa. The Cry proteins have activity against lepidopteran and

CC coleopteran insect pests. Cry1Bf, CryIud and Cry9Fa polynucleotides and
CC polypeptides are useful for obtaining a plant with resistance to insects.
CC Cry polynucleotides are useful for producing transgenic plants which are
CC resistant to insects
XX
SQ Sequence 3687 BP; 1219 A; 640 C; 805 G; 1023 T; 0 U; 0 Other;
Query Match 100.0%; Score 3687; DB 4; Length 3687;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTGACTTCAAAATAGGAAAAATGAGATGAAATATATAAATGCTTTATCGATTCAGCTGTA 60
DB 1 TTGACTTCAAAATAGGAAAAATGAGATGAAATATATAAATGCTTTATCGATTCAGCTGTA 60
QY 61 TCGAATCATTTCCACACAAATGGATCTATCACAGATGCTCGTATGAGGATTCCTTTGTGT 120
DB 61 TCGAATCATTTCCACACAAATGGATCTATCACAGATGCTCGTATGAGGATTCCTTTGTGT 120
QY 121 ATAGCCGAGGGGAATATATCAATCCACTTGTAGCGCATCAACAGTCCAAACGGGTATT 180
DB 121 ATAGCCGAGGGGAATATATCAATCCACTTGTAGCGCATCAACAGTCCAAACGGGTATT 180
QY 181 AACATAGCTGGTAGAATACATAGGTATATAGGCGTACCGTTTCTGGACAAATAGCTAGT 240
DB 181 AACATAGCTGGTAGAATACATAGGTATATAGGCGTACCGTTTCTGGACAAATAGCTAGT 240
QY 241 TTTTATAGTTTTCTTGTGTGTAATATAGCGCGGCGGAGAGATCAGTGGGAAATTTTC 300
DB 241 TTTTATAGTTTTCTTGTGTGTAATATAGCGCGGCGGAGAGATCAGTGGGAAATTTTC 300
QY 301 CTAGAACATGCTGCAACAACTTATAAATCAACAAATACAGAAAATGCTAGGAATACGGCA 360
DB 301 CTAGAACATGCTGCAACAACTTATAAATCAACAAATACAGAAAATGCTAGGAATACGGCA 360
QY 361 CTGCTCGATTACAGGTTTAGGAGATTCCTTTAGAGCCTATCAACAGTCACTTTGAAGAT 420
DB 361 CTGCTCGATTACAGGTTTAGGAGATTCCTTTAGAGCCTATCAACAGTCACTTTGAAGAT 420
QY 421 TGCGTGAACACCGTGATGATGCAAGAACAGAGAGTGTCTTTATACCCCAATATATAGCC 480
DB 421 TGCGTGAACACCGTGATGATGCAAGAACAGAGAGTGTCTTTATACCCCAATATATAGCC 480
QY 481 TTAGAACTTGATTTCTTAAATGGATGCGCTTTTCGCAATTAGAAACCAAGAGTTCCA 540
DB 481 TTAGAACTTGATTTCTTAAATGGATGCGCTTTTCGCAATTAGAAACCAAGAGTTCCA 540
QY 541 TTATTAATGGTATATGCTCAAGCTGCAAAATTTACACCTATTTATTTAGAGATGCTCTCT 600
DB 541 TTATTAATGGTATATGCTCAAGCTGCAAAATTTACACCTATTTATTTAGAGATGCTCTCT 600
QY 601 CTTTTGTGTAGTGAATTTGGGCTTACATCGAGGAAATTCAGGTTATTTATGAGCGCAA 660
DB 601 CTTTTGTGTAGTGAATTTGGGCTTACATCGAGGAAATTCAGGTTATTTATGAGCGCAA 660
QY 661 GTGGAAACACGAGAGATTTCCGACTATTGCGTAGAATGGTATATACAGCTCTAAAT 720
DB 661 GTGGAAACACGAGAGATTTCCGACTATTGCGTAGAATGGTATATACAGCTCTAAAT 720
QY 721 AGCTTGAGAGGGAACAATGCGCAAGTTGGTGGTGGTATTAATCAATTTCCGTTAGATCTA 780
DB 721 AGCTTGAGAGGGAACAATGCGCAAGTTGGTGGTGGTATTAATCAATTTCCGTTAGATCTA 780
QY 781 ACCTTAGGGGTATAGATCTAGTGGCACTATTCAGAGCTATGACACTCGCACTTATCCA 840
DB 781 ACCTTAGGGGTATAGATCTAGTGGCACTATTCAGAGCTATGACACTCGCACTTATCCA 840
QY 841 ATAAATACGAGTGTCTGATTTAAACAGGAAAGTTTATACAGACGCAATTTGAGCAACAGGG 900
DB 841 ATAAATACGAGTGTCTGATTTAAACAGGAAAGTTTATACAGACGCAATTTGAGCAACAGGG 900
QY 901 GTAAATATGCAAGTATGAAATGGTATATAAATGCACTTCGTTTTCGCTATATAGAG 960
DB 901 GTAAATATGCAAGTATGAAATGGTATATAAATGCACTTCGTTTTCGCTATATAGAG 960

DB 901 GTAAATATGCAAGTATGAAATGGTATATAAATGCACTTCGTTTTCGCTATATAGAG 960
QY 961 ACTGCGGTTATCGAAGCCGCACTTACTTGTATTTCTAGAACAACTTACAAATTTTAGC 1020
DB 961 ACTGCGGTTATCGAAGCCGCACTTACTTGTATTTCTAGAACAACTTACAAATTTTAGC 1020
QY 1021 ACTTCAATCAAGTGGAGTGTCTACTAGGCATATAGCTTACTTGGCGGGGACACAAATCAA 1080
DB 1021 ACTTCAATCAAGTGGAGTGTCTACTAGGCATATAGCTTACTTGGCGGGGACACAAATCAA 1080
QY 1081 TCTCGGCCAATAGGAGCGGATTAATACCTCAACGATGGGTCTACCAATCTCTATT 1140
DB 1081 TCTCGGCCAATAGGAGCGGATTAATACCTCAACGATGGGTCTACCAATCTCTATT 1140
QY 1141 AATCCTGTAGATTAATCACTTCTCGAGAGCTATATTTGGACTCAATCATATGAGGA 1200
DB 1141 AATCCTGTAGATTAATCACTTCTCGAGAGCTATATTTGGACTCAATCATATGAGGA 1200
QY 1201 GTGCTTCTATGGGAAATTTACCTTGAACCTTATTTGTTGCTCCCTACTGTTAGATTAA 1260
DB 1201 GTGCTTCTATGGGAAATTTACCTTGAACCTTATTTGTTGCTCCCTACTGTTAGATTAA 1260
QY 1261 TTTAGGAACCTCAGAAATCTTTTGAAGAGGTACTGCTAACTATATAGTCAACCTATGAG 1320
DB 1261 TTTAGGAACCTCAGAAATCTTTTGAAGAGGTACTGCTAACTATATAGTCAACCTATGAG 1320
QY 1321 TCACCTGGGCTTCAATTTAAAGATTCAGAAATCTGAATTTACACAGAAACACAGAACGA 1380
DB 1321 TCACCTGGGCTTCAATTTAAAGATTCAGAAATCTGAATTTACACAGAAACACAGAACGA 1380
QY 1381 CCAAAATATGAATCATATAGTCAATAGTTTATCTACATAGGGCTCAITTTCAAACTTAG 1440
DB 1381 CCAAAATATGAATCATATAGTCAATAGTTTATCTACATAGGGCTCAITTTCAAACTTAG 1440
QY 1441 GTGCATGTACCAGTATATTTCTGGACGCACTAGTGCAGATCGTAAATACCAATAGT 1500
DB 1441 GTGCATGTACCAGTATATTTCTGGACGCACTAGTGCAGATCGTAAATACCAATAGT 1500
QY 1501 TCAGATAGCATACAAATACCAATACCAATACCAATACCAATACCAATACCAATACCTCT 1560
DB 1501 TCAGATAGCATACAAATACCAATACCAATACCAATACCAATACCAATACCAATACCTCT 1560
QY 1561 GTAGTCAGTGGGCCAGATTTTACAGAGGGGATATTAATCCGAACTAACTGTTAGTGT 1620
DB 1561 GTAGTCAGTGGGCCAGATTTTACAGAGGGGATATTAATCCGAACTAACTGTTAGTGT 1620
QY 1621 GTACTAAGTATGGTCTTAAATTTAATATACATCATTTACAGCGGTATCGCGTGAAGTT 1680
DB 1621 GTACTAAGTATGGTCTTAAATTTAATATACATCATTTACAGCGGTATCGCGTGAAGTT 1680
QY 1681 CGTTATGCTGCTTCTCAAAACAAATGGTCTGAGGGTAACTGTCCGAGGGAGTACTCTTTT 1740
DB 1681 CGTTATGCTGCTTCTCAAAACAAATGGTCTGAGGGTAACTGTCCGAGGGAGTACTCTTTT 1740
QY 1741 GATCAAGGATTCCTTAGTACTATAGTGCAAATGAGTCTTTTGACATCTCAATCAATTTAGA 1800
DB 1741 GATCAAGGATTCCTTAGTACTATAGTGCAAATGAGTCTTTTGACATCTCAATCAATTTAGA 1800
QY 1801 TTTGCAAGATTTCTGTTAGTATAGTGCATCTGGCAGTCAAACTGCTGGAATTAAGTATA 1860
DB 1801 TTTGCAAGATTTCTGTTAGTATAGTGCATCTGGCAGTCAAACTGCTGGAATTAAGTATA 1860
QY 1861 AGTAATAATGCAAGTATAGTGCATCTTTTGTATAAATTTCAATTTCAATTTACT 1920
DB 1861 AGTAATAATGCAAGTATAGTGCATCTTTTGTATAAATTTCAATTTCAATTTACT 1920
QY 1921 GCAACCTTCCGAGCAGAAATACGATTTTAGAAGGGCCGCAAGAGCGGTGAATGCTCTGTT 1980
DB 1921 GCAACCTTCCGAGCAGAAATACGATTTTAGAAGGGCCGCAAGAGCGGTGAATGCTCTGTT 1980
QY 1981 ACTAATAACGATTCAGAGATTTGAAACAGATGTCAGAGATTTATCATATTTGATCAAGTA 2040
DB 1981 ACTAATAACGATTCAGAGATTTGAAACAGATGTCAGAGATTTATCATATTTGATCAAGTA 2040

```
Qy 2041 TCCAAATTAGTGGCGTGTATCGATGAAATCTCTAGATGAAAGAGAAATTAATT 2100
Db 2041 TCCAAATTAGTGGCGTGTATCGATGAAATCTCTAGATGAAAGAGAAATTAATT 2100
Qy 2101 GAGAAAGTGAATATGCGAAACGACTCAGTGAATGAAAGAAATTAATTCCAAAC 2160
Db 2101 GAGAAAGTGAATATGCGAAACGACTCAGTGAATGAAAGAAATTAATTCCAAAC 2160
Qy 2161 TTCAATCCATCAATAAGAACACAGACTTCAATATCTACTAATAGCAATCGAATTCACA 2220
Db 2161 TTCAATCCATCAATAAGAACACAGACTTCAATATCTACTAATAGCAATCGAATTCACA 2220
Qy 2221 TCTATCCATGACAACTCTGACATGGAATGTTGGGGAAGTGAACATTAACATCCAGAA 2280
Db 2221 TCTATCCATGACAACTCTGACATGGAATGTTGGGGAAGTGAACATTAACATCCAGAA 2280
Qy 2281 GGAATGACGTAATTAAGAGAAATTAAGTCACTACCGGGGACTTTTAATGAGTGTAT 2340
Db 2281 GGAATGACGTAATTAAGAGAAATTAAGTCACTACCGGGGACTTTTAATGAGTGTAT 2340
Qy 2341 CCGACGTAATTAATCAAAAATAGGAGAGTCGGAATTAAGCTTATCTCGTACCAA 2400
Db 2341 CCGACGTAATTAATCAAAAATAGGAGAGTCGGAATTAAGCTTATCTCGTACCAA 2400
Qy 2401 TTAAGAGGTAATTAAGAGTAAGTCAAGATTTAGAGATATATTTGATTCGTTAATGCG 2460
Db 2401 TTAAGAGGTAATTAAGAGTAAGTCAAGATTTAGAGATATATTTGATTCGTTAATGCG 2460
Qy 2461 AATCATGAACATTTGATGTTCCAGGTACCGAGTCCGTTATGGCCGCTTTCAGTTGAAAGC 2520
Db 2461 AATCATGAACATTTGATGTTCCAGGTACCGAGTCCGTTATGGCCGCTTTCAGTTGAAAGC 2520
Qy 2521 CCAATCGGAAGTCCGGAAGACCGAATCGATCGCACACATTTGAATGGAATCCTGAT 2580
Db 2521 CCAATCGGAAGTCCGGAAGACCGAATCGATCGCACACATTTGAATGGAATCCTGAT 2580
Qy 2581 CTAGATTGTTCTCGAGAGATGGAAGAAATGTCGGCATCATTCCTCATCATTTCTCTTTG 2640
Db 2581 CTAGATTGTTCTCGAGAGATGGAAGAAATGTCGGCATCATTCCTCATCATTTCTCTTTG 2640
Qy 2641 GATATTGATATTTGATGACAGACTTCATGAGAAATCTAGCGGTGTCGGTGTATTCAG 2700
Db 2641 GATATTGATATTTGATGACAGACTTCATGAGAAATCTAGCGGTGTCGGTGTATTCAG 2700
Qy 2701 ATTAAGACGCGAGGAGTCTATGCAAGACTAGGGAATCTGGAATTTATGAAGAGAAACCA 2760
Db 2701 ATTAAGACGCGAGGAGTCTATGCAAGACTAGGGAATCTGGAATTTATGAAGAGAAACCA 2760
Qy 2761 TTATTAGGAGAGCACTGTCGTGTGAAGAGACAGAGAAAAAATGGAGAGACAAACGT 2820
Db 2761 TTATTAGGAGAGCACTGTCGTGTGAAGAGACAGAGAAAAAATGGAGAGACAAACGT 2820
Qy 2821 GAAAACTACAAATTTGAAACAAACAGATATATACAGAGCAAAAGCTGTGATGCT 2880
Db 2821 GAAAACTACAAATTTGAAACAAACAGATATATACAGAGCAAAAGCTGTGATGCT 2880
Qy 2881 TTATTGAGATTTCTCAATATAATAGATTACAAGCGGATACAAACATTTGGCATGATTCAT 2940
Db 2881 TTATTGAGATTTCTCAATATAATAGATTACAAGCGGATACAAACATTTGGCATGATTCAT 2940
Qy 2941 CGGCGAGATAAATTTGATCGAATTCGAGAGCTTATCTGTGAGAAATTTATCTGTTATC 3000
Db 2941 CGGCGAGATAAATTTGATCGAATTCGAGAGCTTATCTGTGAGAAATTTATCTGTTATC 3000
Qy 3001 CCGGGTGAATGCGGAAATTTTGAAGAAATTAAGAGTGCATATATCACTGCAATCTCC 3060
Db 3001 CCGGGTGAATGCGGAAATTTTGAAGAAATTAAGAGTGCATATATCACTGCAATCTCC 3060
Qy 3061 CTATACGATCGGAGAAATGTCGTTAAAAATGCTGATTTAATGATGATGATGCTGG 3120
Db 3061 CTATACGATCGGAGAAATGTCGTTAAAAATGCTGATTTAATGATGATGATGCTGG 3120
```

```
Qy 3121 AATGTTAAAGCGCATGTAGATGTACAAAGAGCCATCACCGTCTCTGCTTGTATCCCA 3180
Db 3121 AATGTTAAAGCGCATGTAGATGTACAAAGAGCCATCACCGTCTCTGCTTGTATCCCA 3180
Qy 3181 GAATGGGAAGCAGAAAGTGTCAAGCAAGTTCGCGTCTGTCCGGGCGTGGCTATATCCTC 3240
Db 3181 GAATGGGAAGCAGAAAGTGTCAAGCAAGTTCGCGTCTGTCCGGGCGTGGCTATATCCTC 3240
Qy 3241 CGTGTACACGCTACAAAGAGGATATGGAGAGGTTGTGTAAACGATCCATGAATCGAG 3300
Db 3241 CGTGTACACGCTACAAAGAGGATATGGAGAGGTTGTGTAAACGATCCATGAATCGAG 3300
Qy 3301 AACAAATACAGCAAGCTTAAATTTAAAACTGTGAAGAGAGGAGTGTATCCAAACGAT 3360
Db 3301 AACAAATACAGCAAGCTTAAATTTAAAACTGTGAAGAGAGGAGTGTATCCAAACGAT 3360
Qy 3361 ACAGGAACGTTGATTAATGATTAATCTGCACACCAAGGTACAGCAGTATGTAATTCGCTAAT 3420
Db 3361 ACAGGAACGTTGATTAATGATTAATCTGCACACCAAGGTACAGCAGTATGTAATTCGCTAAT 3420
Qy 3421 GCTGGATATGAGGATGATATGAAGTTGATCTACAGCATCTGTTAATTAACAAACCGACT 3480
Db 3421 GCTGGATATGAGGATGATATGAAGTTGATCTACAGCATCTGTTAATTAACAAACCGACT 3480
Qy 3481 TATCAAGAGAAACGCTATACAGATGTACGAGAGATATCATTTGTAATGACAGAGGG 3540
Db 3481 TATCAAGAGAAACGCTATACAGATGTACGAGAGATATCATTTGTAATGACAGAGGG 3540
Qy 3541 TATGTGAATTTATCCACCACTACCGCTGTTATATGACAAAGAAATTAGAATATCTTCCCA 3600
Db 3541 TATGTGAATTTATCCACCACTACCGCTGTTATATGACAAAGAAATTAGAATATCTTCCCA 3600
Qy 3601 GAAACCGATAGGTATGATGATTTGAGATTTGAGAAACGGAAGGAAATTTATTTAGACAGC 3660
Db 3601 GAAACCGATAGGTATGATGATTTGAGATTTGAGAAACGGAAGGAAATTTATTTAGACAGC 3660
Qy 3661 GTGGAAATTAATCTCTTATGGAGGATAG 3687
Db 3661 GTGGAAATTAATCTCTTATGGAGGATAG 3687

RESULT 2
AAS02482
ID AAS02482 standard; DNA; 4173 BP.
XX
AC AC
XX XX
DT 29-AUG-2001 (first entry)
XX
DE B. thuringiensis DNA encoding a toxic crystal protein, CryET64.
XX
KW Delta endotoxin; Lepidopteran-active; crystal protein; insecticide;
KW transgenic plant; corn; wheat; soybean; oat; cotton; rice; sorghum;
KW sugarcane; tomato; tobacco; kapok; flax; potato; barley; turf grass;
KW pasture grass; berry; fruit; legume; vegetable; ornamental plant; shrub;
KW cactus; tree cell; gypsy moth; looper; tobacco budworm; spruce budworm;
KW cotton leaf perforator; CryET64; ds.
XX
OS Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
CDS 1..3471
FT /*tag= a
FT /product= "CryET64"
FT /transl_except= (pos:1..3,aa:Met)
XX
XX WO200119859-A2.
XX
XX 22-MAR-2001.
XX
XX 13-SEP-2000; 2000WO-US025361.
XX
XX 15-SEP-1999; 99US-0153995P.
PR
```

XX PA (MONS) MONSANTO CO.
 XX PI Baum JA, Chu C, Donovan WP, Gilmer AJ, Rupar MJ;
 XX DR WPI; 2001-281518/29.
 XX DR P-PSDB; AAU02039.
 XX PT Lepidopteran-active Bacillus thuringiensis delta-endotoxin polypeptides
 XX PT and the polynucleotides that encode them, useful for increasing the
 XX PT insect resistance of plant.
 XX PS Claim 17; Page 133-138; 173pp; English.
 XX CC The sequence encodes a B. thuringiensis Lepidopteran-active delta-
 CC endotoxin, crystal protein CryE64. The Lepidopteran-active B.
 CC thuringiensis delta-endotoxin polypeptides may be used as compositions
 CC that are applied to plant crops to protect them from insect damage. The
 CC polynucleotides may be used in the production of transgenic plants that
 CC express the insecticidal polypeptides and consequently have improved
 CC insect resistance compared to non-transformed plants. Monocotyledonous or
 CC dicotyledonous plants may be protected in this way, for example corn,
 CC wheat, soybean, oat, cotton, rice, rye, sorghum, sugarcane, tomato,
 CC tobacco, kapok, flax, potato, barley, turf grass, pasture grass, berry,
 CC fruit, legume, vegetable, ornamental plant, shrub, cactus and/or tree
 CC cell. A wide range of insects (e.g. gypsy moth, looper, tobacco budworm,
 CC cotton leaf perforator and spruce budworm) may be affected by application
 CC of the insecticidal polypeptides (full details given in specification)
 XX CC
 XX SQ Sequence 4173 BP; 1417 A; 705 C; 878 G; 1173 T; 0 U; 0 Other;
 Query Match 99.4%; Score 3666.2; DB 4; Length 4173;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 3674; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
 QY 1 TTGACTTCAAAATAGGAAAAATGAGATGAATTAATAATGCTTTATCGATCCAGCTGTA 60
 DB 1 TTGACTTCAAAATAGGAAAAATGAGATGAATTAATAATGCTTTATCGATCCAGCTGTA 60
 QY 61 TCGAATCAITTCACACAAATGAGATGCTATACACAGATGCTCGTATTGAGGATTTCTTTGTG 120
 DB 61 TCGAATCAITTCACACAAATGAGATGCTATACACAGATGCTCGTATTGAGGATTTCTTTGTG 120
 QY 121 ATAGCCGAGGGGAATATATCAATCCACTTTGTTAGCGCATCAACAGTCCAAACGGGTATT 180
 DB 121 ATAGCCGAGGGGAATATATCAATCCACTTTGTTAGCGCATCAACAGTCCAAACGGGTATT 180
 QY 181 AACATAGCTGGTAGAATACTAGGTGTATTAGGCGTACCGTTTCTGTGACAAATAGCTAGT 240
 DB 181 AACATAGCTGGTAGAATACTAGGTGTATTAGGCGTACCGTTTCTGTGACAAATAGCTAGT 240
 QY 241 TTTTATAGTTTTCTTTGTTGTAATATATGCGCGGAGAGATCAGTGGGAAATTTTC 300
 DB 241 TTTTATAGTTTTCTTTGTTGTAATATATGCGCGGAGAGATCAGTGGGAAATTTTC 300
 QY 301 CTAGAACATGTCGAACAACTTATAAATCAACAAATACAGAAATGCTAGGAATACGGCA 360
 DB 301 CTAGAACATGTCGAACAACTTATAAATCAACAAATACAGAAATGCTAGGAATACGGCA 360
 QY 361 CTTGCTCGATTACAGGTTTAGAGATTCCTTTAGAGCCTATCAACAGTCACTTGAAGAT 420
 DB 361 CTTGCTCGATTACAGGTTTAGAGATTCCTTTAGAGCCTATCAACAGTCACTTGAAGAT 420
 QY 421 TGCGTAGAAACCGTGATGATGCAAGAACAGAGAGTGTCTTTATACCCCAATATATAGCC 480
 DB 421 TGCGTAGAAACCGTGATGATGCAAGAACAGAGAGTGTCTTTATACCCCAATATATAGCC 480
 QY 481 TTAGAACTTGATTTTCTTAATGCGATCGCGCTTTTCGCAATTAGAAACCAAGAGTTTCCA 540
 DB 481 TTAGAACTTGATTTTCTTAATGCGATCGCGCTTTTCGCAATTAGAAACCAAGAGTTTCCA 540
 QY 541 TTATTAAATGATATGCTCAAGCTGCAAAATTTTACACCTATTATTATTTAGAGATGCTCT 600

541 TTATTAAATGATATGCTCAAGCTGCAAAATTTTACACCTATTATTATTATGAGAGATGCTCT 600
 601 CTTTTTGGTAGTGAAATTTGGGCTTTACATCGCAGAAATTTCAAGCTTATTATGAGCGCAA 660
 601 CTTTTTGGTAGTGAAATTTGGGCTTTACATCGCAGAAATTTCAAGCTTATTATGAGCGCAA 660
 661 GTGGAAACAAACGAGAGATTTATCCGACTATTGCGTAGAATGTTATATACAGGCTTAAAT 720
 661 GTGGAAACAAACGAGAGATTTATCCGACTATTGCGTAGAATGTTATATACAGGCTTAAAT 720
 721 AGCTTGAGAGGACAAATGCGCAAGTTGGTGGCTGTTATAATCAATTCGTCAGATCTA 780
 721 AGCTTGAGAGGACAAATGCGCAAGTTGGTGGCTGTTATAATCAATTCGTCAGATCTA 780
 781 ACCTTAGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGACACTGCACTTATCCA 840
 781 ACCTTAGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGACACTGCACTTATCCA 840
 841 ATAAATACGAGTCTCAGTTAAACAGGGAAGTTTATACAGACCAATTTGAGCAACAGGG 900
 841 ATAAATACGAGTCTCAGTTAAACAGGGAAGTTTATACAGACCAATTTGAGCAACAGGG 900
 901 GTRAAATGCAAGTATGAATTTGGTATATATTAATATGCACTTCGTTTCCGCTATAGAG 960
 901 GTRAAATGCAAGTATGAATTTGGTATATATTAATATGCACTTCGTTTCCGCTATAGAG 960
 961 ACTGCGGTTATCGAAGCCGCACTTACTTTGATTTTCTAGAACAACTTACAAATTTTATG 1020
 961 ACTGCGGTTATCGAAGCCGCACTTACTTTGATTTTCTAGAACAACTTACAAATTTTATG 1020
 1021 ACTTCACTACGATGGAGTCTACTAGGCATATAGCTTACTTGGCGGGGACACAAATCAA 1080
 1021 ACTTCACTACGATGGAGTCTACTAGGCATATAGCTTACTTGGCGGGGACACAAATCAA 1080
 1081 TCTCGGCCAATAGGAGCGGATTAATATCTCAACGCATGGGCTTACCAATCTTCTATT 1140
 1081 TCTCGGCCAATAGGAGCGGATTAATATCTCAACGCATGGGCTTACCAATCTTCTATT 1140
 1141 AATCCTGTGAAGTATTATCTCTCGAGACGTATATTGGACTGAATCATATGACAGGA 1200
 1141 AATCCTGTGAAGTATTATCTCTCGAGACGTATATTGGACTGAATCATATGACAGGA 1200
 1201 GTGCTTCTATGCGGAATTTACCTTGAACTTATTCATGTTGTCCTTCTGTTAGATTAAT 1260
 1201 GTGCTTCTATGCGGAATTTACCTTGAACTTATTCATGTTGTCCTTCTGTTAGATTAAT 1260
 1261 TTTAGAACCCCTCAGAACTATTTTGAAGAGTCTGCTAACTATATAGTCAACCTATGAG 1320
 1261 TTTAGAACCCCTCAGAACTATTTTGAAGAGGTTACTGCTAACTATATAGTCAACCTATGAG 1320
 1321 TCACCTGGGCTTCAATTTAAAGATTCAGAAATTCAGAAATTCACCAAGAAACAAACAGAACGA 1380
 1321 TCACCTGGGCTTCAATTTAAAGATTCAGAAATTCAGAAATTCACCAAGAAACAAACAGAACGA 1380
 1381 CCAAAATTAATGATCATATAGTCAATAGGTTATCTCATAGGGCTCATTTTCAAACTTAGG 1440
 1381 CCAAAATTAATGATCATATAGTCAATAGGTTATCTCATAGGGCTCATTTTCAAACTTAGG 1440
 1441 GTGCATGTACCAAGTATTTCTTGGACGCGCGTAGTGCAGATCGTACAAATACCATTAGT 1500
 1441 GTGCATGTACCAAGTATTTCTTGGACGCGCGTAGTGCAGATCGTACAAATACCATTAGT 1500
 1501 TCAGATAGCAATAACAAATACCATTTGGTAAATCAATTTCAACCTTAAATTCAGGTACCTCT 1560
 1501 TCAGATAGCAATAACAAATACCATTTGGTAAATCAATTTCAACCTTAAATTCAGGTACCTCT 1560
 1561 GTAGTCAGTGGGCCAGGATTTTACAGAGGGGATTAATTCGGAACCTAACGTTAATGTAGT 1620
 1561 GTAGTCAGTGGGCCAGGATTTTACAGAGGGGATTAATTCGGAACCTAACGTTAATGTAGT 1620
 1621 GTACTAAGTATGGTCTTAAATTTTAAATATACATCATCTATTACAGCGGTATCCGCTGAGATT 1680
 1621 GTACTAAGTATGGTCTTAAATTTTAAATATACATCATCTATTACAGCGGTATCCGCTGAGATT 1680

1681 CGTTATGCTGCTCTCTAAACAATGCTGCTGAGGGTAACCTGTCGAGGGAGTACTACTTTT 1740
 1681 CGTTATGCTGCTCTCTAAACAATGCTGCTGAGGGTAACCTGTCGAGGGAGTACTACTTTT 1740
 1741 GATCAAGGATTCCTCTAGTACTATGAGTGCAAAATGAGTCTTTGACATCTCAATCATTTAGA 1800
 1741 GATCAAGGATTCCTCTAGTACTATGAGTGCAAAATGAGTCTTTGACATCTCAATCATTTAGA 1800
 1801 TTTGCGAAGATTCCTCTGAGTATTTAGTGCAATCTGGCAGTCAAACTGCTGGAATAAGTATA 1860
 1801 TTTGCGAAGATTCCTCTGAGTATTTAGTGCAATCTGGCAGTCAAACTGCTGGAATAAGTATA 1860
 1861 AGTAATAATCGAGGTAGACAAAGCTTTTCACTTTGATAAAATTTGAAATTCATTTCAATTTACT 1920
 1861 AGTAATAATCGAGGTAGACAAAGCTTTTCACTTTGATAAAATTTGAAATTCATTTCAATTTACT 1920
 1921 GCAACCTTCGAAGCAGAAATGAGATTTAGAAAGGCGCAAGAGCGGTGAGTCTCTGTTT 1980
 1921 GCAACCTTCGAAGCAGAAATGAGATTTAGAAAGGCGCAAGAGCGGTGAGTCTCTGTTT 1980
 1981 ACTAATACGAATCCAAAGAGATTTGAAACACAGATGTGACAGATTTATCATATTGATCAAGTA 2040
 1981 ACTAATACGAATCCAAAGAGATTTGAAACACAGATGTGACAGATTTATCATATTGATCAAGTA 2040
 2041 TCCAAATTTAGTGGCTGTTTATCGGATGAAATCTGCTTTAGATGAAAGAGAGAAATTTACTT 2100
 2041 TCCAAATTTAGTGGCTGTTTATCGGATGAAATCTGCTTTAGATGAAAGAGAGAAATTTACTT 2100
 2101 GAGAAAGTGAATATGCGAAACGACTCAGTGATGAAAGAACTTACTCCAAAGATCCAAAC 2160
 2101 GAGAAAGTGAATATGCGAAACGACTCAGTGATGAAAGAACTTACTCCAAAGATCCAAAC 2160
 2161 TTCACATCCATCAATGAACACAGACTTTCATATCTACTAATGAGCAATCGAATTTTCA 2220
 2161 TTCACATCCATCAATGAACACAGACTTTCATATCTACTAATGAGCAATCGAATTTTCA 2220
 2221 TCTATCCATGAA CAATCTGAAACATGAGTGTGGGAAAGTGAACATTTCAATCCAGGAA 2280
 2221 TCTATCCATGAA CAATCTGAAACATGAGTGTGGGAAAGTGAACATTTCAATCCAGGAA 2280
 2281 GGAATGACGTATTTAAAGAGATTAAGTCACTACCGGGACTTTTAAATGAGTGTAT 2340
 2281 GGAATGACGTATTTAAAGAGATTAAGTCACTACCGGGACTTTTAAATGAGTGTAT 2340
 2341 CCGACGTATTTATCAAAAAATAGAGAGTCCGAATTTAAAGCTTATCTCCGTACCAA 2400
 2341 CCGACGTATTTATCAAAAAATAGAGAGTCCGAATTTAAAGCTTATCTCCGTACCAA 2400
 2401 TTAAGAGGTATATTGAAGATAGTCAAGATTTAGAGATATATTGATTCGTTATAATGCG 2460
 2401 TTAAGAGGTATATTGAAGATAGTCAAGATTTAGAGATATATTGATTCGTTATAATGCG 2460
 2461 AAACATGAACATTTGATTTCCAGTACCGAGTCCGATGCGCGCTTTTCAGTTGAAGC 2520
 2461 AAACATGAACATTTGATTTCCAGTACCGAGTCCGATGCGCGCTTTTCAGTTGAAGC 2520
 2521 CCAATCGAAGGTGCGGAGAACCGAATCGGATCGCACCAATTTGAAATGGAATCTCTGAT 2580
 2521 CCAATCGAAGGTGCGGAGAACCGAATCGGATCGCACCAATTTGAAATGGAATCTCTGAT 2580
 2581 CTAGATTTGTTCTCTGACAGATGGAGAAAAATGTGCGCATCATTTCCCATCATTTCTCTTTG 2640
 2581 CTAGATTTGTTCTCTGACAGATGGAGAAAAATGTGCGCATCATTTCCCATCATTTCTCTTTG 2640
 2641 GATATTGATATTGATGACAGACTTAGGAAATCTAGCGGTGCGGTGTTTCAAG 2700
 2641 GATATTGATATTGATGACAGACTTAGGAAATCTAGCGGTGCGGTGTTTCAAG 2700
 2701 ATTAAAGACGAGAGAGTCAAGACTAGGAAATCTGGAATTTATTGAGAGAGAACCA 2760
 2701 ATTAAAGACGAGAGAGTCAAGACTAGGAAATCTGGAATTTATTGAGAGAGAACCA 2760

2761 TTATTAGGAGAGCACTGTCTCGTGAAGAGCAGAGAAAAAATGGAGAGCAACAGT 2820
 2761 TTATTAGGAGAGCACTGTCTCGTGAAGAGCAGAGAAAAAATGGAGAGCAACAGT 2820
 2821 GAAAAACTCAATTTGAAAAAACAACCGAGTATATACAGAGGCAAAAGAGCTGTGGATGCT 2880
 2821 GAAAAACTCAATTTGAAAAAACAACCGAGTATATACAGAGGCAAAAGAGCTGTGGATGCT 2880
 2881 TTATTTGTAGATTTCAATATATAGATTACAAGCGGATACAAACATTTGGCATGATTCAT 2940
 2881 TTATTTGTAGATTTCAATATATAGATTACAAGCGGATACAAACATTTGGCATGATTCAT 2940
 2941 GCGGCGATAACTTGTTCATTCGAATTCGAGAGCTTATCTGTGAGAAATTTCTGTTATC 3000
 2941 GCGGCGATAACTTGTTCATTCGAATTCGAGAGCTTATCTGTGAGAAATTTCTGTTATC 3000
 3001 CCGGGTGTAAATCGCGAAATTTTGAAGAAATTAAGAGGTGCGATTTACCTGCAATCTCC 3060
 3001 CCGGGTGTAAATCGCGAAATTTTGAAGAAATTAAGAGGTGCGATTTACCTGCAATCTCC 3060
 3061 CTATACGATCGGAGAAATGTCGTTAAATAATGGTGAATTTAAATGAGATTAGCATGCTG 3120
 3061 CTATACGATCGGAGAAATGTCGTTAAATAATGGTGAATTTAAATGAGATTAGCATGCTG 3120
 3121 AATGTAAGAGGCGATGTAGATGTACAAAGAGCCATCACCGTTCTGCTTGTATCCCA 3180
 3121 AATGTAAGAGGCGATGTAGATGTACAAAGAGCCATCACCGTTCTGCTTGTATCCCA 3180
 3181 GAATGGAGAGCAAGTGTGCAAGCAGTTCGCGTCTGTCGCGGGCGTGCTATATCTC 3240
 3181 GAATGGAGAGCAAGTGTGCAAGCAGTTCGCGTCTGTCGCGGGCGTGCTATATCTC 3240
 3241 CGTGTCAACGCGTACAAAGAGGGATATGGAGGGTGTGTAAACGATCCATGAAATCGAG 3300
 3241 CGTGTCAACGCGTACAAAGAGGGATATGGAGGGTGTGTAAACGATCCATGAAATCGAG 3300
 3301 AACAAATACAGAGCAACTAAAATTTTAAAACTGTGAAAGAGAGGAGTGTATCCAAAGGAT 3360
 3301 AACAAATACAGAGCAACTAAAATTTTAAAACTGTGAAAGAGAGGAGTGTATCCAAAGGAT 3360
 3361 ACAGGAGCGTGTAAATGATTTACTGCACCAAGGTACAGCAGTATGTAATTTCCCGTAAT 3420
 3361 ACAGGAGCGTGTAAATGATTTACTGCACCAAGGTACAGCAGCAGTGTAAATTTCCCGTAAT 3420
 3421 GCTGGATATGAGGATGCATATGAAGTTGATACACAGCATCTGTTAATTAACAAACCGACT 3480
 3421 GCTGGATATGAGGATGCATATGAAGTTGATACACAGCATCTGTTAATTAACAAACCGACT 3480
 3481 TATGAAGAGAAACGATATACAGATGTACGAGAGATAATCATTTGTGATATGACAGAGG 3540
 3481 TATGAAGAGAAACGATATACAGATGTACGAGAGATAATCATTTGTGATATGACAGAGG 3540
 3541 TATGCAATTTATCCACACTTACCAGCTGTTATATGACAAAGAAATTTAGAAATTTCTCCCA 3600
 3541 TATGCAATTTATCCACACTTACCAGCTGTTATATGACAAAGAAATTTAGAAATTTCTCCCA 3600
 3601 GAAACCGATAAGGTATGAGTTGAGATTGGAGAAACCGAAGGAGGAGTTTATTGTAGACAGC 3660
 3601 GAAACCGATAAGGTATGAGTTGAGATTGGAGAAACCGAAGGAGGAGTTTATTGTAGACAGC 3660
 3661 GTGGAATTTACTCTTCTTATGGGGAATAG 3687
 3661 ATAGAATTTACTCTTCTTATGGGGAATAG 3687

RESULT 3
 AAV15222
 ID AAV15222 standard; DNA; 3684 BP.
 XX
 AC AAV15222;
 XX
 DT 27-MAY-1998 (first entry)
 XX

DE Bacillus thuringiensis 158C2c toxin encoding DNA.
 KW Bacillus thuringiensis; 158C2c; toxin; lepidopteran-active; insect;
 KW microbe; transgenic plant; resistant; ss.
 XX Bacillus thuringiensis.
 OS
 FH Key Location/Qualifiers
 FT CDS 1..3684
 FT /*tag= a
 FT /product= "158C2c toxin"
 XX
 XX US5723758-A.
 XX
 XX 03-MAR-1998.
 XX
 XX 23-MAY-1995; 95US-00448170.
 XX
 XX 13-SEP-1991; 91US-00759247.
 PR 01-JUN-1993; 93US-00069902.
 XX
 XX (MYCO) MYCOGEN CORP.
 XX
 XX Steelman S, Narva KE, Cummings DA, Payne J, Cannon RJ;
 PI WPI; 1998-178600/16.
 DR P-PSDB; AAW44321.
 XX
 XX DNA encoding Bacillus thuringiensis toxin proteins - for producing
 FT transgenic plants resistant to attack by lepidopteran pests.
 XX
 XX Claim 7; Col 29-34; 25pp; English.
 XX
 XX The present sequence encodes a 158C2c toxin from Bacillus thuringiensis.
 CC The present invention describes isolated nucleic acid sequences encoding
 CC toxins active against lepidopteran insects. The present invention also
 CC describes a recombinant host transformed with a nucleic acid sequence
 CC encoding a toxin. The nucleic acid sequence can be amplified. The product
 CC is used for producing transgenic plants resistant to attack by
 CC lepidopteran pests. N.B. The numbers in the sequence listing do not
 CC correspond to the SEQ ID NO: s mentioned in the specification e.g. in the
 CC specific listing SEQ ID NO:3, 4, 5 and 6 are said to correspond to the
 CC nucleic acid sequences encoding the toxins, and SEQ ID NO:7, 8, 9 and 10
 CC are said to correspond to the amino acid sequences of the toxins, whereas
 CC in the sequence listing the amino acid sequence is given after the
 CC nucleic acid sequence encoding it (i.e. SEQ ID NO:3 encodes SEQ ID NO:4)
 XX
 XX Sequence 3684 BP; 1232 A; 628 C; 803 G; 1021 T; 0 U; 0 Other;
 SQ
 Query Match 88.6%; Score 3266.6; DB 2; Length 3684;
 Best Local Similarity 93.4%; Pred. No. 0;
 Matches 3449; Conservative 0; Mismatches 229; Indels 15; Gaps 3;
 QY 1 TTGACTTCAATAGGAAATGAGATGAAATATATAATGCTTTATCGATTCAGCTGTA 60
 DB 1 TTGACTTCAATAGGAAATGAGATGAAATATATAATGCTTTATCGATTCAGCTGTA 60
 QY 61 TCGAATCATTCACACAAATGGATCTATCACAGATGCTGATTCAGGATTCCTTGTGT 120
 DB 61 TCGAATCATTCACCAATGAATCATCAACGATGCTGATTCAGGATGATCTTGTGT 120
 QY 121 ATAGCCGAGGGGAATATATCAATCCACTTTGTAGGCGCATCAACAGTCCAAACGGGTATT 180
 DB 121 ATAGCCGAGGGGAACAAATATCGATCCATTTGTAGGCGCATCAACAGTCCAAACGGGTATT 180
 QY 181 AACATAGCTGGTGAATATCTAGTGTATTTAGGCGTACCGTTTCTGCTGGAACAAATAGTAGT 240
 DB 181 AACATAGCTGGTGAATATCTAGTGTATTTAGGCGTACCGTTTCTGCTGGAACAAATAGTAGT 240
 QY 241 TTTTATAGTTTCTTCTGTGTGAATATGCCCCGGCGGAGATCAGTGGGAAATTTTC 300
 DB 241 TTTTATAGTTTCTTCTGTGTGAATATGCCCCGGCGGAGATCCTTGGGAAATTTTC 300

301 CTAGAACATGTGCAACAACTTATAAATCAACAAATACAGAAAATGCTAGGAATACGGCA 360
 DB |||||
 301 CTAGAACATGTGCAACAACTTATAAAGCAACAAAGTAAACAGAAAATAGTAGGATACGGCT 360
 DB |||||
 361 CTTGCTCGAATTACAGGTTTGGGAAATTCCTTTAGAGCCTATCAACAGTCACTTTGAAGAT 420
 QY |||||
 361 CTTGCTCGAATTACAGGTTTGGGAAATTCCTTTAGAGCCTATCAACAGTCACTTTGAAGAT 420
 DB |||||
 421 TGGCTAGAAAACCGTGATGATCAAGAACGAGAAGTGTCTTTTATACCAATATATAGCC 480
 QY |||||
 421 TGGCTAGAAAACCGTGATGATCAAGAACGAGAAGTGTCTTTTATACCAATATATAGCC 480
 DB |||||
 481 TTAGAACTTGAATTTCTTAATGCGATGCGGCTTTTCGCAATTAGAAAACCAAGATTCCA 540
 QY |||||
 481 TTAGAACTTGAATTTCTTAATGCGATGCGGCTTTTCGCAATTAGAAAACCAAGATTCCA 540
 DB |||||
 541 TTATTAATGGTATATGCTCAAGTGCAGAAATTTACACCTATTATTATGAGAGATGCTCT 600
 QY |||||
 541 TTATTAATGGTATATGCTCAAGTGCAGAAATTTACACCTATTATTATGAGAGATGCTCT 600
 DB |||||
 601 CTTTTTGGTAGTGAATTTGGGCTTACATCGCAGGAAATTCAGGTTTATTATGAGCGCCAA 660
 QY |||||
 601 CTTTTTGGTAGTGAATTTGGGCTTACATCGCAGGAAATTCAGGTTTATTATGAGCGCCAA 660
 DB |||||
 661 GTGGAACAAACGAGAGATTTATCCGACTATTGCGTAGAATGGTATTAATACAGGCTTAAAT 720
 QY |||||
 661 GTGGAACAAACGAGAGATTTATCCGACTATTGCGTAGAATGGTATTAATACAGGCTTAAAT 720
 DB |||||
 721 AGCTTGAGAGGACAAATGCGCAAGTGGGTCGTTTAAATCAATTCGCTGAGATCTA 780
 QY |||||
 721 AATTTGAGAGGACAAATGCTGAAAGTGGTTCGATATAATCAATTCGCTGAGACTTA 780
 DB |||||
 781 AGCTTGAGGATTAAGATCTAGTGGCACTATTTCCCAAGCTATGACACTCGACTTATCCA 840
 QY |||||
 781 AGCTTGAGGATTAAGATCTAGTGGCACTATTTCCCAAGCTATGACACTCGGCTTTATCCA 840
 DB |||||
 841 ATAAATACGAGTCTCAGTTTAAACAGGGAATTTATACAGACGCAATTTGGAGCAACAGGG 900
 QY |||||
 841 ATGAATACCAGTCTCAATTTAAACAGAGAAATTTATACAGATCCCAATTTGGAGCAACAAAT 900
 DB |||||
 901 GTAAAT-----ATGCAAGTATGAATGGTATATAATAATGACACTTCGTTTCGGCT 954
 QY |||||
 901 GCACCTTCAGGATTTGCAAGTACGAATGGTATTAATAATGACACTTCGTTTCGGCT 960
 DB |||||
 955 ATAGAGACTGCGGTATCGAAGCCGCACTACTTTGATTTCTAGAAACAACTTCAAAAT 1014
 QY |||||
 961 ATAGAGGCTGCGGTATTTAGGCTCCGCACTACTTTGATTTCCAGAACAGCTTCAAT 1020
 DB |||||
 1015 TTAGCACTTCATCAGATGGAGTGTCTACTAGGCATATCACTTACTTGGCGGGGACACACA 1074
 QY |||||
 1021 TTGAGCGTATTAAAGTCGATGGAGTAACTCAATATATGAATTTACTGGGTGGGACATAGA 1080
 DB |||||
 1075 ATTCAATCTCGGCAATAGAGCGGATTAATACTCTCAACGATGGGTCTACCATACT 1134
 QY |||||
 1081 CTTGAATCCGAAACAAATAGGGGGTCAATTAAGTACCTCCGACACACGGAATACCAATACT 1140
 DB |||||
 1135 TCTATTAACTCTGTGAAGATTATCACTTCTCTCGAGACGTATATTGGACTGAATCATAT 1194
 QY |||||
 1141 TCTATTAACTCTGTGAAGATTATCACTTCTCTCGAGACGTATATTGGACTGAATCATAT 1200
 DB |||||
 1195 GCAGGAGTCTTCTATGGGAAATTTACCTTGAACCTTATTCTATGGTGTCCCTACTGTAGA 1254
 QY |||||
 1201 GCAGGATATAAT-----ACTTCTAACTACTCTCTGTAATGGAGTACTCTTGGGCTAGA 1254
 DB |||||
 1255 TTTAATTTAGAACCTTCAGAACTACTTTTGAAGAGGTACTGCTTAACCTATATAGTCAACC 1314
 QY |||||
 1255 TTTAATTTAGAGAAATCCCTGAAATTTCTTT---AGAGGTAGGCTTCTCTATATCTATAGGG 1311
 DB |||||
 1315 TATGAGTCACTTGGGCTTCAATTTAAAGATTCAGAAATTCAGAAATTCAGCAACAGAAACAA 1374
 QY |||||
 1312 TATAGTGGAGTGGGACACAACTATTTGATTCAGAACTGAATTTACACAGAAACAAACA 1371
 DB |||||
 1375 GAACGACCAAAATATGAATCATATAGTCAATAGGTTATTCACATAGGGGCTCATTTCCAAA 1434
 QY |||||

1372 GAACGACCAATATATGATCTTACAGTCNTAGATTATCTAATATAGACTAATATCAGGA 1431
1435 TCTAGGGTGCAATGACAGTATATCTTGGACGACCCGCTAGTCAGATCGTACAAATPACC 1494
1432 AACACTTTGAGAGCACCAGTATATCTTGGACGACCCGCTAGTCAGATCGTACAAATPACC 1491
1495 ATTAGTTTCAGATAGCAATAACCAATACCATTTGTAAATCATTTCAACCTTAATTCAGGT 1554
1492 ATTAGTTTCAGATAGCAATAACCAATACCATTTGTAAATCATTTCAACCTTAATTCAGGT 1551
1555 ACCTCTGTAGTCAGTGGCCACGAGATTATACAGGAGGGGATATAATCCGAACTAAAGCTTAAT 1614
1552 ACCTCTGTAGTCAGTGGCCACGAGATTATACAGGAGGGGATATAATCCGAACTAAAGCTTAAT 1611
1615 GGTAGTGTACTAAGTATGGGTCTTAAATTTTAAATAATACATCATTTACAGCGGTATCGCGTG 1674
1612 GGTAGTGTACTAAGTATGGGTCTTAAATTTTAAATAATACATCATTTACAGCGGTATCGCGTG 1671
1675 AGAGTTTCGTTATGCTGCTTCTCAAAACAATGGTCTGAGGGTAACTGCGGAGGGAGTACT 1734
1672 AGAGTTTCGTTATGCTGCTTCTCAAAACAATGGTCTGAGGGTAACTGCGGAGGGAGTACT 1731
1735 ACTTTTCATCAAGGATTCCTCTAGTACTATGAGTGCATAATGAGTCTTTTGACATCTCAATCA 1794
1732 ACTTTTCATCAAGGATTCCTCTAGTACTATGAGTGCATAATGAGTCTTTTGACATCTCAATCA 1791
1795 TTTAGATTTTCAGAAATTCCTGTAGGTATTTAGTGCATCTGGCAGTCAAACTGCTGGAATA 1854
1792 TTTAGATTTTCAGAAATTCCTGTAGGTATTTAGTGCATCTGGCAGTCAAACTGCTGGAATA 1851
1855 AGTATAAGTAAATATGCAAGTACGAAACGTTTTCATTTGATAAATGAAATTCATTTCCA 1914
1852 AGTATAAGTAAATATGCAAGTACGAAACGTTTTCATTTGATAAATGAAATTCATTTCCA 1911
1915 ATTACTGCAACCTTCGAAGCAGATACGATTTAGAAAGGCGCAAGAGGCGGTGAATGCT 1974
1912 ATTACTGCAACCTTCGAAGCAGATACGATTTAGAAAGGCGCAAGAGGCGGTGAATGCT 1971
1975 CTGTCTTACTAATACGAATCCAAAGAAATTTGAAACAGATGTGACAGATTATCATATTGAT 2034
1972 CTGTCTTACTAATACGAATCCAAAGAGGTTGAAACAGGTCGTGACAGATTATCATATTGAT 2031
2035 CAAGTATCCAAATTTAGTGGCGTGTATTCGGATGAATCTTCTGATGAATGAAAGAGAGAA 2094
2032 GAAAGTATCCAAATTTAGTGGCGTGTATTCGGATGAATCTTCTGATGAAAGAGAGAA 2091
2095 TTACTTTGAGAAAGTGAATATGCAACGACTCAGTGATGAAAGAACTTACTTCCAGAT 2154
2092 TTACTTTGAGAAAGTGAATATGCAACGACTCAGTGATGAAAGAACTTACTTCCAGAT 2151
2155 CCAAACTTCACATCCATCAATAGCAACCAAGACTTTCATATCTACTAATGAGCAATCGAAT 2214
2152 CCAAACTTCACATCCATCAATAGCAACCAAGACTTTCATATCTACTAATGAGCAATCGAAT 2211
2215 TTCACATCTATCCATGAACCAATCTGAACATGGATGGTGGGAAAGTGAAGAACTTCAATC 2274
2212 TTCACATCTATCCATGAACCAATCTGAACATGGATGGTGGGAAAGTGAAGAACTTCAATC 2271
2275 CAGGAGGAATGACGTTATTTAAGAGAAATTCGTACACTACCGGGGACTTTTAAATGAG 2334
2272 CAGGAGGAATGACGTTATTTAAGAGAAATTCGTACACTACCGGGGACTTTTAAATGAG 2331
2335 TGTATTCGACGTTATTTATCAAAATAAGGAGGTCGGAATTTAAAGCTTATATCTCCG 2394
2332 TGTATTCGACGTTATTTATCAAAATAAGGAGGTCGGAATTTAAAGCTTATATCTCCG 2391
2395 TACCAATTAAGAGGGTATATTGAAGTAGTCAAGATTTAGAGATATATTTGATTCGTTAT 2454
2392 TACCAATTAAGTGGCTATATTGAAGTAGTCAAGATTTAGAGATATATTTGATTCGTTAT 2451
2455 AATCGGAAACATGAACATTTGGATGTTTCCAGGTACCGAGTCCGATGCGCGCTTTTCAGTT 2514

2452 AATCGGAAACATGAACATTTGGATGTTTCCAGGTACCGAGTCCGATATGCGCGCTTTTCAGTT 2511
2515 GAAAGCCCAATTCGGAAGGTGCGAGAACCGAATCGATCGCACCAACATTTTGAATGGAAT 2574
2512 GAAAGCCCAATTCGGAAGGTGCGAGAACCGAATCGATCGCACCAACATTTTGAATGGAAT 2571
2575 CCTGATCTAGATTTCTTCGACAGATGGAGAAATTTGGGCATCATTTCCCATCATTTTC 2634
2572 CCTGATCTAGATTTCTTCGACAGATGGAGAAATTTGGGCATCATTTCCCATCATTTTC 2631
2635 TCTTTGGATATTCATATTTGGATGCACAGACTTCGATGAGAAATCTAGGCGTGTGGTGGTA 2694
2632 TCTTTGGATATTCATTTGGATGCATAGACTTCGATGAGAACTTAGGCGTGTGGTGGTA 2691
2695 TTCAAGATTAAAGACGACGAGGAGTCTATGCAAGACTAGGGAATCTGGAAATTTATTTGAAGAG 2754
2692 TTCAAGATTAAAGACGACGAGGAGTCTATGCAAGACTAGGGAATCTGGAAATTTATTTGAAGAG 2751
2755 AAACCATTTATTAGGAGAGCACTGCTCTGTTGAAAGAGACAGAGAAATTTGGAGAGAC 2814
2752 AAACCATTTATTAGGAGAGCACTGCTCTGTTGAAAGAGACAGAGAAATTTGGAGAGAC 2811
2815 AAACGTGAAATACTCAATTTGGAAACAAACAGAGTATATACAGAGGCAAAAGAGCTGTG 2874
2812 AAACGTGAAATACTCAATTTGGAAACAAACAGAGTATATACAGAGGCAAAAGAGCTGTG 2871
2875 GATGCTTTATTTGTAGATTTCTCAATATATATAGATTACAAGCGGATACAAACATTTGGCATG 2934
2872 GATGCTTTATTTGTAGATTTCTCAATATATAGATTACAAGCGGATACAAACATTTGGCATG 2931
2935 ATTTCATGCGGACAGATAAATCTTGTTCATGCAATTTGAGAGGCTTATCTGTGAGAAATTTATCT 2994
2932 ATTTCATGCGGACAGATAAATCTTGTTCATGCAATTTGAGAGGCTTATCTTTTCAGAAATTTATCT 2991
2995 GTTATCCCGGTGTAATGCGGAAATTTTGAAGAAATTTGAAGGTCGCAATTTACCTGCA 3054
2992 GTTATCCCGGTGTAATGCGGAAATTTTGAAGAAATTTGAAGGTCGCAATTTACCTGCA 3051
3055 ATCTCCCTATACGATCGGAGAAATGTCTGTTAAATAATGGTGAATTTAATAATGGAATTAGCA 3114
3052 ATCTCCCTATACGATCGGAGAAATGTCTGTTAAATAATGGTGAATTTAATAATGGAATTAGCA 3111
3115 TGCTGGAATTTAAAGCGGATAGATGTATACACAGAGCCATCACCGTTCGTCTCTGTTGTT 3174
3112 TGCTGGAATTTAAAGCGGATAGATGTATACACAGAGCCATCACCGTTCGTCTCTGTTGTT 3171
3175 ATCCAGAAATGGAAGCAGAGGTGTCACAGAGGTTCCGCTCTGTCGCGGCGGTGGCTAT 3234
3172 ATCCAGAAATGGAAGCAGAGGTGTCACAGAGGTTCCGCTCTGTCGCGGCGGTGGCTAT 3231
3235 ATCTCCCGTGTCAACGCGTACAAAGAGGGATATGAGAGGGTGTGTAAACGATCCCATGAA 3294
3232 ATCTCCCGTGTCAACGCGTACAAAGAGGGATATGAGAGGGTGTGTAAACGATCCCATGAA 3291
3295 ATCGAGAACATATACAGACGAACTAAATTTAAACCTGTGAAGAGAGGAGTGTATCCA 3354
3292 ATCGAGAACATATACAGACGAACTAAATTTAAACCTGTGAAGAGAGGAGTGTATCCA 3351
3355 ACGGATACAGGAGCGTGAATGATTTATCTGCAACCAAGGTACAGCGATCTGTAATTTCC 3414
3352 ACGGATACAGGAGCGTGAATGATTTATCTGCAACCAAGGTACAGCGATCTGTAATTTCC 3411
3415 CGTAATGCTGGATATGAGGATGATATGAATTTGATCTACAGCATCTGTTAATTTACAAA 3474
3412 CGTAATGCTGGATATGAGGATGATATGAATTTGATCTACAGCATCTGTTAATTTACAAA 3471
3475 CCGACTTTATGAAGAGAAACGATATACAGATGATGAAGAGATTAATCATTTGTGAATATGAC 3534
3472 CCGACTTTATGAAGAGAAACGATATACAGATGATGAAGAGATTAATCATTTGTGAATATGAC 3531
3535 AGAGGGTATGTGAATTTATCCACCACTACAGCTGGTTTATGACAAAGAAATTTAGAAATAC 3594
3532 AGAGGGTATGTGAATTTATCCACCACTACAGCTGGTTTATGACAAAGAAATTTAGAAATAC 3591

Db 1141 TCTATTAACTCTGTAAACATTACAGTTTCACATCTCGAGACGTTTATAGAAACAGATCAATTT 1200
Qy 1195 GCAGGAGTGTCTTATGGGAAATTTACCTTGAACCTATTATCATGTGTCCCTACTGTGTAGA 1254
Db 1201 GCAGGATAAATAT-----ACTTCTAACTACTCTGTGAATGAGTACCTTGGGCTAGA 1254
Qy 1255 TTTTAAATTTAGGACCTCCAGATACATTTTGAAGAGGTACTGTAACTATAGTCAACCC 1314
Db 1255 TTTTAAATTTGGAGAAATCCCTCGAATTCCTCTT---AGAGGTAGCCTTCTCTATCTATAGG 1311
Qy 1315 TATGAGTCACCTGGGCTTCAATTAAGATTCAGAACTGAAATACCAACAGGAAACAA 1374
Db 1312 TATACTGGAGTGGGACACAACTATTTGATTCAGAACTGAAATACCAACAGGAAACAA 1371
Qy 1375 GAACGACCAAAATTAATGAATCATATAGTATAGTGTATCTCACATAGGGCTCATTTCAAA 1434
Db 1372 GAACGACCAAAATTAATGAATCTTACAGTCATAGATTTATCTAATAAGACTAATATCAG 1431
Qy 1435 TCTAGGCTGCATGTACAGTATATTTCTTGACGCGCACCGTAGTCAGATCGTACAAATACC 1494
Db 1432 AACACTTTGAGAGCACCATGATATTTCTTGACGCGCACCGTAGTCAGATCGTACAAATACC 1491
Qy 1495 ATTAGTTTCAGATACATAACCAAAATACCATTTGGTAAATCATTTCAACCTTTAATTCAGGT 1554
Db 1492 ATTAGTTTCAGATACATAACCAAAATACCATTTGGTAAATCATTTCAACCTTTAATTCAGGT 1551
Qy 1555 ACCTCTGTAGTCAGTGGCCCGCAGGATTTACAGGAGGGGATATAATCCGAACTTAACGTTAAT 1614
Db 1552 ACCTCTGTAGTCAGTGGCCCGCAGGATTTACAGGAGGGGATATAATCCGAACTTAACGTTAAT 1611
Qy 1615 GGTAGTGTACTAGTATGGGTCTTAATTTTAAATTAATACATCATTTACAGCGGTATCGCGTG 1674
Db 1612 GGTAGTGTACTAGTATGGGTCTTAATTTTAAATTAATACATCATTTACAGCGGTATCGCGTG 1671
Qy 1675 AGAGTTCGTATGCTGCTCTCAACCAATGCTCTGAGGGTAACTGTCGGAGGGAGTACT 1734
Db 1672 AGAGTTCGTATGCTGCTCTCAACCAATGCTCTGAGGGTAACTGTCGGAGGGAGTACT 1731
Qy 1735 ACTTTTGATCAAGGATTCCTTAGTACTATGAGTCAAAATGAGTCTTTGACATCTCAATCA 1794
Db 1732 ACTTTTGATCAAGGATTCCTTAGTACTATGAGTCAAAATGAGTCTTTGACATCTCAATCA 1791
Qy 1795 TTTAGATTTGCAGAAATTCCTGTAGGTATAGTGCATCTGCGAGTCAAACTGCTGGAATA 1854
Db 1792 TTTAGATTTGCAGAAATTCCTGTAGGTATAGTGCATCTGCGAGTCAAACTGCTGGAATA 1851
Qy 1855 AGTATAAGTAAATAGCAGGTAGCAAACTGTTTCACTTTGATAAATTTGAATTCATTTCCA 1914
Db 1852 AGTATAAGTAAATAGCAGGTAGCAAACTGTTTCACTTTGATAAATTTGAATTCATTTCCA 1911
Qy 1915 ATTACTGCAACCTTCGAAGCAGAAATACGATTTAGAAAGGGCGCAAGAGCGGTGAATGCT 1974
Db 1912 ATTACTGCAACCTTCGAAGCAGAAATAGATTTAGAAAGGGCGCAAGAGCGGTGAATGCT 1971
Qy 1975 CTGTTTACTAATACGAATCCAAAGAAATTTGAAACAGATGTGACAGATTTATCATATTGAT 2034
Db 1972 CTGTTTACTAATACGAATCCAAAGAAATTTGAAACAGATGTGACAGATTTATCATATTGAT 2031
Qy 2035 CAAGTATCCAAATTTAGTGGGCTGTTTATCGGATGAATTCGCTTAGATGAAGAGAGAA 2094
Db 2032 GAAGTATCCAAATTTAGTGGGCTGTTTATCGGATGAATTTCTGTTGGATGAAGAGAGAA 2091
Qy 2095 TTACTTCGAGAAAGTGAATATGCGAAACGACTCAGTGTATGAAGAAACTTTACTCCAAGAT 2154
Db 2092 TTACTTCGAGAAAGTGAATATGCGAAACGACTCAGTGTATGAAGAAACTTTACTCCAAGAT 2151
Qy 2155 CCAAACTTCACATCCATCAATTAAGCAACACAGACTTCATATCTACTAATAGCAATCGAAT 2214
Db 2152 CCAAACTTCACATCCATCAATTAAGCAACACAGACTTCATATCTACTAATAGCAATCGAAT 2211
Qy 2215 TTCACTATTCATTAAGCAATCTGAACATGGATGGTGGGAGTGGAGAACATTACAAATC 2274
Db 2212 TTCACTATTCATTAAGCAATCTGAACATGGATGGTGGGAGTGGAGAACATTACAAATC 2271

Qy 2275 CAGGAAGGAATGACGTTATTTAAAGAGAAATTCGTCACTACCGGGGACTTTTAAATGAG 2334
Db 2272 CAGGAAGGAATGACGTTATTTAAAGAGAAATTCGTCACTACCGGGGACTTTTAAATGAG 2331
Qy 2335 TGTATTCCGACGTTATTTATCAAAATAAGGAGAGTCGGAAATTTAAAGGCTTTATCTCGC 2394
Db 2332 TGTATTCCGACGTTATTTATCAAAATAAGGAGAGTCGGAAATTTAAAGGCTTTATCTCGC 2391
Qy 2395 TACCAATTAAGAGGGTATATTGAAGATAGTCAAGATTTAGAGATATATTGATTCGTTAT 2454
Db 2392 TACCAATTAAGTGCCTATATTGAAGATAGTCAAGATTTAGAGATATATTGATTCGTTAT 2451
Qy 2455 AATCGGAAACATGAACATTTGGATGTTCCAGGTACCGAGTCCGATGCGCGCTTTCAAGTT 2514
Db 2452 AATCGGAAACATGAACATTTGGATGTTCCAGGTACCGAGTCCGATGCGCGCTTTCAAGTT 2511
Qy 2515 GAAAGCCCAATCGAAGTCCGGAGAACCGAATCGATCGCCACCAATTTTGAATGGAAT 2574
Db 2512 GAAAGCCCAATCGAAGTCCGGAGAACCGAATCGATCGCCACCAATTTTGAATGGAAT 2571
Qy 2575 CTTGATCTAGATTTGTTCTCGCAGAGATGGAGAAAAATGTGCGCATCAATCCCATCAATTC 2634
Db 2572 CTTGATCTAGATTTGTTCTCGCAGAGATGGAGAAAAATGTGCGCATCAATCCCATCAATTC 2631
Qy 2635 TCTTTGATATTTGATATTTGGATGCACAGACTTGCATGAGAAATCTAGCGGTGTGGGTGTA 2694
Db 2632 TCTTTGATATTTGATATTTGGATGCATAGACTTGCATGAGAACTTAGCGGTGTGGGTGTA 2691
Qy 2695 TTTCAAGATTTAAGACGCGAGGAGGTCTGCAAGACTAGGAACTTGGAAATTTTAAAGAG 2754
Db 2692 TTTCAAGATTTAAGACGCGAGGAGGTCTGCAAGACTAGGAACTTGGAAATTTTAAAGAG 2751
Qy 2755 AAACCAATTTAGGAGAACCACTGTCTCGTGTGAAGAGACAGAGAAAAAATGGAGAGAC 2814
Db 2752 AAACCAATTTAGGAGAACCACTGTCTCGTGTGAAGAGACAGAGAAAAAATGGAGAGAC 2811
Qy 2815 AAACGTTGAAAACTACAATTTGAAAAAAGAGTATATACAGAGCAAAAGAAAGCTGTG 2874
Db 2812 AAACGTTGAAAACTACAATTTGAAAAAAGAGTATATACAGAGCAAAAGAAAGCTGTG 2871
Qy 2875 GATGCTTTATTTGTAGATTTCTCAATATATAGATTAACAAGGGATACAAACATTTGGCATG 2934
Db 2872 GATGCTTTATTTGTAGATTTCTCAATATATAGATTAACAAGGGATACAAACATTTGGCATG 2931
Qy 2935 ATTCTGCGCGCAGATAAATTTGTTTCATCGAAATTCGAGAGCTTATCTGTGATGATTTATCT 2994
Db 2932 ATTCTGCGCGCAGATAAATTTGTTTCATCGAAATTCGAGAGCTTATCTGTGATGATTTATCT 2991
Qy 2995 GTTATCCCGGGTGTAAATGCGGAAATTTTGAAGAAATTTAGAGGTCCGATTTATCACTGCA 3054
Db 2992 GTTATCCCGGGTGTAAATGCGGAAATTTTGAAGAAATTTAGAGGTCCGATTTATCACTGCA 3051
Qy 3055 ATCTCCCTATACGATCGGAGAAATGTCGTTAAAAATGCTGATTTTAAATGATGATTTAGCA 3114
Db 3052 ATCTCCCTATACGATCGGAGAAATGTCGTTAAAAATGCTGATTTTAAATGATGATTTAGCA 3111
Qy 3115 TGCTGGAATGTAAAAAGGCGCATGTAGATGTACAAACAGAGCCATCACCGTCTGTCTCTGTT 3174
Db 3112 TGCTGGAATGTAAAAAGGCGCATGTAGATGTACAAACAGAGCCATCACCGTCTGTCTCTGTT 3171
Qy 3175 ATCCAGAAATGGGAAGCAGAAAGTGTCAACAGCAGTTCCGCTGTGTCCGGGCGGTGGCTAT 3234
Db 3172 ATCCAGAAATGGGAAGCAGAAAGTGTCAACAGCAGTTCCGCTGTGTCCGGGCGGTGGCTAT 3231
Qy 3235 ATCTCTCGTGTACAGCGTACAAAGAGGATTTGGAGAGGTTGTGTAAACGATCCATGAA 3294
Db 3232 ATCTCTCGTGTACAGCGTACAAAGAGGATTTGGAGAGGTTGTGTAAACGATCCATGAA 3291
Qy 3295 ATCGAGAACCAATACAGACGAACCTAAATTTAAAACTGTGAAGAGAGGAGTGTATCCA 3354
Db 3292 ATCGAGAACCAATACAGACGAACCTAAATTTAAAACTGTGAAGAGAGGAGTGTATCCA 3351

Db 721 AATTTGAGGGGCAAAATGCTGAAAGTTGGTTGGGATATATATCAATTCCTGTAGAGACTTA 780
Qy 781 ACFTTAGGGGATTTAGATCTAGTGGCACTATTTCCAAAGCTATGACACTCGCACTTATCCA 840
Db 781 ACCTAGGAGTATTAGATCTAGTGGCACTATTTCCAAAGCTATGACACGGGTGTTATCCA 840
Qy 841 ATAAATACGAGTCTCAGTTAAACAGGGAAGTTTATACAGACGCAATTTGAGACACAGGG 900
Db 841 ATGAATACCAAGTGTCTCAATTAACAGAGAAATTTATACAGATCCAAATTTGGGAGAACAAAT 900
Qy 901 GTAAT-----ATGGCAAGTATCAATTTGGTATAATAATATGACACCTTCGTTTTCGCT 954
Db 901 GCACCTTCAGGATTTGCAAGTACGAAATGGTTTAAATATGATGACCAATCGTTTTCGCC 960
Qy 955 ATAGAGACTCGGGTATCCGAAGCCCGCATCTACTTGAATTTCTAGAAACAACTTACAAAT 1014
Db 961 ATAGAGCTGCGGTTATAGGCTCCGCATCTACTTGAATTTCCAGAAACAGCTTACAAT 1020
Qy 1015 TTTAGCACTTCATCAAGATGAGTGTACTAGGATATGATCTTACTGGCGGGGGACACA 1074
Db 1021 TTCAGCGTATTAAGTCTGATGAGTAACTACTCAATATATGAATTACTGGGTGGGACATAGA 1080
Qy 1075 ATTCAATCTCGGCCAATAGGAGCGGATTAATACCTCAACGATGGTCTACCNATCT 1134
Db 1081 CTTGAATCGGGAACAATAAGGGGCTATTAGTACCTGGAACACACCGGAAATACCAATCT 1140
Qy 1135 TCTATTAACTCTGTAAATATCATCTCTCTCGAGACGTATATGGAATGGATCATAT 1194
Db 1141 TCTATTAACTCTGTAAATATCACATCTCGAGACGTTTATAGAACAGAACTCATTT 1200
Qy 1195 GCAGGAGTGTCTTATGGGGAATTTACCTTGAACCTATTCAATGGTGTCTTCTGTAGA 1254
Db 1201 GCAGGGAATAAT-----ACTTCTAACTACTCTGTGAATGGAGTACCTTGGGCTAGA 1254
Qy 1255 TTTAAATTTAGGAACCTCTAGATATCTTTTGAAGAGGTACTGTAATAGTCAACCC 1314
Db 1255 TTTAAATTTGAGAAATCCCTCGAATTCCTT---AGAGGTAGCCTTCTCTATCTATAGGG 1311
Qy 1315 TATGAGTCACTGGGCTCAATTAAGAAATTCAGAACTGAAATACCAACAGAAACAACA 1374
Db 1312 TATCTGGAGTGGGACACAATATTGTAATCAGAACTGAAATACCAACAGAAACAACA 1371
Qy 1375 GAACGACAAATATGAATCATATAGTCAATAGTATCTCACATAGGGCTCATTTCCAA 1434
Db 1372 GAACGACAAATATGAATCTTACAGTCAATAGATTTATCTAATATAGACTAAATCAGGA 1431
Qy 1435 TCTAGGCTCATGTACAGTATATCTTGGACCGCACCGTGTAGTCAGATCGTACAAATACC 1494
Db 1432 AACACTTTGAGAGCACAGTATATCTTGGACCGCACCGTGTAGTCAGATCGTACAAATACC 1491
Qy 1495 ATTAGTTTCAGATAGCATACACAAATACCATTTGTAATAATCATTTCAACCTTTAATTCAGGT 1554
Db 1492 ATTAGTTTCAGATAGCATACACAAATACCATTTGTAATAATCATTTCAACCTTTAATTCAGGT 1551
Qy 1555 ACCTCTGTAGTCACTGGGCCAGGATTTACAGAGGGGGATATAATCCGAACCTAACGTTAAT 1614
Db 1552 ACCTCTGTAGTCACTGGGCCAGGATTTACAGAGGGGGATATAATCCGAACCTAACGTTAAT 1611
Qy 1615 GGTAGTGTACTAGTATGGGTCTTAATTTTAAATAATACATCATATACAGCGGTATCGCGTG 1674
Db 1612 GGTAGTGTACTAGTATGGGTCTTAATTTTAAATAATACATCATATACAGCGGTATCGCGTG 1671
Qy 1675 AGATTCGTTATCTGCTCTCAACAAATGGTCTGAGGGTAACTGTCTGGAGGGAGTACT 1734
Db 1672 AGATTCGTTATCTGCTCTCAACAAATGGTCTGAGGGTAACTGTCTGGAGGGAGTACT 1731
Qy 1735 ACTTTTGATCAAGATTCCTAGTACTATGAGTGCAAATGAGTCTTTTGACATCTCAATCA 1794
Db 1732 ACTTTTGATCAAGATTCCTAGTACTATGAGTGCAAATGAGTCTTTTGACATCTCAATCA 1791
Qy 1795 TTTAGATTTGCAGAAATTTCTGTAGGTATTTAGTGCATCTGGCAGTCAAACTGCTGGAATA 1854

Db 1792 TTTAGATTTCCAGAAATTTCTGTAGGTATTTAGTGCATCTGGCAGTCAAACTGCTGGAATA 1851
Qy 1855 AGTATAAGTAAATATGCAAGTAGACAAACGTTTTCATTTGATAAAAATTTGAATTCATTTCCA 1914
Db 1852 AGTATAAGTAAATATGCAAGTAGACAAACGTTTTCATTTGATAAAAATTTGAATTCATTTCCA 1911
Qy 1915 ATTTACTGCAACCTTCGAAGCAGAAATACGATTTTGAAGAGGGCGCAAGAGGGCGGTGAATGCT 1974
Db 1912 ATTTACTGCAACCTTCGAAGCAGAAATATGATTTTGAAGAGGCGCAAGAGGGCGGTGAATGCT 1971
Qy 1975 CTGTTTACTTAATACGAATCCAAAGATTTGAAACAGATGTGACAGATTTATCATATTGAT 2034
Db 1972 CTGTTTACTTAATACGAATCCAAAGAGTTTGAACAGGTGTGACAGATTTATCATATTGAT 2031
Qy 2035 CAAGTATCCAAATTTAGTGGCGTGTATTCGGATGAATTTCTGTCTTAGATGAAAAGAGAGAA 2094
Db 2032 GAAGTATCCAAATTTAGTGGCGTGTATTCGGATGAATTTCTGTTGGATGAAAAGAGAGAA 2091
Qy 2095 TTTACTTGAGAAAGTGAATATGCGAAACGACTCAGTGTAGTGAAGAAACTTTACTCCAAAGAT 2154
Db 2092 TTTACTTGAGAAAGTGAATATGCGAAACGACTCAGTGTAGTGAAGAAACTTTACTCCAAAGAT 2151
Qy 2155 CCAAACTTCACATCCATCAATAGCAACCAAGCTTCATATCTACTATAGTGAAGCAATCCGAAT 2214
Db 2152 CCAAACTTCACATCCATCAATAGCAACCAAGCTTCATATCTACTATAGTGAAGCAATCCGAAT 2211
Qy 2215 TTTCACTCTATCATGAAACAACTCTGAACTGGATGGTGGGAAAGTGAGAACATTTACAATC 2274
Db 2212 TTTCACTCTATCATGAAACAACTCTGAACTGGATGGTGGGAAAGTGAGAACATTTACAATC 2271
Qy 2275 CAGGAAGGAAATGACGTATTTAAAGAGAAATTCGTCACTACCTCCGGGAGCTTTTAATGAG 2334
Db 2272 CAGGAAGGAAATGACGTATTTAAAGAGAAATTCGTCACTACCTCCGGGAGCTTTTAATGAG 2331
Qy 2335 TGTATTCGAGCTGTTTATATCAAAATATAGGAGAGTCCGAAATTTAAAGCTTATACTCCG 2394
Db 2332 TGTATTCGAGCTGTTTATATCAAAATATAGGAGAGTCCGAAATTTAAAGCTTATACTCCG 2391
Qy 2395 TACCAATTAAGAGGGTATATTGAAGATAGTCAAGATTTAGAGATATATTGATTCGTTAT 2454
Db 2392 TACCAATTAAGTGGCTATATTGAAGATAGTCAAGATTTAGAGATATATTGATTCGTTAT 2451
Qy 2455 AATGCGAAACATGAACATTTGGATGTTCCAGGTACCGAGTCCGTATGGCGCTTTTCAGTT 2514
Db 2452 AATGCGAAACATGAACATTTGGATGTTCCAGGTACCGAGTCCGTATGGCGCTTTTCAGTT 2511
Qy 2515 GAAAGCCCAATCGGAGGTGCGGAGAACCGAATCGATCGCACCAATTTTGAATGGAAT 2574
Db 2512 GAAAGCCCAATCGGAGGTGCGGAGAACCGAATCGATCGCACCAATTTTGAATGGAAT 2571
Qy 2575 CTTGATCTAGATTTGTTCTTCGAGAGATGGAGAAAAATGTGCGCATCATTTCCCATCATTTTC 2634
Db 2572 CTTGATCTAGATTTGTTCTTCGAGAGATGGAGAAAAATGTGCGCATCATTTCCCATCATTTTC 2631
Qy 2635 TCTTTGGATTTGATATTTGGATGACAGACTTGTGATGAGAAATCTAGCGGTGTGGGTGGA 2694
Db 2632 TCTTTGGATTTGATTTGGATGATGTTGATGATGTTGATGAGAACCTTAGGCGGTGTGGGTGGA 2691
Qy 2695 TTTCAAGATTTAAGACGAGGAGGTCAATGCAAGACTAGGGAATCTGGAATTTTGAAGAG 2754
Db 2692 TTTCAAGATTTAAGACGAGGAGGTCAATGCAAGACTAGGGAATCTGGAATTTTGAAGAG 2751
Qy 2755 AAACCAATTTAGGAGAACCTGTCTGTTGTAAGAGAGAGAGAGAAAAATTTGGAGAGAC 2814
Db 2752 AAACCAATTTAGGAGAACCTGTCTGTTGTAAGAGAGAGAGAGAAAAATTTGGAGAGAC 2811
Qy 2815 AAACGTGAAAAAATACTCAATTTGAAAAAATAAGTATATACAGAGGCAAAAGAGCTGTG 2874
Db 2812 AAACGTGAAAAAATACTCAATTTGAAAAAATAAGTATATACAGAGGCAAAAGAGCTGTG 2871
Qy 2875 GATGCTTTTATTTGTAGATCTCAATATATATAGATTAAGAGGAGATCAAAACATTTGGAGATG 2934
Db 2872 GATGCTTTTATTTGTAGATCTCAATATATATAGATTAAGAGGAGATCAAAACATTTGGAGATG 2931

Qy	2935	ATTCATCGGCAGATAA	ACTTGTTCATCGAATTCGAGAGC	TTATCTGTGTCAGAA	TATCT	2994
Db	2932	ATTCATCGGCAGATAA	CTTGTTCATCGAATTCGAGAGC	GTATCTTT	CAGAAT	TATCT
Qy	2995	GTTATCCGGGTG	TAATTCGGGAAATTTT	TGAAGAA	TTAGAGGT	CGCATATCACTGCA
Db	2992	GTTATCCAGGTG	TAATTCGGGAAATTTT	TGAAGAA	TTAGAGGT	CGCATATCACTGCA
Qy	3055	ATCTCCCTATACGAT	TCGAGAAATGTCGTTAA	AAATGGTGATTT	TAATATGAT	TAGCA
Db	3052	ATCTCCCTATACGAT	TCGAGAAATGTCGTTAA	AAATGGTGATTT	TAATATGAT	TAGCA
Qy	3115	TGCTGGAATG	TAAAGGCGATGATAG	TGTACAACAGAGCCAT	CACCGTCTCTG	CTCTTGTT
Db	3112	TGCTGGAATG	TAAAGGCGATGATAG	TGTACAACAGAGCCAT	CACCGTCTCTG	CTCTTGTT
Qy	3175	ATCCAGAATGGGA	AGCAGAAGTGTCACAAGCAG	TTCCCGTCTCTCGGGCG	CGTGGCTAT	3234
Db	3172	ATCCAGAATGGGA	AGCAGAAGTGTCACAAGCAG	TTCCCGTCTCTCGGGCG	CGTGGCTAT	3231
Qy	3235	ATCCTCCGTGTCA	GCGGTACAAAGAGGGATATG	GAGGGTTGTGTAACAT	CCATGAA	3294
Db	3232	ATCCTCCGTGTCA	GCGGTACAAAGAGGGATATG	GAGGGTTGTGTAACAT	CCATGAA	3291
Qy	3295	ATCCAGAACAA	TACAGACGAACTAA	AAATTTAA	AAACCTGTAAGAAGAGG	AGGTGTATCCA
Db	3292	ATCCAGAACAA	TACAGACGAACTAA	AAATTTAA	AAACCTGTAAGAAGAGG	AGGTGTATCCA
Qy	3355	ACGGATACAGGA	ACGCTGTAATGATTATAC	TGCAACACCAAGGTACAG	CAGATGTGTAATCC	3414
Db	3352	ACGGATACAGGA	ACGCTGTAATGATTATAC	TGCAACACCAAGGTACAG	CAGATGTGTAATCC	3411
Qy	3415	CGTAATCTGGATAT	GAGGATGTCATCAAGTTG	GATCTACAGCATCTG	TAAATACAAA	3474
Db	3412	CGTAATCTGGATAT	GAGGATGTCATCAAGTTG	GATCTACAGCATCTG	TAAATACAAA	3471
Qy	3475	CCGACTTATGA	GAAGAAAACGTATACAGAT	GTACGAAGAGATATCAT	TGTGTAATGAC	3534
Db	3472	CCGACTTATGA	GAAGAAAACGTATACAGAT	GTACGAAGAGATATCAT	TGTGTAATGAC	3531
Qy	3535	AGGGGTATGTGA	ATTATCCACCACTACCGTCTG	TTATATGACAAAGAA	TTAGAAATAC	3594
Db	3532	AGGGGTATGTGA	ATTATCCACCACTACCGTCTG	TTATATGACAAAGAA	TTAGAAATAC	3591
Qy	3595	TTCCAGAAAAC	CGATAGGTATGATTTGAGAT	TCGGAAGAAACGGAAG	CGGAAGTTATTGTA	3654
Db	3592	TTCCAGAAAAC	CGATAGGTATGATTTGAGAT	TCGGAAGAAACGGAAG	CGGAAGTTATTGTA	3651
Qy	3655	GACAGCGTGA	AAATTACTCCTTTATGGAGGA	ATAG	3687	
Db	3652	GACAGCGTGA	AAATTACTCCTTTATGGAGGA	ATAG	3684	

RESULT 6

AAQ56804

ID AAQ56804 standard; DNA; 4074 BP.

XX XX

AC AAQ56804;

XX

DT	16-OCT-2003	(revised)
DT	16-OCT-2003	(revised)

DT	25-MAR-2003	(revised)
DT	18-OCT-1994	(first entry)

DI 18-OCT-1994 (LIST ENCL) XX

DE *Bacillus thuringiensis* CryIB insecticidal protoxin gene.

XXXXXX

KW Insecticidal crystal protein; ICP; cryIB; Ostrinea nubi

KW European corn borer; Lepidoptera; Pyralidae; toxin; ds.

XX
CC
CC

OS Bacillus thuringiensis; (strain ent
yy

XX	Key	Location/Qualifiers
FH		

ET	key	ET	CDS
186	186	186	186

```
FT FT /*tag= a
```

```
FT FT /product= "CryIB"
```

```
FT FT /note= "insecticidal crystal protoxin; Met initiator
```

```
FT FT codon is TTG"
```

```
XX XX
```

```
PN EP589110-A1.
```

```
XX XX
```

```
XX XX 30-MAR-1994.
```

```
XX XX
```

```
XX XX 19-AUG-1992; 92EP-00402307.
```

```
XX XX
```

```
XX XX 19-AUG-1992; 92EP-00402307.
```

```
XX XX
```

```
PA (PLBZ ) PLANT GENETIC SYSTEMS NV.
```

```
XX XX
```

```
PI Peferoen M, Jansens S, Denolf P;
```

```
XX XX WFI; 1994-102862/13.
```

```
DR DR P-PSDB; AARS0955.
```

```
XX XX
```

```
PT Method to control or combat Ostrinia - utilises Bacillus thuringiensis
```

```
PT cry IB gene/protein for crop prevention.
```

```
XX XX
```

```
XX Claim 1; Page 11-18; 38pp; English.
```

```
XX XX
```

```
CC The CryIB toxin gene (disclosed in EP-408403) has been found to be toxic
```

```
CC to the European corn borer (Ostrinea nubilalis). The use of CryIB
```

```
CC insecticidal crystal protein for protecting crops against O.nubilalis is
```

```
CC claimed. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 16-OCT
```

```
CC -2003 to standardise OS field)
```

Query Match	84.9%	Score 3132	DB 2	Length 4074
Best Local Similarity	91.1%	Pred. No. 0		
Matches 3372: Conservative	0	Mismatches 300	Indels 30	Gaps 3

Qy	1	TTGACTTCAAAATAGGAAAAATGAGATGAAATATTAATGCTTTATCGATTCAGCTGTA	60
Db	186	TTGACTTCAAAATAGGAAAAATGAGATGAAATATTAAT-----GCTGTA	230
Qy	61	TCGAATCATTTCCACACAAATGGATCTATCAACAGATGCTCGTATTGAGGATTCCTTTGTGT	120
Db	231	TCGNAATCATTTCCGACACAAATGGATCTATTACCAGATGCTCGTATTGAGGATAGCTTGTGT	290
Qy	121	ATAGCCGAGGGGAATTAATATCAATCCACTTTGTTAGCGCATCAACAGTCCAAAACGGGTATT	180
Db	291	ATAGCCGAGGGGAACATATTTGATCCATTTGTTAGCGCATCAACAGTCCAAAACGGGTATT	350
Qy	181	AACATAGCTCGTAGAATACTAGTGTATTAGGCGTACCGTTGCTGGACAAATAGCTAGT	240
Db	351	AACATAGCTGTAGATACTAGCGGTATTGGGCGTACCGTTTCTGGACAACTAGCTAGT	410
Qy	241	TTTTATAGTTTTCTTTGGTGTGAATATATGCCCCCGCGGACAGATCAGTGGGAAATTTTC	300
Db	411	TTTTATAGTTTTCTTTGGTGTGAATATGCCCCCGCGGACAGATCAGTGGGAAATTTTC	470
Qy	301	CTAGAACATGTCGAAACAACTTTATAAATCAACAAATCAACAAAATGCTAGGAATACGGCA	360
Db	471	CTAGAACATGTCGAAACAACTTTATAAATCAACAAATCAACAAAATGCTAGGAATACGGCT	530
Qy	361	CTTGCTCGATTACAAGTTTTAGGAGATTCTTTAGAGCCTTATCAACAGTCACTTGAAGAT	420
Db	531	CTTGCTCGATTACAAGTTTTAGGAGATTCTTTAGAGCCTTATCAACAGTCACTTGAAGAT	590
Qy	421	TGGCTAGAAACCGTGATGATGCAAGAACAGAGTGTCTTTTATACCCCAATATATAGCC	480
Db	591	TGGCTAGAAACCGTGATGATGCAAGAACAGAGTGTCTTTTATACCCCAATATATAGCT	650
Qy	481	TTAGAACTTCATTTTTCTTAATGCGATGCCGCTTTTCGCAATTAGAAACCAAGAGTTTCCA	540
Db	651	TTAGAACTTCATTTTTCTTAATGCGATGCCGCTTTTCGCAATTAGAAACCAAGAGTTTCCA	710

QY 541 TTATTAAAGTATATGCTCAAGCTGCAAAATTTACACCTATATATTTGAGAGATGCTCT 600
Db 711 TTATTGATGATATGCTCAAGCTGCAAAATTTACACCTATATATTTGAGAGATGCTCT 770
QY 601 CTTTGTGATGATATGCTCAAGCTGCAAAATTTACACCTATATATTTGAGAGATGCTCT 660
Db 771 CTTTGTGATGATATGCTCAAGCTGCAAAATTTACACCTATATATTTGAGAGATGCTCT 830
QY 661 GTGGAACAAACGAGAGATATTCGGACTATTCGGTGAAGTGGTATATATATATATATATAT 720
Db 831 GTGGAACAAACGAGAGATATTCGGACTATTCGGTGAAGTGGTATATATATATATATATAT 890
QY 721 AGCTTGAGAGGACAAATGCGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 780
Db 891 AGCTTGAGAGGACAAATGCGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 950
QY 781 ACCTTAGGGTATTTAGATCTAGTGGCACTATTCGAAGCTATGACACTGCGCACTTTATCCA 840
Db 951 ACCTTAGGGTATTTAGATCTAGTGGCACTATTCGAAGCTATGACACTGCGCACTTTATCCA 1010
QY 841 ATAAATACGAGTCTCAGTTTAAACAGGAAAGTTTATACAGACGCAATTTGAGCAACAGGG 900
Db 1011 ATAAATACGAGTCTCAGTTTAAACAGGAAAGTTTATACAGACGCAATTTGAGCAACAGGG 1070
QY 901 GTAAATATGCAAGTATGAAATGGTATTAATTAATTAATTAATTAATTAATTAATTAATTA 960
Db 1071 GTAAATATGCAAGTATGAAATGGTATTAATTAATTAATTAATTAATTAATTAATTAATTA 1130
QY 961 ACTCGGGTATTCGAGCCGCACTACTTGTATTTCTAGAAACAACTTACAAATTTTATGAG 1020
Db 1131 GCTCGGGTATTCGAGCCGCACTACTTGTATTTCTAGAAACAACTTACAAATTTTATGAG 1190
QY 1021 ACTTCATCAGATGGAGTGTCTAGGCAATATGATTTACTGGGGGGGACACAAATTTCAA 1080
Db 1191 GCTTCATCAGATGGAGTGTCTAGGCAATATGATTTACTGGGGGGGACACAAATTTCAA 1250
QY 1081 TCTCGGCAATAGAGCGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1140
Db 1251 TCTCGGCAATAGAGCGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1310
QY 1141 AATCCTGTAGATTTATCATTTCTCTCGAGAGATGATTTGAGTGAATCATATGAGGAG 1200
Db 1311 AATCCTGTAGATTTATCATTTCTCTCGAGAGATGATTTGAGTGAATCATATGAGGAG 1370
QY 1201 GTGCTTCTATGGGAAATTTACCTTGAACCTATTTATGATGCTGCTTCTATGATTTAAT 1260
Db 1371 GTGCTTCTATGGGAAATTTACCTTGAACCTATTTATGATGCTGCTTCTATGATTTAAT 1430
QY 1261 TTTAGGAACCTCAGAAATATTTTGAAGAGGTATCTGCTAACTATATAGTCAACCTATGAG 1320
Db 1431 TTTAGGAACCTCAGAAATATTTTGAAGAGGTATCTGCTAACTATATAGTCAACCTATGAG 1490
QY 1321 TCACCTGGGCTTCAATTTAAAGATTCAGAACTGAAATTTACCAAGAGGAAACAGAGGAG 1380
Db 1491 TCACCTGGGCTTCAATTTAAAGATTCAGAACTGAAATTTACCAAGAGGAAACAGAGGAG 1550
QY 1381 CCAAAATTAATGAATCATATAGTATGATTTATCTCATATAGTATTAATTTTACAACTTAGG 1440
Db 1551 CCAAAATTAATGAATCATATAGTATGATTTATCTCATATAGTATTAATTTTACAACTTAGG 1610
QY 1441 GTGATGTACAGATATTTCTGAGCGCAGGATGAGATGAGATGAGATGAGATGAGATGAGAT 1500
Db 1611 GTGATGTACAGATATTTCTGAGCGCAGGATGAGATGAGATGAGATGAGATGAGATGAGAT 1670
QY 1501 TCAGATGAGATTAACAAATACCAATTTGGTAAATCATTTCAACCTTAATTTCAAGTCTCT 1560
Db 1671 CCAAAATGAATACCCAAATTTCCAAATTTGGTAAAGAGCATCCCAACTTCTCAAGGTACCA 1730
QY 1561 GTAGTACGTGGCCAGGATTTACAGGAGGAGATTAATTTCCAACTAAGTAAATTTAGTGTAG 1620
Db 1731 GTTGTAGAGGACAGGATTTACTGGTGGGATTAATTTCTGAGAGAGGATTAATTTAGTGTAG 1790
QY 1621 GTACTAAGTATGGTCTTAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1680

Db 1791 TTTGGACGAAATAGAGTAACTGTTAAACGACCAATTAACCAAAAGATATCTATAGGATTC 1850
QY 1681 CGTTATGCTGCTTCTCAAAACAAATGGTCTGAGGGTAACTGTCGAGGGAGTACTACTACTTT 1740
Db 1851 CGCTATGCTTCAACTGTAGATTTTGTATTTCTTGTATCAGCTGAGGAGTACTACTGTAAT 1910
QY 1741 GATCAAGGATTCCTTCTAGTACTATGATGCAAAATGAGTCTTTTGACATCTCAATCAATTTAGA 1800
Db 1911 AATTTTAGATTTCTCAGTCAATGAACAGTGGAGACGAATAAAATACGGAATTTTGTG 1970
QY 1801 TTTGCAAGATTTCTCTAGTATTTAGTCAATCTGGCAGTCAA--ACTGCTGGAATAGT 1857
Db 1971 AGACGCTGCTTTTACTACCTTTTCTTTTACAAATTTCAAGATATAATTTGCAACGCTCT 2030
QY 1858 ATAAGTAATAATCGAGGTAGACAAAGCTTTTCACTTTGATAAAATTTGAATTTCAATTTCAAT 1917
Db 2031 ATTCAGGCTTTAGTGGAAATGGGAAGTGTATATAGATAAAATTTGAATTTTCCAGTT 2090
QY 1918 ACTGCAACCTTTCGAAGCAGATACGATTTTGAAGGGCGCAAGGGCGTGAATGCTCTG 1977
Db 2091 ACTGCAACCTTTCGAAGCAGATATGATTTTGAAGAGCGCAAGAGGGCGTGAATGCTCTG 2150
QY 1978 TTTACTAATACGAATCCAAAGAGATTTGAAACAGATGTGACAGATTTATATATTTGATCAA 2037
Db 2151 TTTACTAATACGAATCCAAAGAGATTTGAAACAGATGTGACAGATTTATATATTTGATCAA 2210
QY 2038 GTATCCAAATTTAGTGGCTGTTTATCGGATGAATTTCTGCTTAGATGAAAGAGAGAAATTA 2097
Db 2211 GTATCCAAATTTAGTGGCTGTTTATCGGATGAATTTCTGCTTAGATGAAAGAGAGAAATTA 2270
QY 2098 CTTGAGAAAGTGAAATATGCGAAACGACTCAGTGTGATGAAAGAACTTTATCTCCAGATCCA 2157
Db 2271 CTTGAGAAAGTGAAATATGCGAAACGACTCAGTGTGATGAAAGAACTTTATCTCCAGATCCA 2330
QY 2158 AACTTCACATCCATCAATTAAGCAACGAGCTTCTATCTACTACTGAGCAATCGAATTTTC 2217
Db 2331 AACTTCACATCCATCAATTAAGCAACGAGCTTCTATCTACTACTGAGCAATCGAATTTTC 2390
QY 2218 ACATCTATCCATGAAACAACTCTGAAACATGATGGTGGGAGTGGAGAACATTTACAACTCCAG 2277
Db 2391 ACATCTATCCATGAAACAACTCTGAAACATGATGGTGGGAGTGGAGAACATTTACAACTCCAG 2450
QY 2278 GAAAGAAATGACGATTTTAAAGAAATTAAGTCACTACCGGGGACTTTTAAATAGTGT 2337
Db 2451 GAAAGAAATGACGATTTTAAAGAAATTAAGTCACTACCGGGTACTTTTAAATAGTGT 2510
QY 2338 TATCCAGATTTTATTAATCAAAATAGGAGTCCGAATTTAAAGCTTATCTCGCTAC 2397
Db 2511 TATCCAGATTTTATTAATCAAAATAGGAGTCCGAATTTAAAGCTTATCTCGCTAC 2570
QY 2398 CAATTAAGAGGTTATTTGAAGATAGTCAAGATTTTAGAGATATATTTGATTCGTTAAT 2457
Db 2571 CAATTAAGAGGTTATTTGAAGATAGTCAAGATTTTAGAGATATATTTGATTCGTTAAT 2630
QY 2458 GCGAAACATGAAACATTTGGATGTTCCAGGTACCGAGTCCGCTATGGCGCTTTTCAAGTGA 2517
Db 2631 GCGAAACATGAAACATTTGGATGTTCCAGGTACCGAGTCCGCTATGGCGCTTTTCAAGTGA 2690
QY 2518 AGCCGAATCGGAGGTTCCGAGAGAACGAAATCGATCGCACCAATTTTGAATCGAATCCT 2577
Db 2691 AGCCGAATCGGAGGTTCCGAGAGAACGAAATCGATCGCACCAATTTTGAATCGAATCCT 2750
QY 2578 GATCTAGATTTGTTCTGCGAGAGATGGAGAAATTTGCGCATCATTTCCCATCATTTCTCT 2637
Db 2751 GATCTAGATTTGTTCTGCGAGAGATGGAGAAATTTGCGCATCATTTCCCATCATTTCTCT 2810
QY 2638 TTGGATATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 2697
Db 2811 TTGGATATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 2870
QY 2698 AGATTAAGACGAGGAGGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 2757

Db 2871 AAGATTAAAGCCGAGGAGGTCATCGCAAGCATAGGGAATTCGGAATTTATTGAAGAGAAA 2930
 Qy CCATTATTAGGAGAGCACTGCTCGTGTGAAGAGCAGAGAGAAAATGGAGAGACAAA 2817
 Db |||||||
 Qy CCATTATTAGGAGAGCACTGCTCGTGTGAAGAGGCGAGAGAAAATGGAGAGACAAA 2990
 Db |||||||
 Qy CGTGAAAACTTACAAATTTGGAACAAAACGAGTATATACAGAGGCAAAAGAGCTGTGGAT 2877
 Db |||||||
 Qy CGTGAAAACTTACAAATTTGGAACAAAACGAGTATATACAGAGGCAAAAGAGCTGTGGAT 3050
 Qy GCTTTATTGTAGATTCTCAATATAATAGATTACAAGCGGATACAAACATTTGGCATGATT 2937
 Db |||||||
 Qy GCTTTATTGTAGATTCTCAATATAATAGATTACAAGCGGATACAAACATTTGGCATGATT 3110
 Db |||||||
 Qy CATCGGCAGATAAATCTGTTTCATCGAATTCGAGAGGCTTATCTGTGAGAAATATCTGTT 2997
 Db |||||||
 Qy CATCGGCAGATAAATCTGTTTCATCGAATTCGAGAGGCTTATCTGTGAGAAATATCTGTT 3170
 Db |||||||
 Qy ATCCCGGGTGTAAATGCGGAAATTTTGAAGAAATTAGAAGGTGCGAATTCATCTGCAATC 3057
 Db |||||||
 Qy ATCCCGGGTGTAAATGCGGAAATTTTGAAGAAATTAGAAGGTGCGAATTCATCTGCAATC 3230
 Qy TCCCTATACATGCGAGAAATGTCGTTAAATAATGCGTAAATAATGCGTAAATAATGCGTAA 3117
 Db |||||||
 Qy TCCCTATACATGCGAGAAATGTCGTTAAATAATGCGTAAATAATGCGTAAATAATGCGTAA 3290
 Db |||||||
 Qy TGGAAATGTAAGAGGCGATGTAGATGTACAACAGAGCCATCACCGTTCGTCCTGTTGTTATC 3177
 Db |||||||
 Qy TGGAAATGTAAGAGGCGATGTAGATGTACAACAGAGCCATCACCGTTCGTCCTGTTGTTATC 3350
 Db |||||||
 Qy CCAGAAATGGAAGCAGAAAGTGTCAACAGCAGTTCGCGTCTGTCGCGGGTGTGCGTATATC 3237
 Db |||||||
 Qy CCAGAAATGGAAGCAGAAAGTGTCAACAGCAGTTCGCGTCTGTCGCGGGTGTGCGTATATC 3410
 Db |||||||
 Qy CTCGGTGTCAACGGTCAAGAGGGATGTAGAGAGGGTGTGTAAAGATCCATGAAATC 3297
 Db |||||||
 Qy CTCGGTGTCAACGGTCAAGAGGGATGTAGAGAGGGTGTGTAAAGATCCATGAAATC 3470
 Qy GAGAAATACAGAGCACTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 3357
 Db |||||||
 Qy GAGAAATACAGAGCACTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 3530
 Db |||||||
 Qy GATACAGAAACGTTGTAATGATTTACTGTCACCAAGGTTACAGC-----AGTA 3405
 Db |||||||
 Qy GATACAGAAACGTTGTAATGATTTACTGTCACCAAGGTTACAGC-----AGTA 3590
 Qy TGTAAATTCGCGTAAATGCGATGTAGGATGCGATGTAAGTTCATGATGATGATGATGATGAT 3465
 Db |||||||
 Qy TGTAAATTCGCGTAAATGCGATGTAGGATGCGATGTAAGTTCATGATGATGATGATGATGAT 3650
 Db |||||||
 Qy AATTACAAACCGGCTTATGGAAGAGAAACGTATACAGATGTACGAGAGATAATCATTTGT 3525
 Db |||||||
 Qy AATTACAAACCGGCTTATGGAAGAGAAACGTATACAGATGTACGAGAGATAATCATTTGT 3710
 Qy GAATATGACAGAGGATGTGAATTTATCCACCATACAGCTGCTGTTATATGACAAAGAA 3585
 Db |||||||
 Qy GAATATGACAGAGGATGTGAATTTATCCACCATACAGCTGCTGTTATATGACAAAGAA 3770
 Qy TTAGAATACCTCCAGAAACCGGATAGGATGATGATGATGATGATGATGATGATGATGATGAT 3645
 Db |||||||
 Qy TTAGAATACCTCCAGAAACCGGATAGGATGATGATGATGATGATGATGATGATGATGATGAT 3771
 Db |||||||
 Qy TTTATTGTAGACGCGTGAATTTACTCTTTATGGAGGAATAG 3687
 Db |||||||
 Qy TTTATTGTAGACGCGTGAATTTACTCTTTATGGAGGAATAG 3872

RESULT 7
 AAQ64112
 ID AAQ64112 standard; DNA; 3932 BP.
 XX
 AC
 AAQ64112;
 XX

DT 02-FEB-1995 (first entry)
 XX cryET5 gene.
 DE cryET5 gene.
 KW cryET4; cryET5; Lepidoptera; lepidopteran insect; insecticidal; toxin;
 insecticidal crystal protein; ICP; ds.
 XX Bacillus thuringiensis.
 OS
 FH Key Location/Qualifiers
 CDS 67..3756
 FT /*tag= a
 FT misc_feature 2253..2272
 FT /*tag= b
 FT /note= "Oligonucleotide WD162, see AAQ64113)"
 XX
 PN US5322687-A.
 XX
 PD 21-JUN-1994.
 XX
 PF 29-JUL-1993; 93US-00100709.
 XX
 PR 29-JUL-1993; 93US-00100709.
 XX
 PA (ECOG-) ECOGEN INC.
 XX
 PI Tan Y, Jany CS, Donovan WP, Gonzalez JM;
 XX
 DR WPI; 1994-199503/24.
 DR P-PSDB; AAR54074.
 XX
 PT Isolated cryET4 gene and Bacillus thuringiensis cultures transformed with
 this gene - used in compans. against lepidopteran insects.
 PS Disclosure; Col 29-38; 51pp; English.
 XX
 CC B. thuringiensis strain EG5847 exhibits insecticidal activity against
 lepidopteran insects. Two novel toxin genes from B. thuringiensis EG5847
 designated cryET4 and cryET5 produce insecticidal proteins with activity
 against a broad spectrum of lepidopteran insects. The gene sequences are
 given in AAQ64111-12
 XX
 SQ Sequence 3932 BP; 1347 A; 650 C; 840 G; 1095 T; 0 U; 0 Other;
 Query Match 72.9%; Score 2687.2; DB 2; Length 3932;
 Best Local Similarity 83.5%; Pred. No. 0;
 Matches 3088; Conservative 0; Mismatches 593; Indels 15; Gaps 3;
 Qy 1 TTGACTTCAAATAGGAAAAATGAGATGAAATTTATAAATGCTTTATCGATTCACCGGTA 60
 Db 67 TTGACTTCAAATAGGAAAAATGAGATGAAATTTATAAATGCTTTATCGATTCACCGGTA 126
 Qy 61 TCGAATCATTCACACAAATGGATCTATCACCAGATGCTCGTATTGAGGATCTTTTGTGT 120
 Db 127 TGAATCTCTTCCACGCAAAATGAATCTATCACCAGATGCTCGTATTGGAAGATAGCTTTGT 186
 Qy 121 ATAGCCGAGGGAATAATATCAATCCACTTGTGTAGGCGATCAACAGTCCAAACGGGTATT 180
 Db 187 GTAGCCGAGGTGAACATATTCATTCATTTGTAGCGCATCAACAGTCCAAACGGGTATA 246
 Qy 181 AACATAGCTGGTAGAATACTAGGTGTATTTAGGCGTACCGTTTGTCTGGAATAATAGTAGT 240
 Db 247 AACATAGCTGGTAGAATAATTTGGCGGTATTAGGTGTGCGCTTTTGTCTGGAATAATAGTAGT 306
 Qy 241 TTTTATAGTTTCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 300
 Db 307 TTTTATAGTTTCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 366
 Qy 301 CTAGAAATGTGCAACAACTTATAAATCAACAAATAACAGAAAAATGCTAGGATAACGGCA 360
 Db 367 CTGGAACATGTAGAACAACTTATAGACAAACAAAGTAACAGAAAAATAGTAGAATACGGCT 426
 Qy 361 CTTGCTCGATTACAGGTTTAGGAGATTCCTTTAGAGCCTATCAACAGTCACTTGAAGAT 420

Db 427 ATTGCTCGATTAGAGGCTTAGAGAGGCTTATAGATCTTACCAGAGGCTCTTGAAACT 486
Qy |||||
Db 421 TGGCTAGAAAACCGTGATGATGCAAGAACGAGAAAGTGTTCTTTATATACCCAAATATATAGCC 480
Qy |||||
Db 487 TGGTTAGATAACCGAAATGATGCAAGATCAAGAGCAATTAATCTTGAGCGCTATGTTGCT 546
Qy |||||
Db 481 TTAGAACTTGATTTCTTAATGCGATGCGCGCTTTTCGCAATTAAGAAACCAAGAGTTCCCA 540
Qy |||||
Db 547 TTGAACCTTTGACATTACTACTGCTATACCGCTTTTCAGAAATACGAAATAGAAAGTTCCCA 606
Qy |||||
Db 541 TTATTAATGATATGCTCAAGCTGCAAAATTTACACCTATTATTATTCAGAGATGCGCTCT 600
Qy |||||
Db 607 TTATTAATGGTATATGCTCAAGCTGCAAAATTTACACCTATTATTATTATTCAGAGAGCGCATCC 666
Qy |||||
Db 601 CTTTTTGGTAGTGAATTTGGGCTTTACATCGCAGGAAATTCACCGTTATTATGAGCGCAA 660
Qy |||||
Db 667 CTTTTTGGTAGTGAATGGGGAATGCGCATCTCCGATGTATACCAATATTACCAAGAACAA 726
Qy |||||
Db 661 GTGGAACAAACGAGAGATTTATCCGACTATTTGCGTAGAATGGTATAATACAGGTCTAAAT 720
Qy |||||
Db 727 ATCAGATATACAGAGGAATATCTAAACCATTTGCGGTACAAATGGTATAATACAGGGCTAAAT 786
Qy |||||
Db 721 AGCTTGAGGGGCAAAATGCGCGCAAGTTGGGTGGTTATATCAATTCGCTAGAGATCTTA 780
Qy |||||
Db 787 AACTTAAAGAGGGCAAAATGCTGAAAGTTGGTGGGTATATCAATTCGCTAGAGACCTTA 846
Qy |||||
Db 781 ACGTTAGGGGTATTAGATCTAGTGGCACTATTTCCTCAAGCTATGACACTCGCACCTTATCCA 840
Qy |||||
Db 847 ACGTTAGGGGTATTAGATTTAGTAGCCCTATTTCCTCAAGCTATGATATCTCGCACCTTATCCA 906
Qy |||||
Db 841 ATAATATACGATGCTCAGTTTAAACAGGGAAGTTTATACAGACGCAATTTGGAGCAACAGGG 900
Qy |||||
Db 907 ATCAATACGAGTGTCTAGTTTAAACAGAGAAATTTATACAGATCCAAATTTGGGAGAACAAAT 966
Qy |||||
Qy 901 GTAAAT-----ATGGCAAGTATGAATTTGGTATATTAATATGAATGACCTTCTGTTCCGCT 954
Db 967 GCACCTTTCCAGGATTTGCAAGTACGAAATTTGGTTTAAATATGATGACCACTCGTTTCTGCC 1026
Qy |||||
Qy 955 ATAGAGACTGCGGTATTCCGAAGCCGCATCTACTGTGATTTCTAGAACCAACTTTACAAAT 1014
Db 1027 ATAGAGGCTGCCATTTTCAGGCTCCCGCATCTCTGATTTTCAGAACCAACTTTACAAAT 1086
Qy |||||
Qy 1015 TTTAGCACTTTCATCAGATGAGGTGCTACTAGGCATATGACTTACTGCGCGGGGCACACA 1074
Db 1087 TACAGTGCAATCAAGCGGTGAGGTAGCACTCAACATATGAATTTATGGTGGGACATAGG 1146
Qy |||||
Qy 1075 ATTCAATCTCGGCCAATAGGAGGCGGATTAATACCTCAACGATGGGTCTACCA---AT 1131
Db 1147 CTTAACTTCGCGCCCAATAGGAGGGACATTAATACCTCAACACAAAGGACTTTACTTAATAAT 1206
Qy |||||
Qy 1132 ACTTCTATTAACTCTGTAAGATTTATCATTTCTCTCGAGACGATATTGGACTGAAATCA 1191
Db 1207 ACTTCAATTAATCTGTAAACATTAACAGTTACGTCTCGAGACGTTTATAGAACAGAAATCA 1266
Qy |||||
Qy 1192 TATCAGAGTGCCTTCTATGGGAATTTACCTTGAACTTATCATGGTGCCTACTCTGTT 1251
Db 1267 AATCGAGGACAAATAT-----ACTATTACTACTCTGTGAATGAGTACCTTGGGCT 1320
Qy |||||
Qy 1252 AGATTTAATTTTAGGAACCCCTCAGAAATCTTTTGAAGAGAGTACTGTAACTATAGTCAA 1311
Db 1321 AGATTTAATTTTAAACCCCTCAGAAATTTATGAAAGAGGCGCACTACCTACAGTCAA 1380
Qy |||||
Qy 1312 CCCTATGAGTCACTCGGCTTCAATTAAGATTCAGAAACTGAAATTTACCACCGAAACA 1371
Db 1381 CCGTATCAGGAGTTGGGATTTCAATTTATTTGATTCAGAAACTGAAATTTACCACCGAAACA 1440
Qy |||||
Qy 1372 ACAGAACGACCAATTTATGAATCATATAGTACATAGGTTATCTCATATAGGCTCATTTTCA 1431
Db 1441 ACAGAACGACCAATTTATGAATCATATAGTACATAGTATTTCTCATATAGGACTAATCATTA 1500
Qy |||||
Qy 1432 CAATCTAGGGTGCATGTACCAGTATATTCTTTGGACGCAACCGTAGTCAGATCGTACAAAT 1491
Db |||||

Db 1501 GGAAACACTTTTGAGAGCACCAAGTCTATTCTTTGGACCGCATCGTAGTCAGATCGTACGAAT 1560
Qy |||||
Qy 1492 ACCATTAGTTTCAGATAGCATAAACAATAACCAATTTGGTAAATCAATTTCAACTTTAAATCA 1551
Db 1561 ACGATTGAGCAAAATAGAAATTTACAAATACCAATTTGGTAAAGCACTGAATCTTCAATTC 1620
Qy |||||
Qy 1552 GGTACCTCTGTAGTCAGTGGCCAGGATTTTACAGGAGGGGATTAATCCCGAACTAAACGTT 1611
Db 1621 GGTGTTACTGTGTGGAGGGCCAGGATTTTACAGGTGGGATATCTCTCTGTTAGAACAAAT 1680
Qy |||||
Qy 1612 AATGGTAGTGTACTAAGTATGGGTCTTAATTTTAAATAATACATCATTTACAGCGGTATCGC 1671
Db 1681 ACGGTACATTTGGAGATATACGATTAATTAATGTGCCATTTATCCCAAGATATCGC 1740
Qy |||||
Qy 1672 GTGAGAGTTCGTTATGCTGCTTCTCAAAACAATGCTCTGAGGGTAACTGTGCGAGGGAGT 1731
Db 1741 GTAAGGATTCGTTATGCTTCTACTACAGATTTACAATTTTTCACGAGATTAATTTGAAC 1800
Qy |||||
Qy 1732 ACTACTTTTGTATCAGAGATTTCCCTAGTACTATGAGTGCATAATGAGTCTTTTGACATCTCAA 1791
Db 1801 ACTGTTAATATTGTTAATTTCTCAAGAACTATGAATAGGGGGGATAATTTAGAAATATAGA 1860
Qy |||||
Qy 1792 TCATTTAGATTTGCAGAAATTTCTGTAGGTATTAGTCCATCTGSCAGTCAAACTGCTGGA 1851
Db 1861 AGTTTGAAGAACTCGAGGATTTAGTACTCTCTTTTAAATTTTAAATGCCCAAGCACATTC 1920
Qy |||||
Qy 1852 ATAAGTATAAGTAAATATGCAAGGTAGACAAACGTTTCACTTTGATAAAATTTGAATTCATT 1911
Db 1921 ACATGGGTCTCAGAGTTTTTCAAATCAGGAAGTTTATATAGATAGATGCGAAATTTGTT 1980
Qy |||||
Qy 1912 CCAATTTACTCAACCTTTCGAAGCAGATACGATTTTAGAAAGGGCGCAAGAGGCGGTGAAT 1971
Db 1981 CCAGCAGAGTTAACTTTGAGGCGAGAATATGATTTAGAAAGAGCACAAAGGCGGTGAAT 2040
Qy |||||
Qy 1972 GCTCTGTTTACTAATACGAATCCAGAGATTTGAAACAGATGTGACAGATTTATCATATT 2031
Db 2041 GCTCTGTTTACTTCTCAAAATCCAAAGAGATTTGAAACAGATGTGACAGATTTATCATATT 2100
Qy |||||
Qy 2032 GATCAAGTATCCAAATTTAGTGGGTGTTTATCGGATGAAATTTCTGTTAGATGAAAGAGA 2091
Db 2101 GACCAAGTGTCCAATATGTTGGGCATGTTTATCAGATGAATTTGCTTGGATGAGAGCGGA 2160
Qy |||||
Qy 2092 GAATTTACTTGAGAAAGTGAATATGCGAAACGACTCAGTCAATGAAAGAACTTTACTCCAA 2151
Db 2161 GAATTTATTTGAGAAAGTGAATATGCGAAGCACTCAGTCAATGAAAGAACTTTACTCCAA 2220
Qy |||||
Qy 2152 GATCCAAACTTCACATCCATCAATAGCAACACAGACTTTCATATCTACTAATAGCAATCG 2211
Db 2221 GATCCAAACTTCATTCATCAGTGGGCAATTAAGTTTCGCATCCATCGATGGCAATCA 2280
Qy |||||
Qy 2212 AATTTCACTCTATCCATGAACAAATCTGAACATGGATGGTGGGAGTGAGAACATTTACA 2271
Db 2281 AACTTCCCTCTATTTAATGAGCTATCTGAACATGGATGGTGGGAGTGCGAATGTTTACC 2340
Qy |||||
Qy 2272 ATCCAGGAAGGAATGACGTTATTTAAAGAAATTTAGCTACACTTACCGGGGACTTTTAAAT 2331
Db 2341 ATTCCAGGAAGGAATGACGTTATTTAAAGAAATTTAGCTACACTTACCGGGGACTTTTAAAT 2400
Qy |||||
Qy 2332 GAGTGTATTCGAGCGTTATTTATATCAAAAATATAGGAGAGTCCGAAATTTAAAGCTTATACT 2391
Db 2401 GAGTGTATTCGAAATTTATTTATATCAAAAATATAGGAGAGTCCGAAATTTAAAGCTTATACT 2460
Qy |||||
Qy 2392 CGCTACCAATTAAGAGGTATATTGAGATAGTCAAGATTTAGAGATATATTGATTTGATTCGT 2451
Db 2461 CGCTATCAATTAAGAGGTATATTGAGATAGTCAAGATTTAGAGATTTTAAATTTGATTTGATTCGT 2520
Qy |||||
Qy 2452 TATAATGCGAAACATGAAACATTTGATTTTCCAGGTACCGAGTCCGATGATGCGCGCTTTCA 2511
Db 2521 TACAAATGCAAGCATGAAACATTTGATTTCCAGGTACCGATTTCCCTATGCGCGCTTTCA 2580
Qy |||||
Qy 2512 GTTGAAGCCCAATCGGAAGGTGCGGAGAACCGAATCGATGCGCACACATTTTGAATGG 2571
Db 2581 GTTGAAGCCCAATCGGAAGGTGCGGAGAACCAAAATCGATGCGCACCAATTTTGAATGG 2640

Db 247 AACATAGCTGGTAGAATATTGGCGGTATAGGTGTGCGGTTTGTGACCACTAGCTAGT 306
Qy |||||
Db 241 TTTTATAGTTTTCTTTGTTGGTGAATATTGGCCCGCGCAGAGATCAGTGGGAAATTTTC 300
Qy |||||
Db 307 TTTTATAGTTTTCTTTGTTGGGAATATTGGCTAGTGGCAGAGATCCATGGGAATTTTC 366
Qy |||||
Db 301 CTAGAACATGTGCAACAACTTATAATCAACAATAACAGAAATGTGGAATACGGCA 360
Qy |||||
Db 367 CTGGAACATGTAGAACAACTTATAAGAACAAACAGTAAACAGAAAATACTAGGAATACGGCT 426
Qy |||||
Db 361 CTTGCTCGATTACAGGTTTAGGAGATTCCTTTAGAGCCTATCAACAGTCACTTGAAGAT 420
Qy |||||
Db 427 ATTGCTCGATTAGAAAGTCTAGGAAGAGGCTATAGATCTTACCAGCAGGCTCTTGAAGT 486
Qy |||||
Db 421 TGGCTAGAAAACCGGTATGATGCAAGAACGAGAAAGTGTCTTTATATACCCAAATATAGCC 480
Qy |||||
Db 487 TGGTTAGATAACCGAATGATGCAAGATCAAGAGCATTTCTTGAGCGCTATGTTGCT 546
Qy |||||
Db 481 TTAGAACTTGATTTTTCTTTAATGCGATGCGCTTTTTCGCAATTAAGAAACCAAGAGTTCCA 540
Qy |||||
Db 547 TTAGAACTTGCACTTACTGCTATATACCGCTTTTTCAGAAATACGAAATGAAGAGTTCCA 606
Qy |||||
Db 541 TTATTATGTTATGCTCAAGCTGCAAAATTTACACCTATTTATTTGAGAGTGCCTCT 600
Qy |||||
Db 607 TTATTATGTTATGCTCAAGCTGCAAAATTTACACCTATTTATTTGAGAGAGCGCATCC 666
Qy |||||
Db 601 CTTTTCGTAGTGAATTTGGGCTTTACATCGCAGGAAATTCACCGTTATTATGAGCGCAA 660
Qy |||||
Db 667 CTTTTCGTAGTGAATTTGGGAGATGCGCATCTCCGATGTTAACCAATATTACCAGAACAA 726
Qy |||||
Db 661 GTGGAACAAACGAGAGATTTTCGACTATTGCGTAGAATGGTATATACAGGTCCTAAAT 720
Qy |||||
Db 727 ATCAGATATACAGAGGAATATTCAAACCATGCGTACAATGGTATATACAGGCTAAAT 786
Qy |||||
Db 721 AGCTTGAGAGGACAAATGCGCAAGTTGGTGGCTTATTAATCAATTCGTTAGAGATCTA 780
Qy |||||
Db 787 AACTTAAAGAGGACAAATGCTGAAAGTTGGTGGCTATTAATCAATTCGTTAGAGACCTA 846
Qy |||||
Db 781 ACGTTAGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGACACTCGCACCTTATCCA 840
Qy |||||
Db 847 ACGTTAGGGTATTAGATTTAGTAGCCCTATTCCCAAGCTATGATCTCGCACCTTATCCA 906
Qy |||||
Db 841 ATAAATACGAGTGTCTCAGTTAAACAAGGGAAGTTTATACAGCGCAATTTGGAGCAACAGG 900
Qy |||||
Db 907 ATCAATACGAGTGTCTCAGTTAAACAAGAGAAATTTATACAGATCCAAATTTGGGAGAACAA 966
Qy |||||
Db 901 GTAAT-----ATGGCAAGTATGAATGGTATTAATTAATGAATGCACTTCTGTTCCGCT 954
Qy |||||
Db 967 GCACCTTCAGGATTTGCAAGTACGAAATGGTAAATTAATGAATGCACTTCTGTTCCGCT 1026
Qy |||||
Db 955 ATAGAGACTCGGTTATCCGAAGCCGCATCTACTGATTTCTAGAACCAACTTACAAAT 1014
Qy |||||
Db 1027 ATAGAGCTGCAATTTTCAGGCTCCGCACTCTCTGATTTTCAGAACCAACTTACAAAT 1086
Qy |||||
Db 1015 TTTAGCACTTTCATCAGATGAGGTGCTACTAGGCATATGACTTACTGGCGGGGCACACA 1074
Qy |||||
Db 1087 TACAGTGCATCAAGCGTTGGAGTAGCACTCAACATATGAATTTATGGTGGGACATAGG 1146
Qy |||||
Db 1075 ATTCAATCTCGGCCAATAGGAGGCGGATTAATACCTCAACGCAATGGGTCTACCA---AT 1131
Qy |||||
Db 1147 CTTAACTTCGCCCCAATAGGAGGACATTAATACCTCAACACAAGGACTTACTTAATAAT 1206
Qy |||||
Db 1132 ACTTCTATTATCTGTGAAGATTATCACTTCTCTCGAGCGTATATGAGCTGAATCA 1191
Qy |||||
Db 1207 ACTTCAATTAATCTGTGAACATTAACAGTTTACAGTCTCGAGACGTTTATAGAACAGAAATCA 1266
Qy |||||
Db 1192 TATCAGAGAGTCTTCTATGGGAAATTTACCTGAACCTTATTCATGGTGTCCCTACTGTT 1251
Qy |||||
Db 1267 AATCAGGGACAAATAT-----ACTATTACTACTCTGTGAATGAGTACCTTTGGCT 1320
Qy |||||
Db 1252 AGATTTAATTTTAGGAACCCCTCAGAAATCTTTTGAAGAGAGTACTGTCTAACTATAGTCAA 1311
Qy |||||

Db 1321 AGATTTAATTTTATAAAACCCCTCAGAAATATTTATGAAAGAGCGGCCACTACCTACAGTCAA 1380
Qy |||||
Db 1312 CCCTATCAGTCACTCGTGGCTTTCAATTTAAAAGATTTCAGAAAATGAAATACCAACGAGAACAA 1371
Qy |||||
Db 1381 CCGTATCAGGGAGTTGGGATTTCAATTTATTTGATTTTCAGAAAATGAAATACCAACGAGAACAA 1440
Qy |||||
Db 1372 ACAGAACGACCAAAATTTATGAATCATATAGTCAATAGTTTCTCATTAGGCTCATTTCA 1431
Qy |||||
Db 1441 ACAGAACGACCAAAATTTATGAATCATATAGTCAATAGTATTTCTCATATAGGACTAATCAT 1500
Qy |||||
Db 1432 CAATCTAGGCTGCATGTACCAGTATATTTCTTGGACGCAACGCTAGTGCAGATCGTACAAAT 1491
Qy |||||
Db 1501 GGAACAACTTTGAGAGCACCAGTCTATCTTGACGCAATCTGATGAGATCGTACGAAAT 1560
Qy |||||
Db 1492 ACCATTTAGTTCAGATAGCATAAACAATAACCAATTTGTTAAATCATTTCAACCTTTAATTTCA 1551
Qy |||||
Db 1561 ACGATTTGGAACCAATAGAAATTTACAAATACCAATTTGTTGTTAAAGCACATGAATCTTTCA 1620
Qy |||||
Db 1552 GGTACCTCTGCTAGTCACTGCGCCAGGATTTTACAGGAGGGGATATATCCCGAACTAACGTT 1611
Qy |||||
Db 1621 GGTGTTACTGTTGTTGGAGGCGCAGGATTTTACAGGTTGGGATATCTCTCGTAGAACAAAT 1680
Qy |||||
Db 1612 AATGGTAGTGTACTAAGTATAGGTTCTTAAATTTTAAATTAATCATCATACAGCGGTATCGC 1671
Qy |||||
Db 1681 ACGGTTACATTTGGAGATATACGATTTAAATATTAATGTGCCATTTATCCAAAGATATCGC 1740
Qy |||||
Db 1672 GTGAGAGTTCGTTATGCTGCTTCTCAAAACAATGGTCTCGAGGGTAACTGTCGAGGGAGT 1731
Qy |||||
Db 1741 GTAAGGATTCGTTATGCTTCTACTACAGATTTTACAAATTTTTCACGAGAAATTAATGGAAC 1800
Qy |||||
Db 1732 ACTACTTTTGTATCAAGGATTCCTCTAGTACTATGAGTGCATAATGAGTCTTTGACATCTCAA 1791
Qy |||||
Db 1801 ACTGTTAATATTGGTAAATTTCTCAAGAACTATGAATAGGGGGGATAAATTTAGAAATATAGA 1860
Qy |||||
Db 1792 TCAATTTAGATTTTCAGAAATTTCTGTAGTATTTAGTGCATCTGSCAGTCAAACTGCTGA 1851
Qy |||||
Db 1861 AGTTTTAGAACTGCGAGGATTTAGTACTCTCTTTTAAATTTTTTAAATGCCAAAGCACATTC 1920
Qy |||||
Db 1852 ATAAGTATAAGTAAATATGCAAGTAGACAAACCGTTTCACTTTGATAAAATTTGAATTCAT 1911
Qy |||||
Db 1921 ACATGGGTGCTCAGAGTTTTTCAATCAGGAGTTTATATAGATAGAGTCGAATTTGTT 1980
Qy |||||
Db 1912 CCAATTTACTGCAACCTTTCGAAGCAGAAATACGATTTAGAAAAGGCGCAAGAGCGGTGAAT 1971
Qy |||||
Db 1981 CCAGCAGAGTAAATTTGAGGCAAGATATGATTTAGAAAAGAGCACAAAAGCGGTGAAT 2040
Qy |||||
Db 1972 GCTCTGTTTACTTAATACGAATCCAGAGATTTGAAAACAGATGTGACAGATTTATCATATT 2031
Qy |||||
Db 2041 GCTCTGTTTACTTCTTACAAATCCAAAGAGATTTGAAAACAGATGTGACAGATTTATCATATT 2100
Qy |||||
Db 2032 GATCAAGTATCCAAATTTAGTGGCGTGTATTCGATGAATTTCTGTTAGATGAAAAGAGA 2091
Qy |||||
Db 2101 GACCAAGTGTCCAAATATGTTGGCATGTTTATCAGATGAATTTGCTTGGATGAGAGCGA 2160
Qy |||||
Db 2092 GAATTTACTGAGAAAAGTGAATATGCGAAACGACTCAGTGAATGAAAGAAATTTACTCTCAA 2151
Qy |||||
Db 2161 GAATTTATTTGAGAAAAGTGAATATGCGAAGCGACTCAGTGAATGAAAGAAATTTACTCTCAA 2220
Qy |||||
Db 2152 GATCCAACTTCATCCTCAATTAAGCAACCGACTTTCATATCTACTTAATGAGCAATCG 2211
Qy |||||
Db 2221 GATCCAACTTCATCCTCAATTAAGTGGGCAATTAAGTTTCGATCCATCGATGGCAATCA 2280
Qy |||||
Db 2212 AATTTACATCTATCCATGAACCAATCTGAACATCGATGGTGGGGAAGTAGAGAAATTTACA 2271
Qy |||||
Db 2281 AACTTCCCTCTATTAATGAGCTATCTGAACATGATGTTGGGGAAGTGGCAATGTTACC 2340
Qy |||||
Db 2272 ATCCAGGAAGAAATGACGTATTTAAAGAAATTTACGTCACTTACCGGGGACTTTTAAAT 2331
Qy |||||
Db 2341 ATTCCAGGAAGGAATGACGTATTTAAAGAAATTTACGTCACTTACCGGGTACTTTTAAAT 2400
Qy |||||
Db 2332 GAGTGTATTCCGAGCTATTTATCAAAAATAGGAGAGTCCGAAATTTAAAGCTTACT 2391
Qy |||||
Db 2401 GAGTGTATTCCAAATTTATATATCAAAAAATAGGAGAGTCAAGAAATTTAAAGCTTATACG 2460
Qy |||||

QY 2392 CGTACCAATTAGAGGGTATATTGAAGATAGTCAAGATTTAGAGATATATTGATTCGT 2451
 Db |||||
 QY 2461 CGCTATCAATTAAGAGGGTATATTGAAGATAGTCAAGATCTAGAGATTTATTAAATTCGT 2520
 Db |||||
 QY 2452 TATAATCGGAAACATGAAACATTGGATGTTCCAGGTACCGAGTCCGTATGCGCGCTTCA 2511
 Db |||||
 QY 2521 TACAATGCCAAGCATGAAACATTGGATGTTCCAGGTACCGATTTCCCTATGCGCGCTTCA 2580
 Db |||||
 QY 2512 GTTGAAGCCCAATCGGAAGGTGCGGAGAACCGAATCGATCGCGCACACATTTTGAATGG 2571
 Db |||||
 QY 2581 GTTGAAGCCCAATCGGAAGGTGCGGAGAACCAATCGATCGCGCACACATTTTGAATGG 2640
 Db |||||
 QY 2572 AATCCTGATCTAGATTGTTCTCGCAGAGATGAGAGAAAATGTGCGCATCAATCCCATCAT 2631
 Db |||||
 QY 2641 AATCCTGATCTAGATTGTTCTCGCAGAGATGAGAGAAAGATGTGCGCATCAATCCCATCAT 2700
 Db |||||
 QY 2632 TTCTCTTTGATATTTGATATTTGATATGACAGACTTGCATGAGAAATCTAGCGGTGTTGGTG 2691
 Db |||||
 QY 2701 TTCACCTTTGATATTTGATATTTGATATTTGATATTTGATATTTGATATTTGATATTTGAT 2760
 Db |||||
 QY 2692 GTATTCAGGATTAAGACGAGGAGGTCTATGCAAGCTAGCGAATCTGGAATTTATTGAA 2751
 Db |||||
 QY 2761 GTATTCAGGATTAAGACGAGGAGGTCTATGCAAGCTAGCGAATCTGGAATTTATTGAA 2820
 Db |||||
 QY 2752 GAGAAACCATTTATTAGGAGAGCACTGCTCTGTTGAGAGAGCAGAGAGAAAATTTGAGA 2811
 Db |||||
 QY 2821 GAGAAACCATTTATTAGGAGAGCACTGCTCTGTTGAGAGAGCAGAGAGAAAATTTGAGA 2880
 Db |||||
 QY 2812 GACAAAGTGAAGAACTACAAATTTGAGAAACAAACAGAGATATACAGAGGCAAAAGAGCT 2871
 Db |||||
 QY 2881 GACAAAGTGAAGAACTACAAATTTGAGAAACAAACAGAGATATACAGAGGCAAAAGAGCT 2940
 Db |||||
 QY 2872 GTGAGTCTTTATTGTTAGATTTCTCAATATAAGATTACAAGCGGATACAACATTTGGC 2931
 Db |||||
 QY 2941 GTGAGTCTTTATTGTTAGATTTCTCAATATAAGATTACAAGCGGATACAACATTTGGC 3000
 Db |||||
 QY 2932 ATGATTCATCGCGCAGATAAACTTTGTTCAATCGAATTCGAGAGGCTTATCTGTGAGAAATTA 2991
 Db |||||
 QY 3001 ATGATTCATCGCGCAGATAAACTTTGTTCAATCGAATTCGAGAGGCTTATCTTTCAGAAATTA 3060
 Db |||||
 QY 2992 TCTGTTATCCGGGTGTAATGCGGAAATTTTGAAGAAATAGAGGTCCGATATCACT 3051
 Db |||||
 QY 3061 CCGTGTATCCCGGTGTAATGCGGAAATTTTGAAGAAATAGAGGTCAATATCACT 3120
 Db |||||
 QY 3052 GCAATCTCCCTATACGATGCGAGAAATGTCGTTAAATAATGTTGATTTAATAATGATTA 3111
 Db |||||
 QY 3121 GCAATGTCCTTATACGATGCGAGAAATGTCGTTAAATAATGTTGATTTAATAATGATTA 3180
 Db |||||
 QY 3112 GCATGCTGGAATGTAAAGGGCATGTAGATGTACAACAGAGCCATCACCGTTTCTGTCTTT 3171
 Db |||||
 QY 3181 ACATGTTGGAATGTAAAGGGCATGTAGATGTACAACAGAGCCATCATCTTCTGACCTT 3240
 Db |||||
 QY 3172 GTTATCCGAATGCGGAGCAGAGATGTACAAGAGTTCGCTCTGTCGGGGCGTGGC 3231
 Db |||||
 QY 3241 GTTATCCGAATGCGGAGCAGAGATGTACAAGAGTTCGCTCTGTCGGGGCGTGGC 3300
 Db |||||
 QY 3232 TATATCTCTCGTGTACAGAGGTACAAGAGGATATGAGAGGCTTCTGTAAACGATCCAT 3291
 Db |||||
 QY 3301 TATATCTCTCGTGTACAGAGGTACAAGAGGATATGAGAGGCTTCTGTAAACGATCCAT 3360
 Db |||||
 QY 3292 GAAATCCGAGAACATACAGAGCACTAAAATTTTAAACCTGTGAAGAGAGGAGTGTAT 3351
 Db |||||
 QY 3361 GAAATCCGAGAACATACAGAGCACTAAAATTTTAAACCTGTGAAGAGAGGAGTGTAT 3420
 Db |||||
 QY 3352 CCAACGGATACAGAAAGTGTATGATTTATCTGCAACCAAGGTACAGAGATGTAT 3411
 Db |||||
 QY 3421 CCAACGGATACAGAAAGTGTATGATTTATCTGCAACCAAGGTACAGAGATGTAT 3480
 Db |||||
 QY 3412 TCCCGTAACTCGATATGAGATGATATGATTTGATATGATTTGATATGATTTGATATGATTTGAT 3471
 Db |||||
 QY 3481 TCCCGTAACTCGATATGAGATGATATGATTTGATATGATTTGATATGATTTGATATGATTTGAT 3540
 Db |||||

QY 3472 AAACCCGACTTATGAAGAGAAACGTTATACAGATGTACGAGAGATATATCATTTGTAATAT 3531
 Db |||||
 QY 3541 AAACCCGACTTATGAAGAGAAACGTTATACAGATGTACGAGAGATATATCATTTGTAATAT 3600
 Db |||||
 QY 3532 GACAGAGGGTATCTGAATTTATCCACCACCTACACAGCTGGTTATATGACAAAAGAAATTAGAA 3591
 Db |||||
 QY 3601 GACAGAGGGTATCTGAATTTATCCACCACCTACACAGCTGGTTATATGACAAAAGAAATTAGAA 3660
 Db |||||
 QY 3592 TACTTCCCAGAAACCGAATAGGTATGAGATTGAGATTGGAGAAACGGAAGGAAAGTTTATT 3651
 Db |||||
 QY 3661 TACTTCCCAGAAACCGAATAGGTATGAGATTGAGATTGGAGAAACGGAAGGAAAGTTTATT 3720
 Db |||||
 QY 3652 GTAGACAGCGTGAATTTACTCTTATGAGGAATAG 3687
 Db |||||
 QY 3721 GTAGATAGCGTGAATTTACTCTTATGAGGAATAG 3756
 Db |||||
 RESULT 9
 AAT95051
 ID AAT95051 standard; DNA; 3934 BP.
 XX
 AC AAT95051;
 XX
 DT 17-FEB-1998 (first entry)
 XX
 DE DNA encoding Bacillus thuringiensis crystal toxin CryET5.
 XX
 KW EG7283; crystal toxin; CryET5; lepidopteran pest; Lymantria dispar;
 KW Ostrinia nubilalis; Pseudoplusia includens; Plutella xylostella;
 KW Spodoptera exigua; Spodoptera frugiperda; Trichoplusia ni; ds.
 XX
 OS Bacillus thuringiensis.
 XX
 FH Location/Qualifiers
 FT CDS
 FT /*tag= a
 FT /product= "CryET5"
 XX
 US US5679343-A.
 XX
 PD 21-OCT-1997.
 XX
 PF 07-JUN-1995; 95US-00474038.
 XX
 PR 29-JUL-1993; 93US-00100709.
 PR 30-DEC-1993; 93US-00176865.
 XX
 PA (MONS) MONSANTO CO.
 XX
 PI Jany CS, Gonzalez JM, Donovan WP, Tan Y;
 XX
 DR WPI; 1997-525682/48.
 DR P-PSDB; AAW35259.
 XX
 PT Lepidopteran toxic Bacillus thuringiensis crystal protein - useful to
 PT control Lepidopteran pests.
 XX
 PS Example 2; Fig 2; 50pp; English.
 XX
 CC The present sequence encodes the Bacillus thuringiensis EG7283 crystal
 CC toxin CryET5, which, optionally in association with B. thuringiensis
 CC EG7283, can be used against lepidopteran pests. CryET5 is especially
 CC useful for controlling Lymantria dispar, Ostrinia nubilalis, Pseudoplusia
 CC includens, Plutella xylostella, Spodoptera exigua, Spodoptera frugiperda
 CC and Trichoplusia ni
 XX
 SQ Sequence 3934 BP; 1347 A; 650 C; 841 G; 1096 T; 0 U; 0 Other;
 Query Match 72.9%; Score 2687.2; DB 2; Length 3934;
 Best Local Similarity 83.5%; Pred. No. 0;
 Matches 3088; Conservative 0; Mismatches 593; Indels 15; Gaps 3;
 QY 1 TTGACTTCAATAAGGAAAAATGAGATGAATTAATGCTTTATCGATTCGAGCTGTA 60

2212 AATTTCACATCTATCCATGACCAATCTGAACATGGATGGTGGGAAAGTGAGAACATTTACA 2271
 2281 AACTTCCCTCTATTAATGAGCTATCTGAACATGGATGGTGGGAAAGTGAGAACATTTACC 2340
 2272 ATCCAGGAAGAAATGACGATTTAAAGAAATTAAGTACATCACTACCGGGAATTTTAAT 2331
 2341 ATTCCAGGAAGGAATGACGATTTAAAGAAATTAAGTACATCACTACCGGGAATTTTAAT 2400
 2332 GAGTGTATCCGACGATTTATATCAAAAATAGGAGAGTCGGAATTTAAAGCTTATCT 2391
 2401 GAGTGTATCCAAATTTATATCAAAAATAGGAGAGTCGGAATTTAAAGCTTATACG 2460
 2392 CGCTACCAATTAAGAGGATATTTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGT 2451
 2461 CGCTATCAATTAAGAGGATATTTGAAGATAGTCAAGATTTAGAGATATTTGATTCGT 2520
 2452 TATAATCGGAAACATGAACATTTGGATTTCCAGGTACCGAGTCCGATGCGCGCTTTCA 2511
 2521 TACAATGCAAGCATGAACATTTGGATTTCCAGGTACCGATTCCTATGCGCGCTTTCA 2580
 2512 GTTGAAGCCCAATCGAAGTCCGAGACCGAATCGATCGCACACATTTTGAATGG 2571
 2581 GTTGAAGCCCAATCGAAGTCCGAGACCGAATCGATCGCACACATTTTGAATGG 2640
 2572 AATCCTGATCTAGATTTGCTCCTGCAGAGATGGAGAAAATGTGCGCATCATTTCCCATCAT 2631
 2641 AATCCTGATCTAGATTTGCTCCTGCAGAGATGGAGAAAATGTGCGCATCATTTCCCATCAT 2700
 2632 TTCTTTGGATTTGATTTGATTTGATGCAAGATTTGATGATGATGATGATGATGATGATGAT 2691
 2701 TTCACTTTGGATTTGATTTGATTTGATGCAAGATTTGATGATGATGATGATGATGATGAT 2760
 2692 GTATTCAGATTTAGAGCGAGAGGTCATGCAAGATTTGATGATGATGATGATGATGATGAT 2751
 2761 GTATTCAGATTTAGAGCGAGAGGTCATGCAAGATTTGATGATGATGATGATGATGATGAT 2820
 2752 GAGAAACCATTTATAGAGAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2811
 2821 GAGAAACCATTTATGAGAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2880
 2812 GACAAAGTGAAGAACTACAAATTTGGAACAAACGAGTATATACAGAGGCAAAAGAGCT 2871
 2881 GACAAAGTGAAGAACTACAAATTTGGAACAAACGAGTATATACAGAGGCAAAAGAGCT 2940
 2872 GTGAGTCTTTATTTGATGATTTCTCAATATAAGATTTACAGCGGATACAAACATTTGCG 2931
 2941 GTGAGTCTTTATTTGATGATTTCTCAATATAAGATTTACAGCGGATACAAACATTTGCG 3000
 2932 ATGATTCATCGCGGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 2991
 3001 ATGATTCATCGCGGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 3060
 2992 TCTGTTATCCCGGTTAAATGCGGAAATTTTGAAGAAATTAAGAGTTCGATTTACCT 3051
 3061 CCGTATTCAGGTTGATTTGCGGAAATTTTGAAGAAATTAAGAGTTCGATTTACCT 3120
 3052 GCAATCTCCCTATACGATGCGAGAAATGCTGTTTAAAGAAATGCTGATTTTAAATGATTA 3111
 3121 GCAATGCTCTTATACGATGCGAGAAATGCTGTTTAAAGAAATGCTGATTTTAAATGATTA 3180
 3112 GCAATGCTGGAATTAAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3171
 3181 ACAATGTTGAATGTAAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3240
 3172 GTTATCCAGAAATGGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3231
 3241 GTTATCCAGAAATGGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3300
 3232 TATATCTCCGTTGTCAGAGGATCAAGAGGATGATGATGATGATGATGATGATGATGATGATGAT 3291
 3301 TATATCTCTGTTGTCAGAGGATCAAGAGGATGATGATGATGATGATGATGATGATGATGATGAT 3360

3292 GAAATCCAGAACAAATACAGACGAACCTAAATTTAAACCTGTGAAGAGGAAAGTGTAT 3351
 3361 GAAATCCAGAACAAATACAGACGAACCTAAATTTAAACCTGTGAAGAGGAAAGTGTAT 3420
 3352 CAAACCGATACAGAACGTTGATTTATGATTTATCTGCAACCAAGGTACAGAGTATGTAAT 3411
 3421 CAAACCGATACAGAACGTTGATTTATGATTTATCTGCAACCAAGGTACAGAGTATGTAAT 3480
 3412 TCCCGTAAATGCTGGATATGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 3471
 3481 TCCCGTAAATGCTGGATATGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 3540
 3472 AAACCGACTTTATGAAGAGAAACGTTATACAGATGATGATGATGATGATGATGATGATGAT 3531
 3541 AAACCGACTTTATGAAGAGAAACGTTATACAGATGATGATGATGATGATGATGATGATGAT 3600
 3532 GACAGAGGTATGTAATTTATCCACCACTACCAAGTATGATGATGATGATGATGATGATGATGAT 3591
 3601 GACAGAGGTATGTAATTTATCCACCACTACCAAGTATGATGATGATGATGATGATGATGATGAT 3660
 3592 TACTTCCAGAAACCGATTAAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 3651
 3661 TACTTCCAGAAACCGATTAAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 3720
 3652 GTAGACAGCGTGAATTTACTTCTTATGAGGAATAG 3687
 3721 GTAGATAGCGTGAATTTACTTCTTATGAGGAATAG 3756

RESULT 10
 AAT68434
 ID AAT68434 standard; DNA; 3934 BP.
 XX AAT68434;
 AC AAT68434;
 XX AAT68434;
 DT 25-MAR-2003 (revised)
 DT 07-JUL-1997 (first entry)
 XX CryET5 gene.
 XX CryET5 gene.
 KW CryET5; cryET4; Bacillus thuringiensis; insecticidal crystal protein;
 ICP; toxin; CryI protein; lepidopteran insect; insecticide; ds.
 XX Bacillus thuringiensis.
 XX Key Location/Qualifiers
 CDS 67..3756
 FT /*tag= a
 FT /product= "cryET5"
 FT
 XX US5616319-A.
 XX
 XX 01-APR-1997.
 XX
 XX 30-DEC-1993; 93US-00176865.
 XX
 XX 29-JUL-1993; 93US-00100709.
 XX
 XX (MONS) MONSANTO CO.
 XX
 XX Gonzalez JM, Donovan WP, Tan Y, Jany CS;
 WPI; 1997-212077/19.
 DR P-PSDB; AAW17699.
 XX
 XX Bacillus thuringiensis cryET5 gene encoding insecticidal protein - useful
 for control of lepidopteran pests.
 XX
 XX Claim 2; Fig 2; 50pp; English.
 XX
 XX This sequence represents the cryET5 gene of Bacillus thuringiensis (B.t.)
 isolate EG5847. B.t. produces inclusions during sporulation which include
 insecticidal crystal proteins (ICP). ICP toxins are active in insects

CC only after ingestion. Once ingested, the toxic components disrupt the
 CC midgut cells, resulting in cessation of feeding, and eventually death.
 CC The CryI proteins produced by B.t. are active against lepidopteran
 CC insects. The protein encoded by this sequence, and the CryET4 protein
 CC (see AAW17700) belong to the CryI family of ICPs. This sequence can be
 CC used to transform bacteria, which are useful as insecticides against a
 CC wide range of lepidopteran pests, and can be applied to crops, soil and
 CC seeds. The encoded protein, or especially its toxic N terminal region,
 CC can be expressed in plants, to provide protection against lepidopteran
 CC pests. This sequence, or its fragments, can also be used to isolate other
 CC similar genes. (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 3934 BP; 1347 A; 650 C; 841 G; 1096 T; 0 U; 0 Other;

Query Match 72.9%; Score 2687.2; DB 2; Length 3934;
 Best Local Similarity 83.5%; Pred. No. 0;
 Matches 3088; Conservative 0; Mismatches 593; Indels 15; Gaps 3;

QY	1	TTGACTTCAAAATAGGAAATGAGAAATGAAATTAATTAATGCTTTATCGATCCAGCTGTA	60
DB	67	TTGACTTCAAAATAGGAAATGAGAAATGAAATTAATTAATGCTTTATCGATCCAAACGGTA	126
QY	61	TCGAATCATTTCCACACAAATGGATCTATCACAGATGCTGTAATTGAGGATCTTTGTGT	120
DB	127	TCGAATCTTCCAGCGAAATGAATCTATCACAGATGCTGTAATTGAGATAGCTTGTGT	186
QY	121	ATAGCCGAGGGGAATAATATCAATCCACTTGTGTAGCGCATCAACAGTCCAAACGGGTATT	180
DB	187	GTAGCCGAGGTGAACATATTGATCCATTTGTTAGCGCATCAACAGTCCAAACGGGTATA	246
QY	181	AACATAGCTGTAGAAATCTAGGTGTAATTAGGCGTACCGTTTGTGACAAATAGCTAGT	240
DB	247	AACATAGCTGTGTAATATTGGCGTATTAGGTGTGCGGTTTGTGCGACAACTAGCTAGT	306
QY	241	TTTTATAGTTTTCTTGTGTGTAATTATGCGCGCGCGAGAGATCAGTGGGAAATTTTC	300
DB	307	TTTTATAGTTTTCTTGTGTGGGAATTAATGCGCTAGTGGCAGATCATCGGAAATTTTC	366
QY	301	CTAGAACATGTCGAACAACTTATAAATCAACAAATAACAGAAATGCTAGGAATACGGCA	360
DB	367	CTGGAACATGTAGAACAACTTATAAGACACACAGTAACAGAAATCTAGGAATACGGCT	426
QY	361	CTTGCTCGATTAACAGTTTATAGGATTCCTTTAGAGCCTATCAACAGTCACTTGAAGAT	420
DB	427	ATTGCTCGATTAGAAAGTCTAGGAAGAGGCTATAGATCTTACCAGCAGGCTCTTGAAC	486
QY	421	TGCGTAAACCGTGTATGATGCAAGAACGAGTGTCTTTATATACCCCAATATAGCC	480
DB	487	TGCTTAGATAACCGAAATGATGCAAGATCAAGAGCATTTCTTGAGCGCTATGTGCT	546
QY	481	TTAGAACTTGATTTCTTAATGCGATCGCGCTTTTCGCAATTAGAAACCAAGAGTTCCA	540
DB	547	TTAGAACTTGACATTACTGCTATACCGCTTTTCAGAAATACGAATGAAAGATTCCA	606
QY	541	TTATTATGTTATGCTCAAGCTGCAAAATTTACACCTATTATATTGAGAGATGCTCT	600
DB	607	TTATTATGTTATGCTCAAGCTGCAAAATTTACACCTATTATATTGAGAGATGCTCT	666
QY	601	CTTTTGTGTTAGTGAATTTGGGCTTACATCCGAGAAATTTCAACGTTATTATGAGCGCAA	660
DB	667	CTTTTGTGTTAGTGAATTTGGGCTTACATCCGATTTTCAACAAATATTACCAAGAACAA	726
QY	661	GTGGAACAAACGAGAGATTTTCGACTATTTCGTAGAAATGGTATATAACAGTCTTAAAT	720
DB	727	ATCAGATATACAGAGATTTCTAACCATTTGGTACAAATGGTATATAACAGGCTAAT	786
QY	721	AGCTTGAGAGGGAACAAATGCGCAAGTTGGTGGCTTTAATCAATCCGTAGAGATCTA	780
DB	787	AACTTAAGAGGGAACAAATGCTGAAATTTGGTGGCTTAAATCAATCCGTAGAGACCTA	846
QY	781	ACGTTAGGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGACACTCGCACTTATCCA	840
DB	847	ACGTTAGGGGTATTAGATTTAGTGGCTATTCCCAAGCTATGATGATGATGCGACTTATCCA	906

QY	841	ATAAATACGAGTGTCTAGTTTAAACAGGAAAGTTTATACAGACGCAATTTGGAGCAACAGG	900
DB	907	ATCAATACGAGTGTCTAGTTTAAACAGGAAATTTATACAGATCCAAATTTGGAGCAACAA	966
QY	901	GTAAT-----ATGGCAAGTATGAATGGTATTAATTAATTAATTAATTAATTAATTAAT	954
DB	967	GCACCTTCAGGATTTGCAAGTAGCAATTTGGTATTAATTAATTAATTAATTAATTAATTAAT	1026
QY	955	ATAGAGACTCGGTTATCCGAAGCCCGCATCTACTTGAATTTTCTAGAACAACTTTACAAAT	1014
DB	1027	ATAGAGCTGCCATTTTCAGCCCTCCGCACTACTTGAATTTTCCAGAACAACTTTACAAAT	1086
QY	1015	TTTAGCATTTCATCAGATGAGTGTCTATAGGATATAGACTTACTGCGGGGGGCAACA	1074
DB	1087	TACAGTGCATCAAGCCGTTGGAGTAGCACTCAACATATGAATTTATTTGGTGGGACATAGG	1146
QY	1075	ATTCAATCTCGGCAATAGGAGCGGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1131
DB	1147	CTTAACCTTCGCGCAATAGGAGGGACATTAATTAATTAATTAATTAATTAATTAATTAAT	1206
QY	1132	ACTTCTAATTAATCTGTGAATTTATCAATCTTCTCTCGAGACGTATATTGGACTGAATCA	1191
DB	1207	ACTTCAATTAATCTGTGAATTTACAGTTTACGCTCTCGAGACGTATTATAGAACAGATCA	1266
QY	1192	TATGCGAGAGTGTCTTATGCGGAAATTTACCTTGAACCTATTCAATGATGCTGCTTACTGT	1251
DB	1267	AATGCGAGGACAAATAT-----ACTATTACTACTCTCTGTAATGGATGACTTGGGCT	1320
QY	1252	AGATTAATTTTAGGAACTCTCAGATTAATTTTGAAGAGGTACTGCTAATATAGTCAAA	1311
DB	1321	AGATTAATTTTATAAACCTCAGATTAATTTTGAAGAGGCGCCACTACTACAGTCAAA	1380
QY	1312	CCCTATGAGTCACCTGGGCTTCAATTTAAAAGATTTCAGAAATCTGAATTTACCAACAGAA	1371
DB	1381	CCGTATCAGGAGTGGGATTCATTTATTTGATTCAGAAATCTGAATTTACCAACAGAA	1440
QY	1372	ACAGAACGACCAATTAATGAATCATATAGTTCATAGGTTATCTCACATAGGCTCATTTCA	1431
DB	1441	ACAGAACGACCAATTAATGAATCATATAGTTCATAGTTCATCATATAGGACTAATCATA	1500
QY	1432	CAATCTAGGCTGATGATCCAGTATATTCTTGACGCGCAGTGTAGTCAGATCGTACAAT	1491
DB	1501	GGAACACCTTTGAGAGCACCAAGTCTATTCTTGACGCGCATCTGTGCGAGATCGTACGA	1560
QY	1492	ACCATTAGTTTCAGATAGCATAACACAAATACCAATTTGTAATAATCATTTCAACCTTAA	1551
DB	1561	ACGATTTGACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	1620
QY	1552	GGTACCTCTGTAGTGGCCCGCAGGATTTTACAGGAGGGGATATAATTCGAACTTAACG	1611
DB	1621	GGTGTACTTGTGTTGGAGGCGCAGGATTTTACAGGTTGGGATATCTTCTCGTAGAACAA	1680
QY	1612	AATGGTAGTGTACTAAGTATGGTCTTAATTTTAATTAATTAATTAATTAATTAATTAATTA	1671
DB	1681	ACGGTACATTTTGGAGATATACGATTAATTAATTAATTAATTAATTAATTAATTAATTA	1740
QY	1672	GTGAGAGTTGTTATGCTGCTCTCAACAAATGCTCTGAGGTTAATCTGCGGGGAGT	1731
DB	1741	GTAAGGATTCGTTATGCTTCTACTACAGATTTACAATTTTTCACGAGAAATTAATGGA	1800
QY	1732	ACTACTTTTGTATCAAGGATTCCTTAGTACTATGAGTGCATAATGAGTCTTTGACATCTCA	1791
DB	1801	ACTGTTAATTTGGTAAATTTCTCAAGAACATTAATTAATTAATTAATTAATTAATTAATTA	1860
QY	1792	TCATTTAGATTTGCAGAAATTTCTGTAGGTTATTTAGTGCATCTGGCAGTCAAACTGCTG	1851
DB	1861	AGTTTTAGAACTGCAGGATTTAGTACTCTCTTTTAAATTTTAAATGCCCCAAGCAATTC	1920
QY	1852	ATAAGTATAAGTAAATTAATGAGGTAGCAACAACTTTTCACTTTGATTAATAATTTGAT	1911
DB	1921	ACATGGGTGCTCAGAGTTTTCATAATCAGGAAGTTTATATAGATAGTGCAGATTTGTT	1980

QY	1912	CCAATTACTGCAACCTCTCGAAGCAGAAATACGATTTAGAAAGGGCGCAAGAGGGCGGTGAAT	1971
Db	1981	CCAGCAGAGGTAAACATTTGAGGCGAGAATATGATTTAGAAAAGAGCACAAAAGGGCGGTGAAT	2040
QY	1972	GCTCTGTTTACTAATACGAATCCCAAGAAGATTGAAAAACAGATGTGACAGATTTATCATATT	2031
Db	2041	GCTCTGTTTACTCTACAAATCCAAAGAGATTGAAAACAGATGTGACAGATTTATCATATT	2100
QY	2032	GATCAAGTATCCAAATTTAGTGGCGTGTTTATCGGATGAAATCTCTGTTAGATGAAAAGAGA	2091
Db	2101	GACCAAGTGTCCATATATCGTGGCATGTTTATCAGATGAAATTTTGTCTGGATGAGAAGCGA	2160
QY	2092	GAATTTCTTGAGAAAGTGAATAATGCGAAACGACTCAGTGATGAAAGAAACTTATCTCCAA	2151
Db	2161	GAATTTATTTGAGAAAGTGAATAATGCGAAAGCGACTCAGTGATGAAAGAAACTTATCTCCAA	2220
QY	2152	GATCCAACTTCACATCCATCAATAAGCAACACGACTTCATCTCTAATGAGCAATCG	2211
Db	2221	GATCCAAACTTCACATTCATCAGTGGGCAATTAAGTTTCGCATCCATCGATGAGCAATCA	2280
QY	2212	AAATTCACATCTATCCATGAACAATCTGAAACATGGATGGTGGGGAAGTGAGAACATTACA	2271
Db	2281	AACTTCCCCTCTAATATGAGCTATCTGAACATGATGGTGGGGAAGTGCGAATGTTACC	2340
QY	2272	ATCCAGGAAGGAATGACGTATTTAAAGAGAAATTAAGTCACTACACGGGACCTTTTAAAT	2331
Db	2341	ATTCCAGGAAGGAATGACGTATTTAAAGAGAAATTAAGTCACTACACGGGTACTTTTAAAT	2400
QY	2332	GAGTGTATTCGACGTTATTTATATCAAAAATATAGGAGAGTCGGAAATTTAAAGCTTATACT	2391
Db	2401	GAGTGTATTCCAAAATTTATATCAAAAATATAGGAGAGTCAGAAATTTAAAGCTTATACG	2460
QY	2392	CGCTACCAATTTAAGAGAGGTATTTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGT	2451
Db	2461	CGCTATCAATTTAAGAGGTTATTTGAAGATAGTCAAGATCTAGAGATTTATTTAATTCGT	2520
QY	2452	TATTAATCGAAACATGAAACAATTTGGATGTTCAGGTACCGAGTCCGATAGCCGCTTTCA	2511
Db	2521	TACAAATGCAAGCATGAAACAATTTGGATGTTCAGGTACCGATTTCCCTATGCGCGTTTCA	2580
QY	2512	GTTGAAAGCCCAATTCGGAAGGTGCGGAAGAACCGAATCGATCGGCACACAAATTTTGAATGG	2571
Db	2581	GTTGAAAGCCCAATTCGGAAGGTGCGGAAGAACCAAATCGATCGGCACACAAATTTTGAATGG	2640
QY	2572	AATCCTGATCTAGATGTTCTCTGCAGAGATGAGAAAAAATGTGCGCATCAATCCCATCAT	2631
Db	2641	AATCCTGATCTAGATGTTCTCTGCAGAGATGAGAAAAAATGTGCGCATCAATTTCCCATCAT	2700
QY	2632	TTCTCTTTGGATATTGATATTGGAATGCACAGACTTGCATGAGAACTTAGCGGTGTGGGTG	2691
Db	2701	TTCACTTTGGATATTGATTTGGGTGCGACAGACTTGCATGAGAACTTAGCGGTGTGGGTG	2760
QY	2692	GTATTTCAAGATTAAAGACGCGAGGAAGTTCATGCAAGACTAGGGAATCTGGAATTTTATTTGAA	2751
Db	2761	GTATTTCAAGATTAAAGACGCGAGGAAGTATTGCAAGATTAGGAATCTGGAATTTTATCGAA	2820
QY	2752	GAGAAACCATTTATTTAGGAGAGCACTCTCTGCTGTGAAGAGCGAGAGAAAAAATCGAGA	2811
Db	2821	GAGAAACCATTTAATTTGAGAGAGCACTGTCTGTGTGAAGAGCGAGAAAAAATTTGAGA	2880
QY	2812	GACAAACGTGAAAAACTACAATTTGAAAACAAAACGAGTATATACAGAGGCAAAAGAGCT	2871
Db	2881	GACAAACGGGAAAAACTACAAATTTGAAAACAAAACGAGTATATACAGAGGCAAAAGAGCT	2940
QY	2872	GTGGATGCTTTATTTGTAGATTTCTCAATAATAATAGATTTAACGCGGATACAAACATTTGGC	2931
Db	2941	GTGGATGCTTTATTTCGTAGATTCTCAATATGATCAATTAACGCGGATACAAACATTTGGC	3000
QY	2932	ATGATTCATCGCGCAGATAAACTTTGTTTCATCGAATTCGAGAGGCTTATCTGTGAGATTA	2991
Db	3001	ATGATTCATCGCGCAGATAAACTTTGTTTCATCGAATTCGAGAGGCGTATCTTTGAGATTA	3060
QY	2992	TCTGTTATCCCGGGTGTAAATGCGGAAATTTTTCAGAAATTTTAGAAGGTGCGCATTTACCT	3051

Db	3061	CCTGTTATCCAGGTGTAAATGCCGAATTTTGAAGAAATTAGAAAGTCAATTATCACT	3120
Qy	3052	GCAATCTCCCTATACGATGCCAGAAATGTCGTTAAAAATGGTGATTTTAATAATGGATTA	3111
Db	3121	GCAATGTCCTTATACGATGCCAGAAATGTCGTTAAAAATGGTGATTTTAATAATGGATTA	3180
Qy	3112	GCATCTGGAAATGTAAGAGGCATGTAGATGTACAAACAGAGCCATACCGTTCGTGCTCTT	3171
Db	3181	ACATGTTGGAATGTAAAGAGGCATGTAGATGTACAAACAGAGCCATACCGTTCGTGCTCTT	3240
Qy	3172	GTTATCCAGNATGGGAAGCAGAGTGTCAACAGCAGTTCGCGTCTCTCCGGGGCGTGGC	3231
Db	3241	GTTATCCAGAAATGGGAAGCAGAGTGTCAACAGCAGTTCGCGTCTCTCCGGGGCGTGGC	3300
Qy	3232	TATATCTCTCCGTGTACAGCGTACAAAGAGGGATATGAGAGGGTTCGTGTAAACGATCCAT	3291
Db	3301	TATATCTCTCTGTGTACAGCGTACAAAGAGGGATATGAGAGGGTTCGTGTAAACGATCCAT	3360
Qy	3292	GAATTCGAGAACAAATACAGACGAACTAAAAATTTAAAAAAGTGTGAAGAGAGGAGTGTAT	3351
Db	3361	GAATTCGAGAACAAATACAGACGAACTAAAAATTTAAAAAAGTGTGAAGAGAGGAGTGTAT	3420
Qy	3352	CCAAAGGATACAGAAAGTGTAAATGATTTATCTGCACACCAAGGTACAGCAGTATGTAAT	3411
Db	3421	CCAAAGGATACAGAAAGTGTAAATGATTTATCTGCACACCAAGGTACAGCAGTATGTAAT	3480
Qy	3412	TCCCGTAAATGCTGATATGAGGATGCATATGAAGTTGATCTACAGCATCTGTAAATTAC	3471
Db	3481	TCCCGTAAATGCTGATATGAGGATGCATATGAAGTTGATCTACAGCATCTGTAAATTAC	3540
Qy	3472	AAACCGACTTATGAAGAAGAAACGATACAGATGTACGAAGAGATATCAATCTGTGAATAT	3531
Db	3541	AAACCGACTTATGAAGAAGAAACGATACAGATGTACGAAGAGATATCAATCTGTGAATAT	3600
Qy	3532	GACAGAGGTATGTGAATATTCACCACTACAGCTGGTATATGACAAAGAATTTAGAA	3591
Db	3601	GACAGAGGTATGTGAATATTCACCACTACAGCTGGTATATGACAAAGAATTTAGAA	3660
Qy	3592	TACTTCCAGAAACCGATAGGTATGATTCAGATTCGAGAAACGGAAGGAAAGTTTATT	3651
Db	3661	TACTTCCAGAAACAGATACAGTATGATTCAGATTCGAGAAACGGAAGGAAAGTTTATT	3720
Qy	3652	GTACAGACGCTGGAAATTTACTCTTTATGGAGGAATAG	3687
Db	3721	GTAGATAGCTGGAACTACTCTCTCATGGAAGATAG	3756
RESULT 11			
AAV83927			
ID	AAV83927	standard; DNA; 3934 BP.	
XX	AAV83927;		
AC	AAV83927;		
DT	03-MAR-1999	(first entry)	
XX			
DE		DNA encoding a CryET5 protein.	
XX			
KW	CryET4; Bacillus thuringiensis strain B55847; crystal toxin; CryET5;		
KW	Lepidoptera; Helicoverpa zea; resistant strain; Plutella xylostella;		
KW	Spodoptera exigua; S. frugiperda; S. frugiperda; Trichoplusia ni; ds.		
OS	Bacillus thuringiensis.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	67..3756	
FT		/*tag= a	
FT		/product= "CrtET5"	
XX			
PN	US5854053-A.		
XX			
PD	29-DEC-1998.		
XX			

PF 06-JAN-1997; 97US-00779046.
 XX 29-JUL-1993; 93US-00100709.
 PR 30-DEC-1993; 93US-00176865.
 PR 07-JUN-1995; 95US-00474038.
 XX (ECOG-) ECOGEN INC.
 PA
 XX
 PI Donovan WP, Gonzalez JM;
 XX WPI; 1999-094915/08.
 DR P-PSDB; AAW87633.
 XX
 XX New strains EG5847 and EG10368 of *Bacillus thuringiensis* - producing
 PT crystal toxins active against Lepidoptera, particularly *Helicoverpa* zea,
 PR *Plutella xylostella* and *spodoptera* species.
 XX
 XX Example 2; Fig 2A-J; 49pp; English.
 XX
 CC The present sequence encodes a CryET5 protein. The protein is isolated
 CC from a new strain of *Bacillus thuringiensis* (B.t.), strain EG5847 (NRRL B
 CC -21110). EG5847 contains two new crystal toxin genes (cryET4 and cryET5)
 CC that produce proteins active against Lepidoptera. CryET4 is more active
 CC than CryIA(a) against *Helicoverpa* zea, resistant-strains of *Plutella*
 CC *xylostella*, *Spodoptera exigua* and *S. frugiperda*, while CryET5 is more
 CC active than CryIB against *S. frugiperda* and *Trichoplusia ni* (and both are
 CC active against additional insect species)
 XX
 SQ Sequence 3934 BP; 1348 A; 650 C; 840 G; 1096 T; 0 U; 0 Other;
 Query Match 72.9%; Score 2687.2; DB 2; Length 3934;
 Best Local Similarity 83.5%; Pred. No. 0;
 Matches 3088; Conservative 0; Mismatches 593; Indels 15; Gaps 3;
 QY 1 TTGACTTCAATAGGAATGAGATGAATTAATTAATGCTTTATCGATTCAGCTGTA 60
 DB 67 TTGACTTCAATAGGAATGAGATGAATTAATTAATGCTTTATCGATTCAGCTGTA 126
 QY 61 TCGAATCATTCACAAATGATCTATCACAGATGCTCGTATTGAGGATTCCTTTGTGT 120
 DB 127 TCGAATCCTTCCACGCAATGATCTATCACAGATGCTCGTATTGAGGATTCCTTTGTGT 186
 QY 121 ATAGCGGAGGGAATTAATTAATCAATCCACTTGTAGGCGATCAACAGTCCAAACGGGTATT 180
 DB 187 GTAGCGGAGGGAATTAATTAATCAATCCACTTGTAGGCGATCAACAGTCCAAACGGGTATA 246
 QY 181 AACATAGCTGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 DB 247 AACATAGCTGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 306
 QY 241 TTTTATAGTTTCTTGTGTGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
 DB 307 TTTTATAGTTTCTTGTGTGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 366
 QY 301 CTAGAACATGTCGAACAACTTATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 360
 DB 367 CTGGAACATGTAACAACTTATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 426
 QY 361 CTTGCTCGATTCAAGTTTATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 DB 427 ATTGCTCGATTCAAGTTTATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 486
 QY 421 TGGCTAGAACACCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 DB 487 TGGTATGATTAACGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 546
 QY 481 TTAGAACTTGATTTCTTAATGCGATGCGCTTTTCGCAATTAAGAAATTAAGAAATTAAGAAAT 540
 DB 547 TTAGAACTTGATTTCTTAATGCGATGCGCTTTTCGCAATTAAGAAATTAAGAAATTAAGAAAT 606
 QY 541 TTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 DB 607 TTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 666

QY 601 CTTTGTGTAGTGAATTTGGGCTTACATCCAGAGAAATTCACAGTTATTATATGAGCGCAA 660
 DB 667 CTTTGTGTAGTGAATTTGGGCTTACATCCAGAGAAATTCACAGTTATTATATGAGCGCAA 726
 QY 661 GTGGAACAAACGAGAGATTATCCGACTATGCGTAGAATGCGTAGAATGCGTAGAATGCGTAGAAT 720
 DB 727 ATCAGATATACAGAGGAATATTCTAACCAATGCGTAGAATGCGTAGAATGCGTAGAATGCGTAGAAT 786
 QY 721 AGCTTCAGAGGAGCAAAATGCGCAAGTTGGGCTGCTTATAATCAATTCCTGAGAGATCTA 780
 DB 787 AACTTAAGAGGAGCAAAATGCGCAAGTTGGGCTGCTTATAATCAATTCCTGAGAGATCTA 846
 QY 781 ACCTTAGGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGACACTCGCACTTATFCCA 840
 DB 847 ACCTTAGGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGACACTCGCACTTATFCCA 906
 QY 841 ATAAATACGAGTCTCAGTTTAAAGGGAAGTTTATACAGAGCAATTCGAGCAACAGGG 900
 DB 907 ATCAATACGAGTCTCAGTTTAAAGGGAAGTTTATACAGATCCAAATTCGAGCAACAAAT 966
 QY 901 GTAAAT-----ATGGCAAGTATGAATTCGTATAATAATAATCAATTCGTTTTCGGCT 954
 DB 967 GCACCTTCAGGATTCGCAAGTACGAATTCGTTTATAATAATAATCAATTCGTTTTCGGCT 1026
 QY 955 ATAGAGACTGCGGTTATCCGAAGCCGCAATCTACTTGAATTTCTAGAAACAACTTACAAT 1014
 DB 1027 ATAGAGCTGCCATTTTCAGGCTCCGCTACTTGAATTTCTAGAAACAACTTACAAT 1086
 QY 1015 TTTAGCACTTCATCAGATGAGTGTCTACTAGGCATATGACTTACTGGCGGGGACACACA 1074
 DB 1087 TACAGTGCATCAAGCGTTGGAGTAGCACTCAACATGAATTTATTTGGTGGGACATAGG 1146
 QY 1075 ATTCAATCTCGGCAATAGAGGCGGATTAATAATACCTCAACGATGGGTCTACCA---AT 1131
 DB 1147 CTTAATCTCGGCAATAGAGGCGGATTAATAATACCTCAACGATGGGTCTACTAATAAT 1206
 QY 1132 ACTTCTTAAATCTCTGAAGATTATCAATTTCTTCGAGAGCTATATTGGAATGATCA 1191
 DB 1207 ACTTCAATTAATCTCTGAAGATTATCAATTTCTTCGAGAGCTATATTGGAATGATCA 1266
 QY 1192 TATGAGGAGTGTCTTCTATGGGGAATTTACCTTGAACCTTATTCATGCTGCTCCCTACTGTT 1251
 DB 1267 AATGCGAGGACAAATAT-----ACTATTTACTCTCTGTTGAATGGAGTACCTTGGGCT 1320
 QY 1252 AGATTTAAATTTAGGAACCTCAGAACTATCTTTGAAAGAGGTACTGCTAATCTACTAGTCAA 1311
 DB 1321 AGATTTAAATTTAGGAACCTCAGAACTATCTTTGAAAGAGGTACTGCTAATCTACTAGTCAA 1380
 QY 1312 CCTATAGTCACTCGGCTTCAATTTAAAGATTTCAGAACTGAATTTACCCAGAAACA 1371
 DB 1381 CCGTATCAGGAGTTCGGATTCATTTATTTGATTTCAGAACTGAATTTACCCAGAAACA 1440
 QY 1372 ACNAGAGCAAAATTTATGAATCATATAGTCTAGTCTATCTCAGATAGGCTCAATTTCA 1431
 DB 1441 ACNAGAGCAAAATTTATGAATCATATAGTCTAGTCTATCTCAGATAGGCTCAATTTCA 1500
 QY 1432 CAATCTAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1491
 DB 1501 GGAACACTTTGAGAGCACAGTCTATTCTTGAAGCGCATGCTAGTGCAGATTCGATGAT 1560
 QY 1492 ACCATTTAGTTCAGATAGCATAACAAATACCAATTCGTTTAAATTCATTCACCTTAATTTCA 1551
 DB 1561 ACATTTGGACCAAAATAGAAATTCACAAATACCAATTCGTTTAAATTCATTCACCTTAATTTCA 1620
 QY 1552 GGTACCTCTGTAGTCTAGTGGCGCCAGGATTTACAGGAGGGGATATTAATTCGAACTACGTT 1611
 DB 1621 GGTGTTACTGTTGTTGGAGGCGCCAGGATTTACAGGTTGGGGATATTCCTTCGTAGAACAAAT 1680
 QY 1612 AATGTTAGTGTACTAGTATGCTCTTAAATTTTAAATTAATTAATTAATTAATTAATTAATTAAT 1671
 DB 1681 ACGGTTACATTTGGAGATATACGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTCGC 1740

Qy	1672	GTGAGAGTTTCGTTATGCTGCTTCTCAACAACATGCTCTGAGGGGTAACTGTCGGAGGGAGTT	1733
Db	1741	GTAAGGAAATTCGTTATGCTTCTACTACAGATTTACAATTTTTTTCACGAGAAATTAATGTGAACC	1800
Qy	1732	ACTACTTTTGGATCAAGGATTCCTCTAGTACTATGAGTCMAATGAGTCTTTTGACATCTCAA	1791
Db	1801	ACTGTTTAATATTGGTAATTTCTCAAGAACATATGAATAGGGGGGATAAATTTAGAAATATAGA	1860
Qy	1792	TCATTTAGATTTGACAGAATTTCCCTGTAGGTATTAGTGCATCTGGCAGCTCAAACTGCTGGA	1851
Db	1861	AGTTTTAGACTCGAGGATTTAGTACTCTCTTTTAATTTTTTAATGCCAAGCACATTC	1920
Qy	1852	ATAAGTATAAGTAATAATGCAAGGTAGACAAACGTTTCACTTTGATAAAAATTGAATTCATT	1911
Db	1921	ACATGGGTGCTCAGAGCTTTTCAAAACAGGAAGTTTATATAGATACAGTCAAAATTTGTT	1980
Qy	1912	CCAAATTAAGTCTGAGAGCAGATACGATTTAGAAAGGCGCAAGAGGCGGTGAAT	1971
Db	1981	CCAGCAGAGGTAAACATTTGAGGCGAGAAATATGATTTAGAAAGAGCACAAAAGGCGGTGAAT	2040
Qy	1972	GCTCTGTTTACTAATACGAATCCAAAGAAAGATTGAAAAACAGATGTGACAGATTTATCATATT	2031
Db	2041	GCTCTGTTTACTCTACAATCCAAAGAAAGATTGAAAAACAGATGTGACAGATTTATCATATT	2100
Qy	2032	GATCAAGTATCCAAATTTAGTGGCGGTATTATCGGATGAAATTCGTCTTAGATGAAAGAGA	2091
Db	2101	GACCAAGTCCAAATATGGTGGCATGTTTATCAGATGAAATTTGCTTGGATGAGAAGCGA	2160
Qy	2092	GAAATTAATTGAGAAAGTGAATATGCGAAACGACTCAGTATGAAAGAAATTTACTCCAA	2151
Db	2161	GAAATTAATTGAGAAAGTGAATATGCGAAAGCAGTCTAGTATGAAAGAAATTTACTCCAA	2220
Qy	2152	GATCCAAATTTACATCCATCAATTAAGCAACACGACTTTCTATCTACTAATGAGCAATCG	2211
Db	2221	GATCCAAATTTACATTCATCAGTGGCGAATTAAGTTTCGCATCCATCGATGACAAATCA	2280
Qy	2212	AATTTACATCTATPCATGAACAAATCTGAACATGGATGGTGGGGAAGTGAGAACATTTACA	2271
Db	2281	AACCTCCCTCTATTAAATGAGCTATCTGAACATGGATGGTGGGGAAGTGCGAATTTTACC	2340
Qy	2272	ATCCAGAAAGGAATGACGTATTTTAAAGAGAAATTAAGTCACTACCGGGGACTTTTAAT	2331
Db	2341	ATTCCAGAAAGGAATGACGTATTTTAAAGAGAAATTAAGTCACTACCGGGGACTTTTAAT	2400
Qy	2332	GAGTGTATTCCGAGCTATTTATATCAAAAAATAGGAGAGTCGGAATTTAAAGCTTATAC	2391
Db	2401	GAGTGTATTCCAAATTAATTTATATCAAAAAATAGGAGAGTCAGAAATTAAGAGCTTATACG	2460
Qy	2392	CGCTACCAATTAAGAGGGTATATTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGT	2451
Db	2461	CGCTATCAATTAAGAGGGTATATTGAAGATAGTCAAGATCTAGAGATTTATTTAAATTCGT	2520
Qy	2452	TATTAATCGGAAAATATGAAAATTTGGATGTTTCCAGGTAACGAGTCCGATGCGCGCTTTCA	2511
Db	2521	TACAAATGCAAGCATGAAAATTTGGATGTTTCCAGGTAACGATTTCCCTATGCGCGCTTTCA	2580
Qy	2512	GTTGAAAGCCCAATCGGAAGGTGCGGAGAACCGAATCGATGCGCACACATTTTGAATGG	2571
Db	2581	GTTGAAAGCCCAATCGGAAGGTGCGGAGAACCAATCGATGCGCACACATTTTGAATGG	2640
Qy	2572	AATCCTGATCTAGATTTCTCTGAGAGATGGAGAAAAATTTGCGCATCATTTCCCATCAT	2631
Db	2641	AATCCTGATCTAGATTTCTCTGAGAGATGGAGAAAAATTTGCGCATCATTTCCCATCAT	2700
Qy	2632	TTCTCTTTGGATATTGATATTGATATGCACAGACTTTGCAATGAGAAATCTAGCGGTGTGGGTG	2691
Db	2701	TTCACTTTGGATATTGATTTGGGTGCGACAGACTTGCATGAGAACTTAGCGGTGTGGGTG	2760
Qy	2692	GTATTTCAAGATTTAAGACGCGAGGAAGTTCATGCAAGACTAGGGAATCTGGAATTTATTGAA	2751
Db	2761	GTATTTCAAGATTTAAGACGCGAGGAAGTTCATGCAAGATTTAGGAATCTGGAATTTATCGAA	2820
Qy	2752	GAGAAACCATTTATTAGGAAGACGACTCTCTCGTGTGAAGAGACGACAGAAAAAATGGAGA	2811

[illegible]

RESULT 12

ADK98478

ID ADK98478 standard; DNA; 3687 BP.

EX-100

AC ADK98478;

XX
XX
XX

DT	03-JUN-2004 (first entry)	B thuringiensis cry1Bb partial gene sequence SeqID1.
XX		
DE		

XX insecticidal protein; plant; pesticide; gene therapy;
KW lepidopteran insect pest; transgenic plant;
KW insect infestation resistance; monocot; dicot; cry1Bb; gene; ds.
XX
OS Bacillus thuringiensis.

XX Key Location/Qualifiers
FH 1..3687
CDS /tag= a
/product= "B thuringiensis cry1Bb"
/partial
/note= "No start or stop codon"

XX WO2004020636-A1.

XX 11-MAR-2004.

XX 26-AUG-2003; 2003WO-US026510.

XX 29-AUG-2002; 2002US-0407428P.

XX (MONS) MONSANTO TECHNOLOGY LLC.
PA (BOGD/) BOGDANOVA N N.
PA (ROMA/) ROMANO C P.

XX Bogdanova NN, Romano CP;

XX WPI: 2004-269221/25.

XX P-PSDB; ADK98479.

XX New polynucleotide sequence optimized for expression of an insecticidal protein in a plant, useful in the control of Lepidoptera insect pests, and for producing transgenic plants with the ability to resist insect infestations.

XX Disclosure; SEQ ID NO 1; 138pp; English.

XX This invention relates to a novel polynucleotide sequence optimised for expression of an insecticidal protein in a plant. The invention may be useful for the production of pesticides whilst the disclosed sequences may be used for gene therapy. The polynucleotide sequence and methods are useful in the control of lepidopteran insect pests, and for producing transgenic plants with the ability to resist infestations. The invention provides polynucleotide sequences with enhanced, improved and optimised expression in monocot and dicot plant species. The present sequence is that of the (partial) B thuringiensis cry1Bb gene which is related to the invention.

XX Sequence 3687 BP; 1248 A; 621 C; 796 G; 1022 T; 0 U; 0 Other;

Query Match 72.8%; Score 2684.2; DB 12; Length 3687;
Best Local Similarity 83.5%; Pred. No. 0;
Matches 3085; Conservative 0; Mismatches 593; Indels 15; Gaps 3;

QY 1 TTGACCTTCAATAGGAAAATGAGATGAAATATATAATGCTTTATCGATTCCAGCTGTA 60
DB 1 TTGACCTTCAATAGGAAAATGAGATGAAATATATAATGCTTTATCGATTCCACGGTA 60
QY 61 TCGAATCATTCACACAAATGATCTATACCCAGATGCTCGTATTCAGGATCTTTGTGT 120
DB 61 TCGAATCATTCACACAAATGATCTATACCCAGATGCTCGTATTCAGGATCTTTGTGT 120
QY 121 ATAGCCGAGGGAATATCAATCCACTGTTAGCGCATCAACAGTCCAAACGGGTATT 180
DB 121 GTAGCCGAGGGAATATCAATCCACTGTTAGCGCATCAACAGTCCAAACGGGTATA 180
QY 181 AACATAGCTCGTGAATATCTAGTGTATTAGGCGTACCGTTTCTGACAAATAGCTAGT 240
DB 181 AACATAGCTCGTGAATATTTGGCGGTATTAGTGTGCGGTTCCTGGACAACTAGCTAGT 240
QY 241 TTTTATAGTTTCTTGTGTGTAATTATGCGCCCGGCGGACAGATCAGTGGGAAATTTTC 300

DB 241 TTTTATAGTTTCTTGTGTGGAATTTATGCGCCTAGTGGCAGAGATCCATGGGAAATTTTC 300
QY 301 CTAGAACATGTGCAACAACTTATAAATCAACAAATAACAGAAAAATGCTTAGGAATACGGCA 360
DB 301 CTGGAACATGTAGAAACAACTTATAAGACAAACAAAGTAACAGAAAAATAGTACGAGT 360
QY 361 CTGCTCGAATTACAAAGTTTAGGAGATCTCTTTAGAGCCTATCAACAGTCACTTGAAGAT 420
DB 361 ATTGCTCGAATTAGAGGCTCTAGGAAGAGGCTATAGATCTTACAGCAGGCTCTTGAAC 420
QY 421 TGGCTAGAAAAACCGTGATGATCAAGAACGAGAAGTGTCTTTTATACCCAAATATAGCC 480
DB 421 TGGTTAGATAACCGAATGATCAAGATCAAGAGCAATTTCTTGGAGCGCTATGTGCT 480
QY 481 TTAGAACTTTGACATTTACTGCTATACCGCTTTTTCAGAAATACGAAATGCAAGAGTTCCA 540
DB 481 TTAGAACTTTGACATTTACTGCTATACCGCTTTTTCAGAAATACGAAATGCAAGAGTTCCA 540
QY 541 TTATTAATGGTATATGCTCAAGCTGCAAAATTTACACCTATTATTATTTAGAGACGCTCC 600
DB 541 TTATTAATGGTATATGCTCAAGCTGCAAAATTTACACCTATTATTATTTAGAGACGCTCC 600
QY 601 CTTTTTGGTAGTGAATTTTGGGCTTACATCGCAGGAAATTTCAACGTTATTATGAGCCCAA 660
DB 601 CTTTTTGGTAGTGAATTTTGGGCTTACATCGCAGGAAATTTTCCGATGTTAAACCAATATACCAAGAACAA 660
QY 661 GTGGAAACAAACGAGAGATTTATTCGACTATTCGCTAGAAATGCTGATTAATACAGTCTAAAT 720
DB 661 ATCAGATATACAGAGAGATTTATTCGACTATTCGCTAGAAATGCTGATTAATACAGGCTTAAAT 720
QY 721 AGCTTGAGAGGACAAATGCGCGAAGTTGGGTCGTTATTAATCAATTCGCTAGAGATCTA 780
DB 721 AACTTTAAGAGGACAAATGCTCAAAAGTTGGTTCGCGTATTAATCAATTTCCGCTAGAGACCTTA 780
QY 781 AGCTTGAGGCTATTAGATCTAGTGGCACTATTTCCCAAGCTATGCACATCGCACTTATCCA 840
DB 781 AGCTTGAGGCTATTAGATCTAGTGGCCTATTTCCCAAGCTATGATGACTGCACCTTATCCA 840
QY 841 ATAAATACAGTCTCAGTTAAACAGGGAAGTTTATACAGACGCAATTCGAGCAACAGGG 900
DB 841 ATCAATACAGTCTCAGTTAAACAGGGAAGTTTATACAGATCCCAATTCGAGCAACAAAT 900
QY 901 GTAAT-----ATGGCAAGTATGAATGCTGATTAATAATTAATGACCTTCGTTTCGGCT 954
DB 901 GCACCTTCAGGATTTGCAAGTACGAATTTGTTTAAATAATGACCACTCGTTTCGCTGCC 960
QY 955 ATAGAGACTCGGTTATCCGAAGCCGCACTACTTGTATTTTCTAGAACAACTTACAAAT 1014
DB 961 ATAGAGGCTGCCATTTTCAGGCTTCGCACTACTTGTATTTTCCAGAACAACTTACAAAT 1020
QY 1015 TTTAGCACTTCATCACGATGGAGTGTCTACTAGGCAATATGACTTACTGCGGGGCGCACACA 1074
DB 1021 TACAGTGATCAAGCGGTTGGAGTAGCACTCAACATATGAATTTTGGTGGGACATAGG 1080
QY 1075 ATTCAATCTCGGCCAATAGGAGCGGATTAATAATCCTCAACGCAATGG---GTCTACCAAT 1131
DB 1081 CTTAACTTCGGCCCAATAGGAGGACATTAATAATACCTCAACACAGGACTTACTATAAT 1140
QY 1132 ACTTCTATTAACTCTGATAGATTATCATTTCTCTCGAGAGCTATATTGGACTGAATCA 1191
DB 1141 ACTTCAATTAATCCTGTAACTATACAGTTTACGCTTCGAGAGCGTTTATGAACAGATCA 1200
QY 1192 TATGACGAGTGTCTCTATGGGGAATTTACCTTTGAACCTTATTCATGGTGTCCCTACTGTT 1251
DB 1201 AATGAGGACAAATAT-----ACTATTACTCTCTGTAATGAGTACCTTGGCT 1254
QY 1252 AGATTTAATTTTAGGAACCCCTCAGAAATCTTTTGAAGAGGTACTGCTTAATATAGTCAA 1311
DB 1255 AGATTTAATTTTATAAACCCCTCAGAAATTTATGAAGAGGCGGCCACTACCTACAGTCAA 1314
QY 1312 CCCTATGAGTCACTGGGCTTCAATTTAAAGATTGAGAACTGAAATTCACCCAGAAACA 1371
DB 1315 CCGTATCAGGAGTGTGGGATTTCAATTTATTGATTTCAGAACTGAAATTCACCCAGAAACA 1374

Qy	1372	ACGAAACGACCAAAATTATGAATCATATAGTATCAGTAGGTTATCTCACATAGGGCTCATTTCA	1431
Db	1375	ACGAAACGACCAAAATTATGAATCATATAGTATCAGTAGATTTATCTCATATAGGACATAATCATTA	1434
Qy	1432	CAATCTAGGGTGCAATGTACACAGTATATCTTGAGACGCACCGTAGTCAGAGATCGTACAAAT	1491
Db	1435	GGAACACCTTTGAGAGACACCACTTATCTTGGACGCATGCTAGTCAGATCGTACGAAT	1494
Qy	1492	ACCAATTAGTTCAGATAGCATAAACAACAATACCAATGTGTAAATCATTTCAACCTTAATTC	1551
Db	1495	ACGAATGGACCAAAATAGAAATTACACAATACCAATGGTAAAGCACTGAATCTTCATTCA	1554
Qy	1552	GGTACCTCTGTAGTCAGTGGCCACAGGAATTTACAGGAGGGGATATAATCCGAACTACAGTT	1611
Db	1555	GGTGTTACTGTGTGGAGGCCAGGAATTTACAGTGGGGATATCCCTTCGTGAGACAAAT	1614
Qy	1612	AATGGTAGTGTACTAAGTATGGGTCTTAAATTTTAAATAATACATCATTTACAGCGGTATCGC	1671
Db	1615	ACGGGTACATTTGGAGATATACGATTAATAATTAATGTGCCATTTATCCAAAGATATCGC	1674
Qy	1672	GTGAGAGTTCTGGTTATGCTGCTTCTCAACAACATGGTCTGAGGGTAACTGTGCGAGGGAGT	1731
Db	1675	GTAAAGGATTCGTTATGCTTCTCTACACAGATTTACAATTTTTTCACAGAAATTAATGTGAACC	1734
Qy	1732	ACTACTTTTGATCAAGGATTTCCCTAGTACTATGAGTCAAAATGAGTCTTTGACATCTCAA	1791
Db	1735	ACTGTTAATATTTGGTAATTTCTCAAGAACTATGATAGGGGGATTAATTTAGAAATAGA	1794
Qy	1792	TCAATTTAGATTTGCAGAAATTTCCCTGTAGGTATTTAGTGCATCTGGCAGTCAAACTGCTGGA	1851
Db	1795	AGTTTTAGAACTGCAGGATTTAGTACTCTCTTTTAAATTTTTTAAATGCCAAAGCACATTC	1854
Qy	1852	ATAAGTATAAGTAATATGCAAGTACAAACGTTTTCACCTTTCGTAATAATTTGAATTCATT	1911
Db	1855	ACATGGGTGCTCAGAGTTTTTCAAATCAGGAAGTTTATATAGTAGAGTCGAAATTTGTT	1914
Qy	1912	CCAATTACTGCAACCTTCGAAGCAGATACGATTTAGAAAAGGGCGCAAGAGCGGTGAAT	1971
Db	1915	CCAGCAGAGTAAACATTTGAGGCAGATAATGATTTAGAAAAGACACAAAAGGCGGTGAAT	1974
Qy	1972	GCTCTGTTTACTAATACGAATCCAAGAGATTTGAAAACAGATGTGACAGATTATCATATT	2031
Db	1975	GCTCTGTTTACTTCTACAAATCCAAGAAAGATTTGAAAACAGATGTGACAGATTATCATATT	2034
Qy	2032	GATCAAGTATCCAAATTTAGTGGCGTGTATTCGGATGAATTTCTGCTTAGATGAAAAGAGA	2091
Db	2035	GACCAAGTCCAAATATGGTGGCATGTTTATCAGATGAATTTTTCCTTGGATGAGAGCGA	2094
Qy	2092	GAATTACTTCAGAAAAGTGAATATGCGAAACGATCAGTGATGAAAGAACTTACTCCAA	2151
Db	2095	GAATTAATTTGAGAAAAGTGAATATGCGAAGCGACTCAGTGATGAAAGAACTTACTCCAA	2154
Qy	2152	GATCCAACTTCACATCCATCAATTAAGCAACAGACTTCATATCTACTAATAGCAATCG	2211
Db	2155	GATCCAACTTCACATTCATCAGTGGGCAATTAAGTTTCGCATCCATCGATGAGCAATCA	2214
Qy	2212	AAATTCACATCTATPCCATGAACAACTCGAACTGGATGGTGGGAAAGTGAGAACATTACA	2271
Db	2215	AACTTCCCTCTAATTAATGAGCTATCTGAACATGGATGGTGGGAAAGTGCGAATGTACC	2274
Qy	2272	ATCCAGGAAGGAATGACGTAATTTAAGAGAAATTAAGTCACTACCGGGACTTTTAAT	2331
Db	2275	ATTGAGGAAGGAATGACGTAATTTAAGAGAAATTAAGTCACTACCGGGACTTTTAAT	2334
Qy	2332	GAGTGTATCCGACGTAATTTATATCAAAAAATAGGAGAGTCGGAATTTAAAGCTTATACT	2391
Db	2335	GAGTGTATCCAAATTTATATCAAAAAATAGGAGAGTCAGAAATTAAGCTTATACG	2394
Qy	2392	CGCTACCAATTAAGAGGGTATATGAAGATAGTCAAGATTTAGAGATATATTTTGATTCGT	2451
Db	2395	CGCTATCAATTAAGAGGGTATATGAAGATAGTCAAGATCTAGAGATTTATTTTAATTCGT	2454

```

|||||
3535 GACAGAGGATGTGAATTTATCCACAGTACCAGCTGGTTATGTGACAAAGAAATTAGAA 3594
3592 TACTTCCCGAAGAACCGAATAGGTATGGATTGGAGATTGGAGAAACGGAAGGAGTTTATT 3651
3595 TACTTCCCGAAGAACAGATACAGTATGGATTGGAGATTGGAGAAACGGAAGGAGTTTATT 3654
3652 GTACAGAGCGTGAATTTACTCTTATGGAGAA 3684
3655 GTAGATAGCGTGAATTTACTCTTATGGAGAA 3687

RESULT 13
AA504854
ID   AAS04854 standard; DNA; 3627 BP.
XX
AC   AAS04854;
XX
DT   07-SEP-2001 (first entry)
XX
DE   Bacillus thuringiensis DNA encoding partial mutant Cry1Ba.
XX
KW   Crystal protein; Cry1a; Cry1Ba; moth; butterfly; Colorado potato beetle;
KW   db; mutant.
XX
OS   Bacillus thuringiensis.
XX
FH   Key
FT   CDS
FT   1..3627
FT   /*tag= a
FT   /product= "Cry1Ba"
FT   /partial
FT   /note= "No stop codon"
FT   sig_peptide
FT   1..57
FT   /*tag= b
FT   mat_peptide
FT   58..3651
FT   /*tag= c
FT   mutation
FT   replace(1464,A)
FT   /*tag= d
FT   mutation
FT   replace(1467,T)
FT   /*tag= e
XX
PN   EP1099760-A1.
XX
PD   16-MAY-2001.
XX
PF   09-NOV-1999; 99EP-00203723.
XX
PR   09-NOV-1999; 99EP-00203723.
XX
(PYRO-) CPRO-DLO CENT PLANTENVERDELINGS REPROD.
XX
PI   De Maagd RA, Bosch HJ;
XX
DR   WPI; 2001-337141/36.
XX
DR   P-PSDB; AAU02094.
XX
PT   New hybrid Bacillus thuringiensis hybrid toxins comprising structural
PT   domains derived from at least 2 different crystal proteins, such as
PT   Cry1a and Cry1Ba, and having insecticidal activity, useful for combating
PT   insects.
XX
PS   Example; Page 22-23; 43pp; English.
XX
CC   The sequence encodes B. thuringiensis (Bt) crystal protein Cry1Ba,
CC   mutated to allow cloning of domain III or domains I and II, to make the
CC   hybrid protoxins of the invention. The hybrid toxins of the invention,
CC   having structural domains I, II and III in this order starting from the N
CC   -terminal derived from at least 2 different crystal proteins, are useful
CC   for protecting plants against pest insects, e.g. moths, butterflies and
CC   Colorado potato beetle or for combating insects
XX

```

```

SQ   Sequence 3627 BP; 1184 A; 648 C; 820 G; 975 T; 0 U; 0 Other;
Query Match      71.3%; Score 2630.2; DB 4; Length 3627;
Best Local Similarity 83.4%; Pred. No. 0;
Matches 3081; Conservative 0; Mismatches 533; Indels 81; Gaps 5;

QY   2   TCAGCTTCAATAGGAAATAGAAATGAAATATATAATGCTTTATCGATTCCAGCTGTAT 61
    |||||
DB   2   TGACTTCAAATAGGAAATAGAAATGAAATATATAAT-----GCTGTAT 46
    |||||
QY   62   CGAATCATTTCCACACAAATGGATCTATCACAGATGCTCGTATTGGAGATTCTTTGTGA 121
    |||||
DB   47   CGAATCATTTCCGACAAATGGATCTATTACCAGATGCTCGTATTGGAGTAGCTTGTGA 106
    |||||
QY   122  TAGCCGAGGGGAATATATCAATCCACTTGTAGCCATCAACAGTCCAAACGGGTATT 181
    |||||
DB   107  TAGCCGAGGGGAACAATATCGATCCATTTGTAGCGCATCAACAGTCCAAACGGGTATT 166
    |||||
QY   182  ACATAGCTGTAGATAGTATGAGGCGTACCGTTTGTGACAAATAGCTAGTT 241
    |||||
DB   167  ACATAGCTGTAGATAGTATGAGGCGTATGCGGTTCCTGCTGACAACTAGCTAGTT 226
    |||||
QY   242  TTTATAGTTTTCTTGTGTGTAATTTATGCCCCCGCGCAGAGATCAGTGGGAAATTTTCC 301
    |||||
DB   227  TTTATAGTTTTCTTGTGTGTAATTTATGCCCCCGCGCAGAGATCAGTGGGAAATTTTCC 286
    |||||
QY   302  TAGAACATGTCGAACAACTTTATAAATCAACAAATAACAGAAATGCTAGGAATACGGCAC 361
    |||||
DB   287  TAGAACATGTCGAACAACTTTATAAATCAACAAATAACAGAAATGCTAGGAATACGGCTC 346
    |||||
QY   362  TTGCTCGATTACAGGTTTAGGAGATTCTTTAGAGCTTATCAACAGTCACTTGAAGATT 421
    |||||
DB   347  TTGCTCGATTACAGGTTTAGGAGATTCTTTCAGAGCTTATCAACAGTCACTTGAAGATT 406
    |||||
QY   422  GCTAGAAAACCGTGATGATGCAAGAACGAGAGTGTCTTTATATACCAATATATAGCCT 481
    |||||
DB   407  GCTAGAAAACCGTGATGATGCAAGAACGAGAGTGTCTTTATATACCAATATATAGCTT 466
    |||||
QY   482  TAGAACTTGATTTTCTTAATGCGATGCCGCTTTTCGCAATTAGAAAACCAAGAGTTCCAT 541
    |||||
DB   467  TAGAACTTGATTTTCTTAATGCGATGCCGCTTTTCGCAATTAGAAAACCAAGAGTTCCAT 526
    |||||
QY   542  TATTATGTTATATGCTCAAGCTGCAAAATTACACCTATTTATTATTGAGAGATGCCCTCTC 601
    |||||
DB   527  TATTGATGTTATATGCTCAAGCTGCAAAATTACACCTATTTATTATTGAGAGATGCCCTCTC 586
    |||||
QY   602  TTTTTCGTAGTGAAATTTGGGCTTTACATCGCAGAAATTCACCGTTATTATTGAGCGCAAG 661
    |||||
DB   587  TTTTTCGTAGTGAAATTTGGGCTTTACATCGCAGAAATTCACCGTTATTATTGAGCGCGCAAG 646
    |||||
QY   662  TGGACAAACGAGAGATTATTCGACTATTTCGCTAGAAATGGTATTAATACAGGTTCTAAATA 721
    |||||
DB   647  TGGAACGACGAGAGATTATTCGACTATTTCGCTAGAAATGGTATTAATACAGGTTCTAAATA 706
    |||||
QY   722  GCTTGAGAGGACAAATGCCGCAAGTTGGTGCTTATTAATCAATTCCTGAGAGATCTAA 781
    |||||
DB   707  GCTTGAGAGGACAAATGCCGCAAGTTGGTGCTTATTAATCAATTCCTGAGAGATCTAA 766
    |||||
QY   782  CGTTAGGGTATTAGATCTAGTGGCACTATTCGCAAGCTATGACACTCGCACATTATCCAA 841
    |||||
DB   767  CGTTAGGGTATTAGATCTAGTGGCACTATTCGCAAGCTATGACACTCGCACATTATCCAA 826
    |||||
QY   842  TAAATACGAGTGTCTCAGTTTAAACAGGGAAGTTTATACAGACGCAATTTGGAGCAACAGGGG 901
    |||||
DB   827  TAAATACGAGTGTCTCAGTTTAAACAGGGAAGTTTATACAGACGCAATTTGGAGCAACAGGGG 886
    |||||
QY   902  TAAATATGCAAGTATGAATTTGGTATTAATAATGCACTTCGCTTTTCGGTTATATAGAGA 961
    |||||
DB   887  TAAATATGCAAGTATGAATTTGGTATTAATAATGCACTTCGCTTTCTCTGCGCATAGAGG 946
    |||||
QY   962  CTGCGGTTATCCGAACCGCGCATCTACTTGAATTTCTAGAACAACTTACAAATTTTAGCA 1021
    |||||
DB   947  CTGCGGTTATCCGAACCGCGCATCTACTTGAATTTCTAGAACAACTTACAAATTTTAGCG 1006
    |||||

```


1022 CTTTCATCAGATGGAGTGTCTACTAGGCATATGACTTACTCGCGGGGCACACAATTTCAAT 1081
1007 CTTTCATCAGATGGAGTGTCTACTAGGCATATGACTTACTCGCGGGGCACACAATTTCAAT 1066
1082 CTCGGCCAAATAGGAGCGGGAATTAATACTCAACGCATGGGTCTACCAATCTTCTATTAA 1141
1067 CTCGGCCAAATAGGAGCGGGAATTAATACTCAACGCATGGGTCTACCAATCTTCTATTAA 1126
1142 ATCTGTGAAGATATCATCTTCTCTCGAGACGTATATTTGGAATGATATATGCGAGGAG 1201
1127 ATCTGTGAAGATATCATCTTCTCTCGAGACGTATATTTGGAATGATATATGCGAGGAG 1186
1202 TGCTTCTATCGGGGAATTTACTCTTGAACCTATTCTATGGTGTCCCTACTGTTAGATTTAAAT 1261
1187 TGCTTCTATCGGGGAATTTACTCTTGAACCTATTCTATGGTGTCCCTACTGTTAGATTTAAAT 1246
1262 TTAGGAACCTCTAGATATCTTTTGAAGAGGTACTGCTAACTATAGTCAACCTATGAGT 1321
1247 TTACGAACCTCTAGATATTTCTCATAGAGGTACCGCTAACTATAGTCAACCTATGAGT 1306
1322 CACCTGGCTTCAATTAAGATTTAGAACTCAAGTCTGCTAACTATAGTCAACCTATGAGT 1381
1307 CACCTGGCTTCAATTAAGATTTAGAACTCAAGTCTGCTAACTATAGTCAACCTATGAGT 1366
1382 CAAATATGATCATATAGTATAGTATCTCATAGAGGTCTCATTTCAATCTAGGG 1441
1367 CAAATATGATCATTTACAGTACAGGTATCTCATATAGTATAAATTTTACAACTCAGGG 1426
1442 TGCAATGACAGTATATCTTTGAGCAGCAGGTAGTGCAGATCTGTAACAATCAATTAGTT 1501
1427 TGAATGTACCGGTATATCTTTGAGCAGCAGGTAGTGCAGATCTGTAACAATCAATTAGTT 1486
1502 CAGATAGATAACACAAATACCAATCTGTAAGATTTCAATCAACCTTAAATTCAGGTACCTCTG 1561
1487 CAAATAGATACCCAAATCCCAATGGTAAGATCTCCGAACTTCTCAAGGTACCACGTG 1546
1562 TAGTCAGTGGCCAGGATTTTACAGGAGGGATATAATCCGAACTAAACGTTAAATGGTGTAGTG 1621
1547 TTGTTAGAGACCAAGATTTACTGGTGGGATATCTTCGAAGAACGAATCTGGTGGAT 1606
1622 TACTAGTATGGGTCTTAATTTTAAATATACATCATACAGGTATCGGTGAGAGTTC 1681
1607 TTGGAACCGATTAAGATTAAGTGTAAACCGACCAATTAACAAAGATATCGTATAGGATTC 1666
1682 GTTATGCTGCTTCTCAAAACAATGGTCTCTGAGGTAACTGTCTGAGGAGGTACTACTTTTG 1741
1667 GCTATGCTTCAACTGTAGATTTTGAATTTCTTTGTATCACTGGAGGTACTACTGTAAATA 1726
1742 ATCAAGGATTCCTAGTATGATGAGTGCAAAATGAGTCTTTTGACATCTCAATCAATTTAGAT 1801
1727 ATTTTAGATTCCTACGTACAATGAACAGTGGAGACGAACCTAAATACGGAAATTTTGTGA 1786
1802 TTGCAAAATTTCTGTAGGTATTTAGTGATCTGGCAGTCAACTGCTGGAATAGATATAA 1861
1787 GAGCTGCTTTTACTACACCTTTTACTTTTACAAATTTCAAGATATAATTCGAACGTCTA 1846
1862 GTAATAATGAGGTAGACAAACG- - -TTTCACCTTTGATAAAATTTGAATTCATTCCAATTA 1918
1847 TTCAAGGCCTTAGTGAATGGGAAGTGTATATAGATATAATTTGAATTTTCCGTTA 1906
1919 CTGCAACCTTTGAGGAGGAGATTTAGAAAGGCGCAAGGCGGTGAATGCTCTGT 1978
1907 CTGCAACCTTTGAGGAGGAGATTTAGAAAGGCGCAAGGCGGTGAATGCTCTGT 1966
1979 TTACTAATACGAATCAAGAGATTTCAAAACAGATGTGACAGATATCATATTTGATCAAG 2038
1967 TTACTAATACGAATCAAGAGATTTCAAAACAGATGTGACAGATATCATATTTGATCAAG 2026
2039 TATCCAAATTTAGTGGCGTGTATTCGGATGAATTTCTGCTTAGATGAAAGAGAGAAATTAAC 2098
2027 TATCCAAATTTAGTGGATTTGTTTATCAGATGAATTTTGTCTGATGAAAGAGAGAAATTTGT 2086

2099 TTGAGAAATGAAATATGCAAAACGACTCAGTGTGAAAGAACTTACTTCAAGATCCAA 2158
2087 CCGAGAAAGTCAAAATGCAAGAGCGACTCAGTGTAGCGGGAATTTACTTCAAGATCCAA 2146
2159 ACTTCACTCCATCAATAAGCAACCAAGACTTCATATCTACTAATAGCAATCGAATTTCA 2218
2147 ACTTCAAGAGGATCAATAGCAACCAAGC- - - - - 2175
2219 CATCTATCCATGNAACNAATCTGAACATGGATGGTGGGAAGTGAGACATTTACAACTCAGG 2278
2176 - - - - - CGTGGCTGGAGAGGAAGTACAGATATTTACCATCCAAAG 2212
2279 AAGGAATACGCTATTAAAGAGAAATTTAGCTCACACTACCGGGGACTTTTAAATGAGTGT 2338
2213 GAGGAGATGACGTATTTCAAAGAGAAATTTAGCTCACACTACCGGGTACCGTGTAGTGTGT 2272
2339 ATCCGACGTATTTATATCAAAAATAGGAGAGTTCGGAATTTAAAGCTTATATCTCGCTACC 2398
2273 ATCCAAACGTATTTATATCAGAAAATAGATGAGTCGAAATTTAAAGCTTATATCCCGTTATG 2332
2399 AATTAGAGGGTATTTGAAGATAGTCAAGATTTTGAAGATATATTTGATTCGTTAAATG 2458
2333 AATTAGAGGGTATTTGAAGATAGTCAAGATTTTGAAGATTTATTTGATCCGTTACAAATG 2392
2459 CGAAACATCAAAACATTTGGATTTTCCAGGTACCGAGTCCGTATGCGCGCTTTTCAGTTGAAA 2518
2393 CAAACACGAATAGTAAATGTGCCAGCACGGTTCCTTATGCGCGCTTTTCAGCCCAA 2452
2519 GCCCAATCGGAAGGTGCGGAGAACCGAATCGATGCGCACCAATTTTGAATGGAATCTGT 2578
2453 GTCCAAATCGGAAGGTGCGGAGAACCGAATCGATGCGCGCACCACTTTGAATGGAATCTGT 2512
2579 ATCTAGATTTGCTTCGAGAGATGAGAAAAATTTGCGCATCATTTCCCATCTTTCTCTT 2638
2513 ATCTAGATTTGCTTCGAGAGACGGGAAAAATTTGCGCATCATTTCCCATCTTTCACT 2572
2639 TGGATATTTGATATTTGATGTCACAGACTTTGCAATGAGAATCTAGGCGTGTGGGTATTCA 2698
2573 TGGATATTTGATTTGATGTCACAGACTTTAAATGAGGACTTAGGTGTATGGGTGATATTCA 2632
2699 AGATTAAGACCGCAGGAAGGTCTATGCAAGCTAGGGAATCTGGAATTTTATGAGAGAAAC 2758
2633 AGATTAAGACCGCAGGAAGGTGCCATGCAAGCTAGGGAATCTAGAGTTTCTCGAAGAGAAAC 2692
2759 CATTATTTAGGAGAACCACTGTCTGTGTGAAGAGACAGAGAAAAATTTGAGAGACAAAC 2818
2693 CATTATTTAGGAGAACCACTGTCTGTGTGAAGAGACCGGAGAGAGTGTGAGAGACAAAC 2752
2819 GTGAAAACTACAATTTGAAAAACAAACCGAGTATATACAGAGCAAAAGAGCTGTGGATG 2878
2753 GAGAGAAACCTGCAGTTGGAACAAATATTTTATAAAGAGCAAAAGAACTCTGTAGATG 2812
2879 CTTTATTTGTAGATTTCTCAATATATAGTTTACAGCGGATACAAACATTTGCGCATGATTC 2938
2813 CTTTATTTGTAAACTCTCAATATGATAGTATCAAGTGGATACGAACTATCGCGATGATTC 2872
2939 ATGCGCGCAGATAAACTCTGTTTCAATCAATTTCCAGAGCGCTTATCTGTCAAGATTTATCTGTATA 2998
2873 ATGCGCGCAGATAAAACCGGTTCAAGAACTCCGGGAACGTTATCTGCAAGTGTCTGTGA 2932
2999 TCCCGGTGTAAATGCGGAAATTTTGAAGAAATTTAAGAGGTGCGCAATTTACTGCAATCT 3058
2933 TTCCAGGTGTCAATGCGGCCATTTTTCGAAGAATTTAGAGGGACGTTATTTTACAGCGTAT 2992
3059 CCTATACGATCGAGAAATGTCGTTTAAATTTGATTTTAAATTAATGATAGCATGCT 3118
2993 CCTTATATGATCGGAGAAATGTCATTTAAATTTGGCGATTTCAATGATGCTTATTATGCT 3052
3119 GGAATGTAAGAGGCGCATGTAGATGTACAA- - - - - CAGAGCCATCACCGTTCCTGCTTTGTTA 3175
3053 GGAAGTGAAGGTCATGTAGATGTAGAGAGAGCAAAACCAACCGTTCGCTTCTGTTA 3112
3176 TCCCAAGATGGAGACAGAGTGTCAAGCAGTTCGCGTCTGTCCGGGGCGTGCCTATA 3235

P-PSDB; AAU00421.

Novel hybrid insecticidal toxin useful for controlling insects such as Spodoptera exigua and Plutella xylostella, comprises domains I and II from CryIF or CryIB toxin joined to domain III from CryIC toxin.

Claim 7; Page 88-89; 99pp; English.

The present sequence encodes for 1 of 3 novel hybrid insecticidal toxins (AAU00419-AAU00422) and is designated BNC15. BNC15 comprises domains I and II from the CryIbA toxin at the N-terminus joined to domain III from CryIcA toxin at the C-terminus. In the 1186 amino acid FFC1 hybrid sequence, the junction between the CryIbA and CryIcA toxin domains corresponds to FFC1 residues 446-454. In the 1221 amino acid BNC13 and BNC15 hybrid sequences, the junction between the CryIbA and CryIcA toxin domains is residues 482-488 in the BNC13 hybrid, and residues 491-494 in the BNC15 hybrid. The hybrid toxins are constructed by cloning and in vivo recombination. The hybrid toxins are useful for controlling an insect such as Spodoptera exigua (beet armyworm), Manduca sexta (tobacco hornworm), Plutella xylostella (diamondback moth), Ostrinia nubilalis (European corn borer), Spodoptera frugiperda (fall armyworm), and Heliothis virescens (tobacco budworm) which are major causes of vegetable, fruit or ornamental flower crop losses. The nucleotide sequences encoding the hybrid toxins are useful for producing an insect-resistant plant by introducing the nucleotide sequence into the plant preferably a transgenic plant. The nucleotide sequences can also be expressed in microorganisms such as a virus, bacterium and fungus and the toxin produced used as an insecticidal agent. Baculoviruses engineered with the nucleotide sequence encoding a hybrid toxin can be used to infect insects in vivo resulting in their death. The hybrid toxins have a greater toxicity level than either of their parent toxins alone

Sequence 3663 BP; 1190 A; 650 C; 832 G; 991 T; 0 U; 0 Other;

Query Match	69.0%	Score 2544.4	DB 4	Length 3663
Best Local Similarity	82.1%	Pred. No. 0		
Matches 3065	Conservative 0	Mismatches 546	Indels 123	Gaps 7
Qy	2	TGACTTCAAATAGCAAAAATAGAGAAATGAAATATATAAATGCTTTATCGATTCAGCTGCAGCTGAT	61	
Db	2	TGGCTTCAATAGCAAAAATAGAGAAATGAAATATATAAAT-----GCTGTAT	46	
Qy	62	CGAATCAATCCACAACAAATGGATCTATCACCAGATGCTCGTATTCAGGATCTTTGTGTGA	121	
Db	47	CGAATCAATCCGCACAAATGCATCTATTAACCAGATGCTCGTATTCAGGATAGCTTGTGTGA	106	
Qy	122	TAGCCGAGGGGAATAATATCAATCCACTTGTATAGCGCATCAACAGTCCNAACGGGTATTA	181	
Db	107	TAGCCGAGGGGAACAAATATCATGATCCATTTGTTAGCGCATCAACAGTCCNAACGGGTATTA	166	
Qy	182	ACATAGCTGGTAGAATACTAGGTGTATTAGGCGTACCGTTTGTCTCGACAAATAGCTAGTGT	241	
Db	167	ACATAGCTGGTAGAATACTAGGCGTATTGGGCGTACCGTTTGTCTCGACAACTAGCTAGTGT	226	
Qy	242	TTTATAGTTTCTTGTGGTGAATTTATGSCCCCGCGGAGAGATCAGTGGGAAATTTTCC	301	
Db	227	TTTATAGTTTCTTGTGGTGAATTTATGSCCCCGCGGAGAGATCAGTGGGAAATTTTCC	286	
Qy	302	TAGAACATGTGCAACAACTTATAAATCAACAAATAACAGAAATGCTAGGAATACGGCAC	361	
Db	287	TAGAACATGTGCAACAACTTATAAATCAACAAATAACAGAAATGCTAGGAATACGGCTC	346	
Qy	362	TTGCTCGAATTACAAGGTTTAGGAGATTCCTTTTAGAGCCCTATCAACAGTCCACITTTGAAGATT	421	
Db	347	TTGCTCGAATTACAAGGTTTAGGAGATTCCTTCAGAGCCCTATCAACAGTCCACITTTGAAGATT	406	
Qy	422	GGCTAGAAAAACCGTGTAGTATCAAGAAACGAGAAGTGTCTTTTATACCCAATATATAGCCT	481	
Db	407	GGCTAGAAAAACCGTGTAGTATCAAGAAACGAGAAGTGTCTTTTATACCCAATATATAGCTT	466	
Qy	482	TAGAACTTGATTTTTCTTAAATCCGATGCGCTTTTCGCAATTTAGAAACCAAGAGTTCCAT	541	
Db	467	TAGAACTTGATTTTTCTTAAATCCGATGCGCTTTTCGCAATTTAGAAACCAAGAGTTCCAT	526	

		Best local similarity	8a.r.14	0; Mismatches	546; Indels	123; Gaps
		Matches	3065; Conservative			
Qy	2	TGACTTCAAATAGGAAAAATGAGAAATGAAATATATAAATGCTTTATCGATTCCAGCTGTAT	61			
Db	2	TGGCTTCAAATAGGAAAAATGAGAAATGAAATATATAAAT-----GCTGTAT	46			
Qy	62	CGAATCAATTCACACAAATGGATCTATCCACAGATGCTCGTATTCAGGAATTCCTTGTGTATA	121			
Db	47	CGAATCAATTCGCCACAAATGGATCTATTAACAGATGCTCGTATTCAGGATAGCTTGTGTATA	106			
Qy	122	TAGCCGAGGGGAAATAATCAATCCACTGTGTAGCGCATCAACAGTCCAAACGGGTATTA	181			
Db	107	TAGCCGAGGGGAAACAATATCGATCAATTTGTAGCGCATCAACAGTCCAAACGGGTATTA	166			
Qy	182	ACATAGCTGGTAGAATACTAGTGTGTATTAGGCGTACCGTTTGCTCGACAAATAGCTAGTT	241			
Db	167	ACATAGCTGGTAGAATACTAGGCGTATTGGGGGTACCGTTTGCTCGACAACTAGCTAGTT	226			
Qy	242	TTTATAGTTTTCTTGTTGGTGAAATTAATGSCCGCGGCAGAGATCAGTGGGAAATTTTCC	301			
Db	227	TTTATAGTTTTCTTGTTGGTGAAATTAATGSCCGCGGCAGAGATCAGTGGGAAATTTTCC	286			
Qy	302	TAGAACATGTCGAACAACTTAATAATCAACAAATAACAGAAAAATCGTAGGAATACGGCAC	361			
Db	287	TAGAACATGTCGAACAACTTAATAATCAACAAATAACAGAAAAATCGTAGGAATACGGCTC	346			
Qy	362	TTGCTCGAATTACAAGGTTTAGAGATTCCTTTTAGAGCCCTATCAACAGTCACATTGAAGATT	421			
Db	347	TTGCTCGAATTACAAGGTTTAGAGATTCCTTCAGAGCCCTATCAACAGTCACATTGAAGATT	406			
Qy	422	GGCTAGAAAAACCGTGTGATGATCAAGAAACGAGAAGTGTCTTTTATACCCAATATATAGCCT	481			
Db	407	GGCTAGAAAAACCGTGTGATGATCAAGAAACGAGAAGTGTCTTTATACCCAATATATAGCTT	466			
Qy	482	TAGAACTGTGATTTTTCTTAATCCGATGCCGCTTTTCGCAATTAGAAAAACCAAGAAGTTCAT	541			
Db	467	TAGAACTGTGATTTTTCTTAATCCGATGCCGCTTTTCGCAATTAGAAAAACCAAGAAGTTCAT	526			

Qy	542	TATTAATGGGTATATGCTCAAGCTGCAAATTTACACCTTATTATTATTCAGAGATGCGCTCTC	601
Db	527	TATTTGATGGGTATATGCTCAAGCTGCAAAATTTACACCTTATTATTATTGAGAGATGCGCTCTC	586
Qy	602	TTTTTTGGTGTAGTGAATTTTGGGCTTACATCGCAGGAAATTCACGTTATTATGAGCGCCAAAG	661
Db	587	TTTTTTGGTGTAGTGAATTTTGGGCTTACATCGCAGGAAATTCACGCTATTATTATGAGCGCCAAAG	646
Qy	662	TGGAACAAAACGAGAGATTTATTTCCGACTATTTCGCGTAGAATGGTATAATACACAGGTCTAAATA	721
Db	647	TGGAACGAAACGAGAGATTTATTTCCGACTATTTCGCGTAGAATGGTATAATACACAGGTCTAAATA	706
Qy	722	GCTTTGAGAGGGAAGAAATGCGCGAAGTTTGGGTGCGTTATAATCAATTCGCTAGAGATCTAA	781
Db	707	GCTTTGAGAGGGAAGAAATGCGCGAAGTTTGGGTGCGTTATAATCAATTCGCTAGAGATCTAA	766
Qy	782	CGTTAGGGGTATTAGATCTAGTGGCACCTATTTCCCAAGCTATGACACATCGCACTTATATCCAA	841
Db	767	CGTTAGAGATATTAGATCTAGTGGCACCTATTTCCCAAGCTATGACACATCGCACTTATATCCAA	826
Qy	842	TAAATACGAGTGCTCAGTTTAAACAGGGAAGTTTATACAGACGCAATTTGGAGCAACAGGGG	901
Db	827	TAAATACGAGTGCTCAGTTTAAACAGGGAAGTTTATACAGACGCAATTTGGAGCAACAGGGG	886
Qy	902	TAAATATGSCAAGTATGAATTTGGTATAATAATATGCAACCTTCGTTTTCCGCTATAGAGA	961
Db	887	TAAATATGSCAAGTATGAATTTGGTATAATAATATGCAACCTTCGTTTTCCGCTATAGAGG	946
Qy	962	CTCGGGTTATCCGAAGCCCGCATCTACTTGATTTTTCTAGAACAACTTACAAATTTTTAGCA	1021
Db	947	CTCGGGCTATCCGAAGCCCGCATCTACTTGATTTTTCTAGAACAACTTACAAATTTTTAGCG	1006
Qy	1022	CTTCATCACGATGGAGTGCTATAGGCAATATGACTTACTGGCGGGGGCAACAAATTCAT	1081
Db	1007	CTTCATCACGATGGAGTAAATCTAGGCAATATGACTTATGCGGGGGGGCAACAGATTCAT	1066
Qy	1082	CTCGGCCAATAGGAGCGGATTAATTAACCTCAACGCAATGGTCTACCAATACTTCTATTA	1141
Db	1067	CTCGGCCAATAGGAGCGGATTAATTAACCTCAACGCAATGGGCTTACCAATACTTCTATTA	1126
Qy	1142	ATCCTGTAAGATTATCAATTTCTCTCGAGACGTAATTTGGACTGAAATCATATGCAAGGAG	1201
Db	1127	ATCCTGTAAACATTTACGGTTGCGACTCTCGAGACGTTTATAGGACTGAAATCATATGCAAGGAG	1186
Qy	1202	TGCTTCTATCGGGAAATTTACTTGAAACCTATCATATGGTGTCCTCTACCTGTTTGGATTTAAAT	1261
Db	1187	TGCTTCTATCGGGAAATTTACTTGAAACCTATCATATGGTGTCCTCTACCTGTTTGGATTTAAAT	1246
Qy	1262	TTAGGAACCCCTCAGAATACTTTTGAAAGAGGTACTGCTAACTATAGTCAACCCCTATGAGT	1321
Db	1247	TTACGAACCCCTCAGAAATATTTCTGATAGAGGTACCGCTAACTATAGTCAACCTTATGAGT	1306
Qy	1322	CACCTGGGCTTCAATTAAGAATTCAGAACTGAAATTCACACCGAAGAAACACAGAACGAC	1381
Db	1307	CACCTGGGCTTCAATTAAGAATTCAGAACTGAAATTCACACCGAAGAAACACAGAACGAC	1366
Qy	1382	CAAAATATGAATCATATAGTTCATAGGTTATCTCATATAGGCTCATTTTCAATCTAGGG	1441
Db	1367	CAAAATATGAATCTTACAGTCACAGTTATCTCATATAGGTTAATTTTACATCCAGGG	1426
Qy	1442	TGCATGTACAGGTATATCTTTGGACGACCGTAGTGAGATCGGPACAAAATACCAATTAGTT	1501
Db	1427	TGAATGTACCGGTATATCTTTGGACGCAATCGTAGTGAGATCGGPACAAAATACCAATTAGTT	1486
Qy	1502	CAGATACATACACAAATACCATTTGGTAAATCATTTCAACCTTAAATTCAGGTACCTCTG	1561
Db	1487	CAGAGAAATTAATCAAAATACCTTTAGTGAAGGATTTAGAGTTTGGGGGGGACCTCTG	1546
Qy	1562	TAGTCAGTGGCCACAGGATTTTACAGGAGGGGATATAATCCGAACCTAAACGTTTAAATGGTAGTG	1621
Db	1547	TCATTAACAGACACAGGATTTTACAGGAGGGGATATCCCTTCGAAGAAATACCTTTGGTGTATT	1606

Qy	1622	TACTAAGTAGTGGGCTCTTAATTTTAAATAATACATCATTA	CHGCCGATATCGCGTGGAGTTC	1681
Db	1607	TTGTATCTCTACAAGTCAATATTAATTTACCAATTACC	CAAGATACCGTTTAAAGATTTTC	1666
Qy	1682	GTATATCGCTTCTCT-----CAAA	CAATGGTCTCTGAGGGTAAC	1720
Db	1667	GTACGCTTCCAGTAGGGATGACGAGTTATAGTATTA	ACAGGAGCGGCATCCACAGGAG	1726
Qy	1721	TCGGAGGGAGTACTACTTTTGGATCAAGGATTCCTCTAGTACT	TATGAGTGC AAAATGAGTCTTT	1780
Db	1727	TGGGAGCCAAAGTTAGTGTAATATGCCCTCTTCAGAAA	ACTATGGAATAGGGGAGAACT	1786
Qy	1781	TGACATCTCAATCATTTAGATTTGCAAGATTTCCCTGTAGGTAT	TATGTGCATCTGGCAGTC	1840
Db	1787	TAACATCTAGAACATTTAGATATACCGATTTTAGT---	AATCCTTTTTCATTTAGAGCTA	1843
Qy	1841	AAACTGCTGGAATAAGTATATAGTAA-----	TAATGCAGGTAGAC	1879
Db	1844	ATCCAGATATAATTTGGGATAAGTGAAACAACCTCTATTTGGT	GCAGGTCTTATTAGTAGCG	1901
Qy	1880	AAACGTTTCACTTTGTATAAAAATGAAATTCATTC	CCAATTACTGCAACCTTCGAAAGCAGAAAT	1939
Db	1904	GTGAACCTTTATATAGATATAAATTTGAAATTTATTT	CTAGCAGATGCAACATTTGAAGCAGAAAT	1963
Qy	1940	ACGATTTAGAAAGGGCGCAAGAGCGGTGAATGCTCTGTTT	ACTAATATAGAAATCCAAAGAA	1999
Db	1964	CTGATTTAGAAAGAGCACAAAGCGGTGAATGCCCTGTTT	ACTTCTTCCAAATCAAAATCG	2023
Qy	2000	GATTTGAAAACAGATGTGACAGATTTATCATATTTGAT	CAAGTATCCAAATTTAGTGGCGTGTT	2059
Db	2024	GGTTAAAAACCGATGTGACGGATTTATCATATGAT	CAAGTATCCAAATTTAGTGGATGTT	2083
Qy	2060	TATCGGATGAATTCGTCTTAGATGAAAAGAGAGAA	TTACTTTGAGAAAGTGAAATATGCGGA	2119
Db	2084	TATCAGATGAATTTGTCTGATGAAAAGCGAGAA	TTGTCCGAGAAAGTCAACATGCGGA	2143
Qy	2120	AACGACTCAGTGTAGAAAGAACTTACTCCAAGAT	CCAAACTTCACATCCATCAATAAGC	2179
Db	2144	AGCGACTCAGTGTAGGCGGAATTTTACTTCAAGAT	CCAAACTTCAGAGGGATCAATAGAC	2203
Qy	2180	AACGAGACTTCATATCTACTAATGAGCAATCGAA	TTTCACATCTATCCATGAACAATCTG	2239
Db	2204	AACGAGAC-----	-----	2211
Qy	2240	AACATGATGGTGGGAAGTGAGAACATTTACAAT	CCAGGAAGAAATGACGTATTTAAAG	2299
Db	2212	--CGTGGCTGGAGAGAGATGACAGATATTA	CCATCCAGGAGAGATGACGTATTCAGAG	2269
Qy	2300	AGAAATACGTACACTACCGGGTACCGGTTGATGAGT	GCTATCCAAAGTATTTATATCAGA	2329
Db	2270	AGAATTAGGTGCACTACCGGTACCGGTTGATGAGT	GCTATCCAAAGTATTTATATCAGA	2329
Qy	2360	AAATAGGAGAGTCCGAAATTTAAAGCTTTATCTCGCT	ACCNAATTTAAGAGGGTATTTGAAG	2419
Db	2330	AAATAGATGAGTCCGAAATTTAAAGCTTTATAC	CCCGTTATGAAATTTAAGAGGGTATTTCCAAG	2389
Qy	2420	ATAGTCAAGATTTTAGAGATATTTTGATTCGTTTAT	ATGCGAAACATGAAACATTCGATG	2479
Db	2390	ATAGTCAAGACTTTAGAAATCTATTTGATCGGTTA	CAATGCAAAACAGAAATAGTAATG	2449
Qy	2480	TTCCAGGTACCGAGTCCGTATGCGCGCTTT	CAGTTGAAAAGCCCAATCCGAGGTGCGGAG	2539
Db	2450	TGCCAGGCACGGGTCTCTTATGCGCGCTT	TCACGCCAAAGTCCAAATCCGAAAGGTGGAG	2509
Qy	2540	AACCGAATCGATCGGCACACATTTTGAATGGAAT	CTCTGATCTAGATTTGTTCTCTGCAGAG	2599
Db	2510	AACCGAATCGATCGCGGCCACACTTTGAATGGAAT	CCTGATCTAGATTTGTTCTCTGCAGAG	2569
Qy	2600	ATGAGAGAAATCTGCGCATCATTTCCCATCTTTCT	TTTGGATATTTGATTTGGATGCA	2659
Db	2570	ACGGGAAAAAATGTGCACATCATTTCCATTT	CACCTTGGATATTTGATTTGGATGTA	2629
Qy	2660	CAGACTTGATGAGAATCTAGGCGGTGGGTGAT	TTTCAAGATTTAAGACGCAAGAAAGGTC	2719

QY 2 TGACTTCAAAATAGGAAATAGGAATGAAATATATAATGCTTTATCGATTCCAGCTGTAT 61
 Db 2 TGGCTTCAAAATAGGAAATAGGAATGAAATATATAATGCTTTATCGATTCCAGCTGTAT 46
 QY 62 CGAATCAATCCACAAATGATCTATCACCAGATGCTCGTATTGAGGATCTTTTGTGTA 121
 Db 47 CGAATCAATCCGACAAATGATCTATCACCAGATGCTCGTATTGAGGATGCTTTGTGTA 106
 QY 122 TAGCCGAGGGAATATATCAATCCACTTGTAGCGCATCAACAGTCCAAACGGGTATTA 181
 Db 107 TAGCCGAGGGAACAAATATCGATCCATTTGTAGCGCATCAACAGTCCAAACGGGTATTA 166
 QY 182 ACATAGCTGTAGGAATAGTGTATTTAGCGGTACCGTTTGTGGCAATATAGCTAGTT 241
 Db 167 ACATAGCTGTAGGAATAGTGTATTTAGCGGTACCGTTTGTGGCAATATAGCTAGTT 226
 QY 242 TTTATAGTTTTCTTGTGTGTAATTTAGCGGTACCGTTTGTGGCAATATAGCTAGTT 301
 Db 227 TTTATAGTTTTCTTGTGTGTAATTTAGCGGTACCGTTTGTGGCAATATAGCTAGTT 286
 QY 302 TAGAATGTGCAACAACTTATTAATCAACAAATTAACAGAAATGCTAGGAATACGGCAC 361
 Db 287 TAGAATGTGCAACAACTTATTAATCAACAAATTAACAGAAATGCTAGGAATACGGCCTC 346
 QY 362 TTGCTGATTTACAGGTTTAGGAGATTCCTTTAGAGCCTATCAACAGTCACTTTGAAGATT 421
 Db 347 TTGCTGATTTACAGGTTTAGGAGATTCCTTTAGAGCCTATCAACAGTCACTTTGAAGATT 406
 QY 422 GGCTAGAAAACCGTGATGATGCAAGAACGAGAGTGTCTTTATACCCAAATATATAGCCT 481
 Db 407 GGCTAGAAAACCGTGATGATGCAAGAACGAGAGTGTCTTTATACCCAAATATATAGCCT 466
 QY 482 TAGAATGTGATTTCTTAATGCGATGCGCTTTTTCGCAATTTAGAAACCAAGAGTTCCAT 541
 Db 467 TAGAATGTGATTTCTTAATGCGATGCGCTTTTTCGCAATTTAGAAACCAAGAGTTCCAT 526
 QY 542 TATTAAATGATATGCTCAAGCTGCAAAATTTACACCTATTATTATTCAGAGAGTGCCTCTC 601
 Db 527 TATTAAATGATATGCTCAAGCTGCAAAATTTACACCTATTATTATTCAGAGAGTGCCTCTC 586
 QY 602 TTTTGTAGTGAATTTGGGCTTACATCGCAGGAAATTCACGTTATTATGAGCGCCAAAG 661
 Db 587 TTTTGTAGTGAATTTGGGCTTACATCGCAGGAAATTCACGTTATTATGAGCGCCAAAG 646
 QY 662 TGGAAACAAACGAGATTTATCCGACTATTGCGGTAGAAATGCTTAATACAGGTTCTAAATA 721
 Db 647 TGGAAACAAACGAGATTTATTCGACTATTGCGGTAGAAATGCTTAATACAGGTTCTAAATA 706
 QY 722 GCTTTAGAGGGAACAAATGCGCAAGTTGGGTGCGTTATATCAATTCGCTAGAGATCTAA 781
 Db 707 GCTTTAGAGGGAACAAATGCGCAAGTTGGGTGCGTTATATCAATTCGCTAGAGATCTAA 766
 QY 782 CGTTAGGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGACACTCGCACTTATCCAA 841
 Db 767 CGTTAGGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGACACTCGCACTTATCCAA 826
 QY 842 TAAATACAGTGTCTAGTTAAACAGGGAATTTATACAGCGCAATTTGGAGCAACAGGGG 901
 Db 827 TAAATACAGTGTCTAGTTAAACAGGGAATTTATACAGCGCAATTTGGAGCAACAGGGG 886
 QY 902 TAAATATGGAAGTATCAATTTGGTATTAATATGCACTTCGTTTTCGCTATAGAGA 961
 Db 887 TAAATATGGAAGTATCAATTTGGTATTAATATGCACTTCGTTTTCGCTATAGAGA 946
 QY 962 CTCGGTTATCCGAAGCCCGCATCTACTGATTTTCTAGAACAACTTTACAAATTTTAGCA 1021
 Db 947 CTCGGTTATCCGAAGCCCGCATCTACTGATTTTCTAGAACAACTTTACAAATTTTAGCG 1006
 QY 1022 CTTTCATCAGATGAGTGTCTACTAGGATATGACTTACTGGCGGGGCAACAAATTCAT 1081
 Db 1007 CTTTCATCAGATGAGTGTCTACTAGGATATGACTTACTGGCGGGGCAACAAATTCAT 1066

QY 1082 CTCGGCAATAGGAGCGGATTAATACTCAACGATGGGTCTACCAATCTTCTATTATTA 1141
 Db 1067 CTCGGCAATAGGAGCGGATTAATACTCAACGATGGGTCTACCAATCTTCTATTATTA 1126
 QY 1142 ATCCTGTAAAGATPATCATTTCTCTCGAGACGTATATTGGACTGAATCATATGCGAGG 1201
 Db 1127 ATCCTGTAAAGATPATCATTTGCGATCTCGAGACGTATATTAGGACTGAATCATATGCGAGG 1186
 QY 1202 TGCTTCTATGGGAATTTACCTTGAACCTTATCATGGTGTCCCTACTGTGTAGATTAAAT 1261
 Db 1187 TGCTTCTATGGGAATTTACCTTGAACCTTATCATGGTGTCCCTACTGTGTAGATTAAAT 1246
 QY 1262 TTAGGAACCTCTCAGATATCTTTTGAAGAGTACTGTCTAACTATAGTCAACCTTATGAGT 1321
 Db 1247 TTAGGAACCTCTCAGATATTTCTGATAGAGTACCGTAACTATATAGTCAACCTTATGAGT 1306
 QY 1322 CACCTGGGCTTCAATTTAAAGATTTAGAAATCTGAAATTCACCCAGAAACAAAGAACGAC 1381
 Db 1307 CACCTGGGCTTCAATTTAAAGATTTAGAAATCTGAAATTCACCCAGAAACAAAGAACGAC 1366
 QY 1382 CAAATTTAGATCATATAGTCTAGGTATCTCACATAGGGCTCATTTCAATCTTAGGG 1441
 Db 1367 CAAATTTAGATCATTTACAGTCAAGGTATCTCATATAGGTATAATTTTCAATCTTAGGG 1426
 QY 1442 TGCAATGTACAGTATATTTCTTGACGACACCGTATGTCAGATCGTACAAATACCAATTAGT 1501
 Db 1427 TGAATGTACCGGTATATTTCTTGACGACACCGTATGTCAGATCGTACAAATACCAATTAGT 1486
 QY 1502 CAGATAGCAATAACAAATACCAATTTGGTAAATTCATTTCAACCTTTAAATTCAGGTACCTCTG 1561
 Db 1487 CAGAGAGATTAATCAATACCTTTAGTGAAGAGATTTAGAGTTTGGGGGGGACCCTCTG 1546
 QY 1562 TAGTCAATGCGCCAGAGATTTACAGGAGGGGATATAATTCGAACTAAAGTTTAAATGGTAGTG 1621
 Db 1547 TCATTCAGGACAGGATTTACAGGAGGGGATATCTTCGAGAAATACCTTTGGTGATT 1606
 QY 1622 TACTAAGTATGGGTCTTAATTTTAAATAATCATCATTTACAGCGGTATTCGCGTACAGAGTTC 1681
 Db 1607 TTGATCTCTACAGTCAATATTAATTTACCAATTTACCAAGATACCGTTTAAAGATTTC 1666
 QY 1682 GTTATGCTGCTTCT-----CAACAAATGGTCTCGAGGGTAACTG 1720
 Db 1667 GTTATGCTTCCAGTAGGGATGCAACGATTTATAGTATTTAACAGAGCGGCAATCCACAGGAG 1726
 QY 1721 TCGGAGGAGTACTACTTTTGTATCAAGGATTCCTTAGTACTATGAGTGCATAATGAGTCTT 1780
 Db 1727 TGGAGCGCAAGTTAGTGAATATGCTCTTCAGAAACTATGGAATAGGGGAGACT 1786
 QY 1781 TGACATCTCAATCATTTAGATTTGAGAAATTTCTCTGAGGTATTTAGTGCATCTGGCAGTC 1840
 Db 1787 TAACATCTAGAACATTTAGATATACCGATTTTAGT---AATCTTTTTCATTTTAGAGCTA 1843
 QY 1841 AAATCTGCTGAATPAAGTAAAGTAA-----TAATGCAAGGTAGAC 1879
 Db 1844 ATCCAGATATAATTTGGGATAAGTGAACACCTCTATTTTGGTGCAGGTTCTTATTAGTAGCG 1903
 QY 1880 AAACGTTTCACTTTGATATAAAATTTGAATTTCAATTTACTGCAACCTTCGAAAGCAGAAT 1939
 Db 1904 GTGAATCTTATATAGATAAAATTTGAATTTATTTCTGAGATGCAACATTTGAGCAGAAAT 1963
 QY 1940 ACGATTTAGAAAGCGGCGCAAGAGCGGTGAATGCTCTGTTTACTTAATACGAATCCAGAA 1999
 Db 1964 CTGATTTAGAAAGCAGCAACAAAGCGGTGAATGCCCTGTTTACTTCTTCCAATCAATTCG 2023
 QY 2000 GATTGAAAACAGATGTCAGAGATTTATATTTGATCAAGTATCCAAATTTAGTGGCGGTT 2059
 Db 2024 GGTATAAAACCGATGTCAGCGATTTATCATTTGATCAAGTATCCAAATTTAGTGGATTTGT 2083
 QY 2060 TATCGGATGAATTTCTGCTTAGATGAAAGAGAGAAATTTACTTGAAGAGTCAAAATATGCGA 2119
 Db 2084 TATCAGATGAATTTTGTCTGATGAAAGAGAGAAATTTGTCGAGAAAGTCAACATGCGA 2143
 QY 2120 AACGACTCAGTGTAGAAAGAAACTTACTCCAAGATCCAACTTCAATCCATCAATCAATAGC 2179

This Page Blank (uspto)

1	3566.2	99.4	4173	4	US-09-661-322A-37	Sequence 37, Appli
2	3266.6	88.6	3684	1	US-08-448-170-7	Sequence 7, Appli
3	3266.6	88.6	3684	1	US-08-361-803-5	Sequence 5, Appli
4	3260.2	88.4	3684	4	US-09-661-322A-62	Sequence 62, Appli
5	3133.6	85.0	4074	1	US-08-377-690-1	Sequence 1, Appli
6	2887.2	72.9	3934	1	US-08-100-709-3	Sequence 3, Appli
7	2887.2	72.9	3934	1	US-08-176-865-3	Sequence 3, Appli
8	2687.2	72.9	3934	1	US-08-474-038-3	Sequence 3, Appli
9	2687.2	72.9	3934	2	US-08-779-046-3	Sequence 3, Appli
10	2687.2	72.9	3934	2	US-08-881-340-3	Sequence 3, Appli
11	1933.4	48.6	3522	1	US-08-040-751-4	Sequence 4, Appli
12	1793.4	48.6	3522	1	US-08-291-368-1	Sequence 1, Appli
13	1793.4	48.6	3522	2	US-08-962-190-1	Sequence 1, Appli
14	1793.4	48.6	3522	5	PCT-US95-10310-1	Sequence 1, Appli
15	1791.8	48.6	3522	6	5164180-3	Sequence 1, Appli
16	1791.8	48.6	3522	6	5164180-3	Patent No. 5164180
17	1662	45.1	4106	1	US-08-434-823-1	Patent No. 5164180
18	1662	45.1	4106	1	US-08-457-366-1	Sequence 1, Appli
19	1581.6	42.9	3558	3	US-09-178-252-22	Sequence 1, Appli
20	1581.6	42.9	3558	4	US-09-826-660-22	Sequence 22, Appli
21	1501	40.7	3766	1	US-08-032-364-1	Sequence 22, Appli
22	1495.6	40.6	3624	1	US-07-951-715A-6	Sequence 1, Appli
23	1495.6	40.6	3624	2	US-08-459-448A-6	Sequence 6, Appli
24	1495.6	40.6	3624	3	US-08-459-595A-6	Sequence 6, Appli
25	1495.6	40.6	3624	3	US-08-459-504B-6	Sequence 6, Appli
26	1495.6	40.6	3624	3	US-08-459-444-6	Sequence 6, Appli
27	1495.6	40.6	3624	3	US-09-053-549-7	Sequence 7, Appli

QY 301 CTAGAACATGTCGAACAACTTATAAATCAACAAATAACAGAAAAATGCTAGGAATACGGCA 360
 DB 301 CTAGAACATGTCGAACAACTTATAAATCAACAAATAACAGAAAAATGCTAGGAATACGGCA 360
 QY 361 CTTGCTCGATTACAAGGTTTAGGAGATTCCTTTTAGAGCCTATCAACAGTCACTTTGAAGAT 420
 DB 361 CTTGCTCGATTACAAGGTTTAGGAGATTCCTTTTAGAGCCTATCAACAGTCACTTTGAAGAT 420
 QY 421 TGGCTAGAAAACCGTGATGATGACGACGACGAGAGTGTCTTTATATCCCAATATATAGCC 480
 DB 421 TGGCTAGAAAACCGTGATGATGACGACGACGAGAGTGTCTTTATATCCCAATATATAGCC 480
 QY 481 TTAGAACTTGATTTCTTAATGCGATGCGCTTTTCGCAATTAGAAACCAAGAAAGTTCCA 540
 DB 481 TTAGAACTTGATTTCTTAATGCGATGCGCTTTTCGCAATTAGAAACCAAGAAAGTTCCA 540
 QY 541 TTATTAATGTPATATGCTCAAGCTGCAAAATTTACACCTATTATTATTGAGAGATGCGCTCT 600
 DB 541 TTATTAATGTPATATGCTCAAGCTGCAAAATTTACACCTATTATTATTGAGAGATGCGCTCT 600
 QY 601 CTTTTTGGTAGTAATTTGGGCTTACATCGCAGGAAATTCACGTTATTATGAGCGCAA 660
 DB 601 CTTTTTGGTAGTAATTTGGGCTTACATCGCAGGAAATTCACGTTATTATGAGCGCAA 660
 QY 661 GTGAAACAAACGAGAGATTTATCCGACTATTGCGTAGAATGGTATAATACAGGTCTAAAT 720
 DB 661 GTGAAACAAACGAGAGATTTATCCGACTATTGCGTAGAATGGTATAATACAGGTCTAAAT 720
 QY 721 AGCTTGAGAGGGAACAAATGCGCAAGTTGGGTGCGTTTAAATCAATTTCCGTAGAGATCTA 780
 DB 721 AGCTTGAGAGGGAACAAATGCGCAAGTTGGGTGCGTTTAAATCAATTTCCGTAGAGATCTA 780
 QY 781 ACGTTAGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGACACTCGCACTTATCCA 840
 DB 781 ACGTTAGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGACACTCGCACTTATCCA 840
 QY 841 ATAATAACGAGTGTCTAGTTTAAACAGGGAAGTTTATACAGACGCAATGGAGCAACAGGG 900
 DB 841 ATAATAACGAGTGTCTAGTTTAAACAGGGAAGTTTATACAGACGCAATGGAGCAACAGGG 900
 QY 901 GTAATAATGCGAAGTATGAATGGTATAATAATGAATGAATGAATGAATGAATGAATGAAT 960
 DB 901 GTAATAATGCGAAGTATGAATGGTATAATAATGAATGAATGAATGAATGAATGAATGAAT 960
 QY 961 ACTCGGTTATCCGAAGCCGATCTACTTGTATTTCTAGAACAACTTACAAATTTTATAGC 1020
 DB 961 ACTCGGTTATCCGAAGCCGATCTACTTGTATTTCTAGAACAACTTACAAATTTTATAGC 1020
 QY 1021 ACTTCATCAGATGGAGTGTCTAGGCATATGACTTACTGGCGGGGGGACACAAATTCAA 1080
 DB 1021 ACTTCATCAGATGGAGTGTCTAGGCATATGACTTACTGGCGGGGGGACACAAATTCAA 1080
 QY 1081 TCTCGGCAATAGAGGCGGANTTAAATACCTCAACGATGGGTCTACCAATCTTCTATT 1140
 DB 1081 TCTCGGCAATAGAGGCGGANTTAAATACCTCAACGATGGGTCTACCAATCTTCTATT 1140
 QY 1141 AATCCTGTAGATTTATCATTTCTCTCGAGACGTATATTGGACTGAATCATATGACGGA 1200
 DB 1141 AATCCTGTAGATTTATCATTTCTCTCGAGACGTATATTGGACTGAATCATATGACGGA 1200
 QY 1201 GTGCTTCTATGGGAAATTTACCTTGAACCTTATTCATGGTGTCCCTACTGTAGATTTAAT 1260
 DB 1201 GTGCTTCTATGGGAAATTTACCTTGAACCTTATTCATGGTGTCCCTACTGTAGATTTAAT 1260
 QY 1261 TTTAGGAACCTCAGAAATCTTTTGAAGAGGTAATCTGCTAACTATATAGTCAACCTATGAG 1320
 DB 1261 TTTAGGAACCTCAGAAATCTTTTGAAGAGGTAATCTGCTAACTATATAGTCAACCTATGAG 1320
 QY 1321 TCACCTGGGCTTCAATTTAAAGATTTCAGAACTGAATTTACCACAGAAACAAACAGACGA 1380
 DB 1321 TCACCTGGGCTTCAATTTAAAGATTTCAGAACTGAATTTACCACAGAAACAAACAGACGA 1380
 QY 1381 CCAAAATTAATGAATCATATAGTCATAGTTTATCTCACATAGGGCTCAATTCACAAATCTAGG 1440

DB 1381 CCAAAATTAATGAATCATATAGTCATAGTTTATCTCACATAGGGCTCAATTCACAAATCTAGG 1440
 QY 1441 GTGCATGTACAGTATATTTCTTGACGCGACCGTAGTGCAGATCGTACAAATACCAATAGT 1500
 DB 1441 GTGCATGTACAGTATATTTCTTGACGCGACCGTAGTGCAGATCGTACAAATACCAATAGT 1500
 QY 1501 TCAGATAGCATACACAAATACCAATTTGGTAAATCATTTCAACCTTAATTCAGGTACCTCT 1560
 DB 1501 TCAGATAGCATACACAAATACCAATTTGGTAAATCATTTCAACCTTAATTCAGGTACCTCT 1560
 QY 1561 GTAGTCAGTGGCCAGGATTTACAGGAGGGGATATTAATCCGAACCTAACGTTAATGGTAGT 1620
 DB 1561 GTAGTCAGTGGCCAGGATTTACAGGAGGGGATATTAATCCGAACCTAACGTTAATGGTAGT 1620
 QY 1621 GTACTAAGTATGGTCTTAATTTTAAATATACATCATTTGACATCTCAATCATTTAGA 1680
 DB 1621 GTACTAAGTATGGTCTTAATTTTAAATATACATCATTTGACATCTCAATCATTTAGA 1680
 QY 1681 CGTTATGCTGCTTCTCAACAAATGGTCTGAGGGTAACCTGTCGAGGGAGTACTACTTTT 1740
 DB 1681 CGTTATGCTGCTTCTCAACAAATGGTCTGAGGGTAACCTGTCGAGGGAGTACTACTTTT 1740
 QY 1741 GATCAAGGATTCCTCTAGTACTATGAGTGCATAATGAGTCTTTGACATCTCAATCATTTAGA 1800
 DB 1741 GATCAAGGATTCCTCTAGTACTATGAGTGCATAATGAGTCTTTGACATCTCAATCATTTAGA 1800
 QY 1801 TTTGCGAAGATTCCTGTAGGTATTAGTGCATCTGGCAGTCAAACTGCTGGAATAAGTATA 1860
 DB 1801 TTTGCGAAGATTCCTGTAGGTATTAGTGCATCTGGCAGTCAAACTGCTGGAATAAGTATA 1860
 QY 1861 AGTAATAATGCAGGTAGACAAACGTTTCACTTTGATAAAATGAAATTCATTCCAATTTACT 1920
 DB 1861 AGTAATAATGCAGGTAGACAAACGTTTCACTTTGATAAAATGAAATTCATTCCAATTTACT 1920
 QY 1921 GCAACCTTCGAAGCAGAAATACGATTTAGAAAGGCGCAAGAGGCGGTGAATGCTCTGTTT 1980
 DB 1921 GCAACCTTCGAAGCAGAAATACGATTTAGAAAGGCGCAAGAGGCGGTGAATGCTCTGTTT 1980
 QY 1981 ACTAATACGAATCCAGAGATTTGAAAACAGATGTGACAGATTTATCATTTGATCAAGTA 2040
 DB 1981 ACTAATACGAATCCAGAGATTTGAAAACAGATGTGACAGATTTATCATTTGATCAAGTA 2040
 QY 2041 TCCAAATTTAGTGGCTGTTTATCGGATGAATCTGCTTAGATGAAAAGAGAGAAATTTACTT 2100
 DB 2041 TCCAAATTTAGTGGCTGTTTATCGGATGAATCTGCTTAGATGAAAAGAGAGAAATTTACTT 2100
 QY 2101 GAGAAAGTGAATATATGCGAAACGACTCAGTGTATGAAAGAACTTACTTCCAAAGATCCAAAC 2160
 DB 2101 GAGAAAGTGAATATATGCGAAACGACTCAGTGTATGAAAGAACTTACTTCCAAAGATCCAAAC 2160
 QY 2161 TTCAATCCATCAATTAAGCAACAGATTTCAATCTACTAATGAGCAATCGAATTTTCA 2220
 DB 2161 TTCAATCCATCAATTAAGCAACAGATTTCAATCTACTAATGAGCAATCGAATTTTCA 2220
 QY 2221 TCTATCCATGAACAACTGAAACATGATGCTGGGGAAGTGAGAACTTACCAATCCAGGAA 2280
 DB 2221 TCTATCCATGAACAACTGAAACATGATGCTGGGGAAGTGAGAACTTACCAATCCAGGAA 2280
 QY 2281 GGAATGACGTATTTAAAGAGAAATTAAGTGCACACTACCGGGGACTTTTAAATGAGTGTAT 2340
 DB 2281 GGAATGACGTATTTAAAGAGAAATTAAGTGCACACTACCGGGGACTTTTAAATGAGTGTAT 2340
 QY 2341 CCGAGGTATTTATCAAAAATAGAGAGTCCGAATTTAAAGCTTATACTCGCTACCAA 2400
 DB 2341 CCGAGGTATTTATCAAAAATAGAGAGTCCGAATTTAAAGCTTATACTCGCTACCAA 2400
 QY 2401 TTAAGAGGGTATATTCAAGATAGTCAAGATTTAGAGATATTTGATTCCTTATTAATGCG 2460
 DB 2401 TTAAGAGGGTATATTCAAGATAGTCAAGATTTAGAGATATTTGATTCCTTATTAATGCG 2460
 QY 2461 AAAATGAAACATTTGATGTTCCAGGTACCGAGTCCGATGCGGCTTTCAGTTGAAAGC 2520

|||||TCGAATCATTCGCGACAAATGAATCTATCAACCGATGCTCGTATTAGGATAGCTTGTGTT 120
Db
121 ATAGCCGAGGGAATATATATCAATCCACTGTTAGCGCATCAACAGTCCAAACGGGTATT 180
Qy
121 ATAGCCGAGGGAACAAATATCGATCCATTTGTTAGCGCATCAACAGTCCAAACGGGTATT 180
Db
181 AACATAGCTGTGAGAACTACTAGGTGTTATTAGCGGTACCGTTGCTGGACAAATAGCTAGT 240
Qy
181 AACATAGCTGTGAGAACTACTAGGTGTTATTAGCGGTACCGTTGCTGGACAAATAGCTAGT 240
Db
241 TTTTATAGTTTTCTTTGTTGTAATTTATGCGCCCGCGCGAGAGATCAGTGGGAATTTTC 300
Qy
241 TTTTATAGTTTTCTTTGTTGTAATTTATGCGCCCGCGCGAGAGATCAGTGGGAATTTTC 300
Db
301 CTAGAACATGTCGAACAACTTATTAATCAACAAATAACAGAAATGCTAGGAATACGGCA 360
Qy
301 CTAGAACATGTCGAACAACTTATTAAGCAACAAAGTAAACAGAAATACTAGGGATACGGCT 360
Db
361 CTGCTCGATTACAAGTTTATAGGAGATTCCTTTAGAGCCTATCAACAGTCACTTGAAGAT 420
Qy
361 CTGCTCGATTACAAGTTTATAGGAGATTCCTTTAGAGCCTATCAACAGTCACTTGAAGAT 420
Db
421 TGGCTAGAAAACCGTGTATGTCGAAGAACGAGAGTGTCTTTATACCCAAATATATAGCC 480
Qy
421 TGGCTAGAAAACCGTGTATGTCGAAGAACGAGAGTGTCTTTATACCCAAATATATAGCC 480
Db
481 TTGAACTGTGATTTCTTAATGCGATGCGCGTTCGCAATTAAGAACTTGAAGTTTCCA 540
Qy
481 TTGAACTGTGATTTCTTAATGCGATGCGCGTTCGCAATTAAGAACTTGAAGTTTCCA 540
Db
541 TTATTAATGTTATATGCTCAAGCTGCAAAATTTACACCTATTTATTTAGAGATGCTCT 600
Qy
541 TTATTAATGTTATATGCTCAAGCTGCAAAATTTACACCTATTTATTTAGAGATGCTCT 600
Db
601 CTTTTTGGTAGTAATTTGGGCTTTACATCGCAGAAATTCACCGTATTATGAGCGCCAA 660
Qy
601 CTTTTTGGTAGTAATTTGGGCTTTACATCGCAGAAATTCACCGTATTATGAGCGCCAA 660
Db
661 GTGGAAACAGAGAGATTTCCGACTATGCGTAGAATGTTGTAATATACAGGTCTAAAT 720
Qy
661 GTGGAAACAGAGAGATTTCCGACTATGCGTAGAATGTTGTAATATACAGGTCTAAAT 720
Db
721 AGCTTGAGAGGACAAATGCGCAAGTTGGGTGGTTTAAATCAATTCGTTAGAGATCTA 780
Qy
721 AATTTGAGAGGACAAATGCTGAAGTTGGTGGATATATCAATTCGTTAGAGATCTA 780
Db
781 ACGTTAGGGTATTAGATCTAGTGGCACTATTCGCAAGCTATGACATCGCACTTATCCA 840
Qy
781 ACGTTAGGGTATTAGATCTAGTGGCACTATTCGCAAGCTATGACATCGCACTTATCCA 840
Db
841 ATAAATACGAGTCTCAGTTAACAGGGAAGTTTATACAGCGCAATTTGGAGCAACAGGG 900
Qy
841 ATAAATACGAGTCTCAGTTAACAGGGAAGTTTATACAGCGCAATTTGGAGCAACAGGG 900
Db
901 GTAATATATGAGTATGAAATGTTGGTATTAATTAATTAATGACCTTCGTTTCGCT 954
Qy
901 GCACTTCAGGATTTGCAAGTACGAAATGGTATTAATTAATTAATGACCATGTTTCGCT 954
Db
955 ATAGAGACTGCGGTTATCCGAGCCCGCATCTACTTGAATTTCTAGAACAACTTACAAAT 1014
Qy
955 ATAGAGACTGCGGTTATCCGAGCCCGCATCTACTTGAATTTCTAGAACAACTTACAAAT 1014
Db
961 ATAGAGCTGCGGTTATAGGCGCTCCGCACTACTTGAATTTTCAGAACAGCTTACAAAT 1020
Qy
1015 TTTTAGCACTCATCAGATGAGTCTAGGAGATGCTAGGAGATGCTAGGCGGGGACACACA 1074
Qy
1021 TTAGCGGTATTAAGTCCAGTGAATTAATCAATATATGAATTTACTGGGTGGGACATAGA 1080
Db
1075 ATTCAATCTCGGCAATAGGAGCGGATTAATTAATCACTCAACGATGGGTCTACCAATACT 1134
Qy
1081 CTTGAATCGGCAATTAAGGGGTCAATTAAGTACCTCGACACAGGAAATACCAATACT 1140
Db
1135 TCTATTAATCTGTGAAGATTTATCTTCTCTGAGACGTTATTTGGACTGAATCATAT 1194
Qy

1141 TCTATTAATCTGTAAACATTTACAGTTTACATCTCGACGCTTTATAGAACAGAAATCATTT 1200
Db
1195 GCAGGAGTGTCTTATGCGGAAATTTACCTTGAACCTTATCATGTGTCTTACTTGTGTAGA 1254
Qy
1201 GCAGGAGTAAAT 1254
Db
1255 TTTTAAATTTTAGGACCTCTCAGAACTATTTTGAAGAGGTACTCTACTACTAGTCAACCC 1314
Qy
1255 TTTTAAATTTTAGGAGAAATCCCTGAAATTCCTTT---AGAGGTAGCTTCTCTACTATATAGG 1311
Db
1315 TATGAGTCACCTCGGCTTCAATTTAAAGATTCAGAACTGAAATTTACCCAGAGAAACAA 1374
Qy
1312 TATACTGGAGTGGGACACAACTATTTGATTCAGAACTGAAATTTACCCAGAGAAACAA 1371
Db
1375 GAACGACAAATTTATGAATCATATAGTATAGTATATCTCACATAGGGCTCATTTTCAAA 1434
Qy
1372 GAACGACAAATTTATGAATCTTACAGTCATAGATTTATCTAATATAGACTAATATCAGA 1431
Db
1435 TCTAGGCTGCATGTPACCAGTATATCTTGGACCGCAGTGTAGTCAGATCGTACAAATACC 1494
Qy
1432 AACACTTTGAGAGCACCGATATATCTTGGACCGCAGTGTAGTCAGATCGTACAAATACC 1491
Db
1495 ATTAGTTTACATAGCATAACAAATACCAATTCGTTAAATCATTTCAACCTTAATTCAGGT 1554
Qy
1492 ATTAGTTTACATAGCATAACAAATACCAATTCGTTAAATCATTTCAACCTTAATTCAGGT 1551
Db
1555 ACCTCTGTAGTACGTCGCGCCAGGATTTACAGAGGGGATATATTCGGAACCTAACGTTAAT 1614
Qy
1552 ACCTCTGTAGTACGTCGCGCCAGGATTTACAGAGGGGATATATTCGGAACCTAACGTTAAT 1611
Db
1615 GGTAGTGTACTAAGTATGGGTCTTAATTTTAAATAACATCATTTACAGCGGTATCGCGTG 1674
Qy
1612 GGTAGTGTACTAAGTATGGGTCTTAATTTTAAATAACATCATTTACAGCGGTATCGCGTG 1671
Db
1675 AGAGTTTCTGTTATGCTCTCTCAACAAATGCTCTCGAGGTAACTGTGCGAGGGAGTACT 1734
Qy
1672 AGAGTTTCTGTTATGCTCTCTCAACAAATGCTCTCGAGGTAACTGTGCGAGGGAGTACT 1731
Db
1735 ACTTTTGTATCAAGGATTCCTAGTACTATGAGTGCAGAAATGAGTCTTGACATCTCAATCA 1794
Qy
1732 ACTTTTGTATCAAGGATTCCTAGTACTATGAGTGCAGAAATGAGTCTTGACATCTCAATCA 1791
Db
1795 TTTAGATTTGCAAAATTTCTGTAGGTATTTAGTGCATCTGGCAGTCAAACTGCTGGAATA 1854
Qy
1792 TTTAGATTTGCAAAATTTCTGTAGGTATTTAGTGCATCTGGCAGTCAAACTGCTGGAATA 1851
Db
1855 AGTATAGTAAATTAATGAGGTAGACAAACGTTTCACTTTGATATAAATGAAATTCATTTCCA 1914
Qy
1852 AGTATAGTAAATTAATGAGGTAGACAAACGTTTCACTTTGATATAAATGAAATTCATTTCCA 1911
Db
1915 ATTACTGCAACCTTCGAAGCAGAAATACGATTTAGAAAGGCGCAAGAGCGGTGAATGCT 1974
Qy
1912 ATTACTGCAACCTTCGAAGCAGAAATACGATTTAGAAAGGCGCAAGAGCGGTGAATGCT 1971
Db
1975 CTGTTTACTAATACGAAATCCAGAGATTCAGAAACAGATGTCAGACATTTATCATATTGAT 2034
Qy
1972 CTGTTTACTAATACGAAATCCAGAGAGTTGAAACAGGTGTGACAGATTTATCATATTGAT 2031
Db
2035 CAAGTATCCAAATTTAGTGGCGTATTATCGGATGAAATCTGCTTTAGATGAAAGAGAGAA 2094
Qy
2032 GAAGTATCCAAATTTAGTGGCGTATTATCGGATGAAATCTGCTTTGGATGAAAGAGAGAA 2091
Db
2095 TTAATTTGAGAAAGTGAATATATGCAACGACTCAGTGTAGTGAAGAACTTACTTCCAGAT 2154
Qy
2092 TTAATTTGAGAAAGTGAATATATGCAACGACTCAGTGTAGTGAAGAACTTACTTCCAGAT 2151
Db
2155 CCAAACTTCACTCCATCAATTAAGCAACAGACTTTCATATCTACTAATGAGCAATCGAAT 2214
Qy
2152 CCAAACTTCACTCCATCAATTAAGCAACAGACTTTCATATCTACTAATGAGCAATCGAAT 2211
Db
2215 TTTCAATCTATCCAGAACTCTGAACTGAGTGTGGGAGTGAAGCAATTCATCAATC 2274
Qy
2212 TTTCAATCTATCCAGAACTCTGAACTGAGTGTGGGAGTGAAGCAATTCATCAATC 2271
Db

QY 2275 CAGGAAGGAATGACGTAATTTAAAGAGAAATTAAGTCAACCTACCGGGGACCTTTAAATGAG 2334
DB 2272 CAGGAAGGAATGACGTAATTTAAAGAGAAATTAAGTCAACCTACCGGGGACCTTTAAATGAG 2331
QY 2335 TGTTATCCGAGCTATTTATATCAAAAATAGGAGTCCGGAATTAAGAGCTTTATACCTGC 2394
DB 2332 TGTTATCCGAGCTATTTATATCAAAAATAGGAGGCGGAATTAAGAGCTTTATACCTGC 2391
QY 2395 TACCAATTAAGAGGCTATTTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGTTAT 2454
DB 2392 TACCAATTAAGTGGCTATTTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGTTAT 2451
QY 2455 AATCGGAACATGAAACATTCGATGTTTCCAGGTACCGAGTCCGATAGGCGCGCTTTCAAGT 2514
DB 2452 AATCGGAACATGAAACATTCGATGTTTCCAGGTACCGAGTCCGATAGGCGCGCTTTCAAGT 2511
QY 2515 GAAAGCCCAATCGGAAGTGGGAGAACCGAATCGATGCGCACCAATTTTGAATGGAAT 2574
DB 2512 GAAAGCCCAATCGGAAGTGGGAGAACCGAATCGATGCGCACCAATTTTGAATGGAAT 2571
QY 2575 CCTGATCTAGATTTGTTCTCGAGAGATGGAGAAAATGTGCGCATCAFTTCCCATCTTC 2634
DB 2572 CCTGATCTAGATTTGTTCTCGAGAGATGGAGAAAATGTGCGCATCAFTTCCCATCTTC 2631
QY 2635 TCTTTGGATATGATATTTGGATGACAGACTTGCAATGAGAAATCTAGGCGTGTGGTGTA 2694
DB 2632 TCTTTGGATATGATATTTGGATGACAGACTTGCAATGAGAAATCTAGGCGTGTGGTGTA 2691
QY 2695 TTCAGATTAAGACGCGAGAGGTCNTCAGACTAGGGAATCTGGAAATTTTGAAGAG 2754
DB 2692 TTCAGATTAAGACGCGAGAGGTCNTCAGACTAGGGAATCTGGAAATTTTGAAGAG 2751
QY 2755 AAAACATTTATGAGGAAGCACTGTCTGCTGAAGAGCAGAGAGAGAAAATGAGAGAC 2814
DB 2752 AAAACATTTATGAGGAAGCACTGTCTGCTGAAGAGCAGAGAGAGAAAATGAGAGAC 2811
QY 2815 AAACGTGAAAACCTACAATTTGGAACAAAACAGTATATACAGAGGCAAGAGAGCTGTG 2874
DB 2812 AAACGTGAAAACCTACAATTTGGAACAAAACAGTATATACAGAGGCAAGAGAGCTGTG 2871
QY 2875 GATCCTTTATTTAGATTTCTCAATATATATAGATACAGCGGATACAAACATTTGGCATG 2934
DB 2872 GATCCTTTATTTAGATTTCTCAATATATATAGATACAGCGGATACAAACATTTGGCATG 2931
QY 2935 ATTCATCGCGCAGATAAACTTTGTTTCATCGAATTCGAGAGGCTTATCTGTCAAGATTTATCT 2994
DB 2932 ATTCATCGCGCAGATAAACTTTGTTTCATCGAATTCGAGAGGCTTATCTGTCAAGATTTATCT 2991
QY 2995 GTTATCCCGGTGTAAATGCGGAAATTTTGAAGAAATTTAGAGGTCGCAATTCACCTGCA 3054
DB 2992 GTTATCCCGGTGTAAATGCGGAAATTTTGAAGAAATTTAGAGGTCGCAATTCACCTGCA 3051
QY 3055 ATCTCCCTATACGATGCGAGAAATGTGTTAAAATGTTGATTTTAAATAGGATAGCA 3114
DB 3052 ATCTCCCTATACGATGCGAGAAATGTGTTAAAATGTTGATTTTAAATAGGATAGCA 3111
QY 3115 TGCTGGAATGTAAAGGCGATGTAGATGTACAACAGAGCCATCACCGTTCTGCTCCTGTT 3174
DB 3112 TGCTGGAATGTAAAGGCGATGTAGATGTACAACAGAGCCATCACCGTTCTGCTCCTGTT 3171
QY 3175 ATCCAGAAATGGGAAGCAGAGTGTCAACAGCAGTTCGCGTCTGTCCGGGCGTGGCTAT 3234
DB 3172 ATCCAGAAATGGGAAGCAGAGTGTCAACAGCAGTTCGCGTCTGTCCGGGCGTGGCTAT 3231
QY 3235 ATCTCCGTGTCAAGCGTCAAGAGGATATGAGAGGTTGTGTAAACGATCATGAA 3294
DB 3232 ATCTCCGTGTCAAGCGTCAAGAGGATATGAGAGGTTGTGTAAACGATCATGAA 3291
QY 3295 ATCCAGAACATACAGAGCACTAAATTTAAAACCTGTGAGAGAGGAGTATCCCA 3354
DB 3292 ATCCAGAACATACAGAGCACTAAATTTAAAACCTGTGAGAGAGGAGTATCCCA 3351

QY 3355 ACGGATACAGGAACGCTGTAATGATTTATCTGCACACCGAGGTACAGCGAGTATGTAATTC 3414
DB 3352 ACGGATACAGGAACGCTGTAATGATTTATCTGCACACCGAGGTACAGCGAGTATGTAATTC 3411
QY 3415 CGTAATCTCGATATGAGGATGATATGAAGTTCATCTACAGCATCTGTTAAATTTACAAA 3474
DB 3412 CGTAATCTCGATATGAGGATGATATGAAGTTCATCTACAGCATCTGTTAAATTTACAAA 3471
QY 3475 CCGACTTTATGAAGAAGAAACGATATACAGATGTACGAAGAGATAATCATTTGTGAATATGAC 3534
DB 3472 CCGACTTTATGAAGAAGAAACGATATACAGATGTACGAAGAGATAATCATTTGTGAATATGAC 3531
QY 3535 AGGGGTATGTAATTTATCCACCTACCTACCTGTTATATGACAAAAGAAATTTAGATATAC 3594
DB 3532 AGGGGTATGTAATTTATCCACCTACCTACCTGTTATATGACAAAAGAAATTTAGATATAC 3591
QY 3595 TTCCAGAAACCGATTAAGGTATGATTTGAGATTCGAGAAACGGAAGGAGGATTTATTGTA 3654
DB 3592 TTCCAGAAACCGATTAAGGTATGATTTGAGATTCGAGAAACGGAAGGAGGATTTATTGTA 3651
QY 3655 GACAGCGTGAATTTACTCTTTATCGGAGGAATAG 3687
DB 3652 GACAGCGTGAATTTACTCTTTATCGGAGGAATAG 3684

RESULT 3

US-08-961-803-5
; Sequence 5, Application US/08961803
; Patent No. 6150589
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel
; APPLICANT: Cummings, David A.
; APPLICANT: Cannon, Raymond J. C.
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Stelman, Steve
; TITLE OF INVENTION: No. 6150589el Bacillus thuringiensis Isolate Denoted
; TITLE OF INVENTION: B.t. PSI58C2, Active Against Lepidopteran Pests, and Genes
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jay M. Sanders
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,803
; FILING DATE: 31-OCT-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,902
; FILING DATE: 01-JUNE-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/448,170
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: N/S 102DCD1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100

TELEFAX: (352) 372-5800
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3684 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-08-961-803-5

Query Match 88.6%; Score 3266.6; DB 3; Length 3684;
 Best Local Similarity 93.4%; Pred. No. 0;
 Matches 3449; Conservative 0; Mismatches 229; Indels 15; Gaps 3;

Qy	1	TTGACTTCAAAATAGGAAATGAGAAATGAAATATATAATGCTTTATCGATTTCAGACTGTA	60
Db	1	TTGACTTCAAAATAGGAAATGAGAAATGAAATATATAATGCTTTATCGATTTCAGACTGTA	60
Qy	61	TGCAATCATTTCCACACAAATGGATCTATCACAGATGCTCGTATFGAGGATTTCTTTGT	120
Db	61	TGCAATCATTTCCGACAAATGAATCTATCAACCGATGCTCGTATFGAGGATAGCTTGT	120
Qy	121	ATAGCCAGGGGAAATATATCAATCCACTGTTAGCGCATCAACAGTCCAAACGGGTATT	180
Db	121	ATAGCCAGGGGAAATATATCAATCCACTGTTAGCGCATCAACAGTCCAAACGGGTATT	180
Qy	181	AACATAGCTGTAAGTACTAGGTGATATAGGCGTACCGTTTCTGCGACAAATAGCTAGT	240
Db	181	AACATAGCTGTAAGTACTAGGTGATATAGGCGTACCGTTTCTGCGACAAATAGCTAGT	240
Qy	241	TTTATATAGTTTCTTTGTTGGTGAATATAGCCCGCGCGAGAGATCAGTGGGAAATTTTC	300
Db	241	TTTATATAGTTTCTTTGTTGGTGAATATAGCCCGCGCGAGAGATCCTTGGGAAATTTTC	300
Qy	301	CTAGAACATGTGGAACAACTTAATTAATCAACAAATACAGAAATGCTAGGAATACGGCA	360
Db	301	CTAGAACATGTGGAACAACTTAATTAATCAACAAATACAGAAATACAGGAATACGGCT	360
Qy	361	CTTGCTCGATTACAAGGTTTAGGAGATTCTTTAGAGCCTATCAACAGTCACTTTGAAGAT	420
Db	361	CTTGCTCGATTACAAGGTTTAGGAGATTCTTTAGAGCCTATCAACAGTCACTTTGAAGAT	420
Qy	421	TGGCTAGAAAACCGTGATGATGCAAGAACGAGAGTGTCTTTATACCCCAATATATAGCC	480
Db	421	TGGCTAGAAAACCGTGATGATGCAAGAACGAGAGTGTCTTTATACCCCAATATATAGCC	480
Qy	481	TTAGAACTTGATTTTCTTAATGCGATGCGCTTTTCGCAATTAGAAAACCAAGAGTTCCA	540
Db	481	TTAGAACTTGATTTTCTTAATGCGATGCGCTTTTCGCAATTAGAAAACCAAGAGTTCCA	540
Qy	541	TTATTATGTTATATGCTCAAGCTGCAAAATTTACACCTATTATTATTGAGAGATGCTCT	600
Db	541	TTATTATGTTATATGCTCAAGCTGCAAAATTTACACCTATTATTATTGAGAGATGCTCT	600
Qy	601	CTTTTTCGTAGTGAATTTGGGCTTTACATCGCAGGAAATTTCAACGTTATTATGAGCGCAA	660
Db	601	CTTTTTCGTAGTGAATTTGGGCTTTACATCGCAGGAAATTTCAACGTTATTATGAGCGCAA	660
Qy	661	GTGAAACAAACGAGAGATTTATTCGACTATTCGCTAGAAATGAGTATATACAGGCTTAAT	720
Db	661	GTGAAACAAACGAGAGATTTATTCGACTATTCGCTAGAAATGAGTATATATACAGGCTTAAT	720
Qy	721	AGCTTTGAGGGGCAAAATGCGCAAGTTGGGTGGTATATCAATTCGTTAGAGATCTA	780
Db	721	AATTTGAGAGGGAACAAATGCTGAAAGTTGGTGGGATATATCAATTCGTTAGAGATCTA	780
Qy	781	ACGTTAGGGGTATTAGTCTAGTGGCACTATTTCGAAGCTATGACACTCGCACTTATCCA	840
Db	781	ACGTTAGGGGTATTAGTCTAGTGGCACTATTTCGAAGCTATGACACTCGCACTTATCCA	840
Qy	841	ATAAATACAGTGTCTAGTTAAAGGGAAGTTTATACAGCGCAATTTGGAGCAACAGG	900
Db	841	ATGAATACAGTGTCTCAATTAACAGGAAATTTTATACAGATCCAATTTGGGAGAACAAAT	900

Qy	901	GTAAAT-----ATGGCAAGTATGAATGGTATATAATGAATGACACCTTCGTTTTCGGCT	954
Db	901	GCACCTTCAGGATTTGCAAGTACGAATGGTTAAATAATGAATGACACCATCGTTTTCGTC	960
Qy	955	ATAGAGACTCGGTTATCCGAAGCCCGCATCTACTTGATTTCTAGAACAACTTACAAT	1014
Db	961	ATAGAGGCTCGGTTATTTAGGCTCCGCATCTACTTGATTTCCAGAACAGCTTACAAT	1020
Qy	1015	TTTAGACATTCATCAGATGGAGTGTCTAGGATATGATCTTACTCGCGGGGACACACA	1074
Db	1021	TTGAGCGTATTAAGTTCGATGGAGTAATCTCAATATATGAATTAATCTGGTGGGACATAGA	1080
Qy	1075	ATTCAATCTCGGCCAATAGGAGCGGATTAATAATACCTCAACGCGATGGGTCTTACCAAT	1134
Db	1081	CTTGAATCGGCAACAAATAGGGGCTCATTAACTACCTCGACACACGGAATACCAAT	1140
Qy	1135	TCATTAATCTGTAGATTAATCATCTTCTCTCGAGACGTATATTTGGAGTGAATCATAT	1194
Db	1141	TCTATTAACTCTGTAAATTTACAGTTTCAATCTCGAGACGTTTATAGAACAGAAATCAT	1200
Qy	1195	GCAGGAGTGTCTTATGGGGAATTTACCTTGAACCTATTTCATGCTGCTCTTCTGTTAGA	1254
Db	1201	GCAGGGGATAAATAT-----ACTTCTAACTACTCTCTGTAATGGAGTACCTTTGGGCT	1254
Qy	1255	TTTAAATTTTAGGAACCTCAGAAATACCTTTTGAAGAGGTACTGCTAACTATAGTCAACCC	1314
Db	1255	TTTAAATTTAGGAATATCCCTGTAATTTCTCTT--AGAGTAGCCTTCTCTATATATAGG	1311
Qy	1315	TATGAGTCACTCGGCTTCAATTTAAAGATTCAGAACTGAAATACCAACAGAAACAAACA	1374
Db	1312	TATAGTGGAGTGGGACACAACTATTTGATTCAGAACTGAAATTTACCAACAGAAACAAACA	1371
Qy	1375	GACGACCAATATTAATGAATCATATAGTATAGTATCTCACATAGGCTTCAATTTCAACA	1434
Db	1372	GACGACCAATATTAATGAATCTTACAGTATAGATTTCTAATATAGACTAATATACAGGA	1431
Qy	1435	TCTAGGTCATGTATCCAGTATATTTTGGACGCGCAGTGTAGTCAGATCGTACAAATACC	1494
Db	1432	AACACTTTGAGAGCACCAGTATATTTCTGGACGCGCAGTGTAGTCAGATCGTACAAATACC	1491
Qy	1495	ATTAGTTTCAATAGCATAAACACAAATACCAATTTGGTAAATCATTTCAACCTTAACT	1554
Db	1492	ATTAGTTTCAATAGCATAAACACAAATACCAATTTGGTAAATCATTTCAACCTTAACT	1551
Qy	1555	ACCTCTGTAGTCACTGGCCCGCAGGATTTACAGGAGGGGATATAATCCGAACTAACT	1614
Db	1552	ACCTCTGTAGTCACTGGCCCGCAGGATTTACAGGAGGGGATATAATCCGAACTAACT	1611
Qy	1615	GGTAGTCTACTAAAGTATGGGTCTTAAATTTTAAATAATACATCATTTACAGCGGTAT	1674
Db	1612	GGTAGTCTACTAAAGTATGGGTCTTAAATTTTAAATAATACATCATTTACAGCGGTAT	1671
Qy	1675	AGAGTTCGTTATGCTTCTTCAAAACAAATGGTCTTGGAGGTAACTTCGGAGGGAGTACT	1734
Db	1672	AGAGTTCGTTATGCTTCTTCAAAACAAATGGTCTTGGAGGTAACTTCGGAGGGAGTACT	1731
Qy	1735	ACTTTTCATCAAGGATTCCTCTAGTACTATGAGTCAAAATGAGTCTTTGACATCTCAAT	1794
Db	1732	ACTTTTCATCAAGGATTCCTCTAGTACTATGAGTCAAAATGAGTCTTTGACATCTCAAT	1791
Qy	1795	TTTAGATTTTCAGAAATTTCTGTAGGTATTAGTGCATCTGSCAGTCAAACTTCGTTGAATA	1854
Db	1792	TTTAGATTTTCAGAAATTTCTGTAGGTATTAGTGCATCTGSCAGTCAAACTTCGTTGAATA	1851
Qy	1855	AGTAAATGATTAATGAGGTAGCAAAAGTTTCACTTGTGATAAATTAATTAATTTCAAT	1914
Db	1852	AGTAAATGATTAATGAGGTAGCAAAAGTTTCACTTGTGATAAATTAATTAATTTCAAT	1911
Qy	1915	ATTACTGCAACCTTCGAGGACAGAAATCGATTTAGAAAAGGGCGCAAGAGCGGCTGAAT	1974
Db	1912	ATTACTGCAACCTTCGAGGACAGAAATCGATTTAGAAAAGGGCGCAAGAGCGGCTGAAT	1971

QY 1975 CTGTTTACTAATACGAATCCAAAGAGATTGAAAACAGAGTGTGACAGATTATCATATTGAT 2034
Db 1972 CTGTTTACTAATACGAATCCAAAGAGATTGAAAACAGAGTGTGACAGATTATCATATTGAT 2031
QY 2035 CAAGTATATCCAAATTTAGTGGCGGTGTTTATCGGATGAATTTCTGTTAGATGAAAGAGAGAA 2094
Db 2032 GAAGTATCCAAATTTAGTGGCGGTGTTTATCGGATGAATTTCTGTTGATGAAAGAGAGAA 2091
QY 2095 TTACTTGAGAAAGTGAATATGCGAAACGACTCAGTGTGATGAAAGAACTTTACTCCAAGAT 2154
Db 2092 TTACTTGAGAAAGTGAATATGCGAAACGACTCAGTGTGATGAAAGAACTTTACTCCAAGAT 2151
QY 2155 CCAAACTTCACATCCATCAATTAAGCAACACGACTTCATATCTACTTAATGAGCAATCGAAT 2214
Db 2152 CCAAACTTCACATCCATCAATTAAGCAACACGACTTCATATCTACTTAATGAGCAATCGAAT 2211
QY 2215 TTCACTATCTATCCATGAACAATCTGAACATCGATGGTGGGGAAGTGTGAGAACATTTACAATC 2274
Db 2212 TTCACTATCTATCCATGAACAATCTGAACATCGATGGTGGGGAAGTGTGAGAACATTTACAATC 2271
QY 2275 CAGGAAGGAAATGACGTATTTAAAGAGAAATTAACGTACACCTACCGGGGACTTTTAAATGAG 2334
Db 2272 CAGGAAGGAAATGACGTATTTAAAGAGAAATTAACGTACACCTACCGGGGACTTTTAAATGAG 2331
QY 2335 TGTTATCGAGCTATTTATATCAAAAATAGAGAGTCCGAAATTAAGCTTTATCTCGC 2394
Db 2332 TGTTATCGAGCTATTTATATCAAAAATAGAGAGTCCGAAATTAAGCTTTATCTCGC 2391
QY 2395 TACCAATTTAGAGGGTATTTAGAGATAGTCAAGATTTAGAGATATATTTGATTCGTTAT 2454
Db 2392 TACCAATTTAGAGGGTATTTAGAGATAGTCAAGATTTAGAGATATATTTGATTCGTTAT 2451
QY 2455 AATCGGAAACATGAAACATTTGGATGTTCCAGGTACCGAGTCCGATGGCCGCTTTTCAGTT 2514
Db 2452 AATCGGAAACATGAAACATTTGGATGTTCCAGGTACCGAGTCCGATGGCCGCTTTTCAGTT 2511
QY 2515 GAAAGCCCAATCGAAGGTGCGGAGAACCGAATCGATCGCGCACCAATTTTGAATGGAAT 2574
Db 2512 GAAAGCCCAATCGAAGGTGCGGAGAACCGAATCGATCGCGCACCAATTTTGAATGGAAT 2571
QY 2575 CCTGATCTAGATTTGTTCTCGCAGAGATGAGAAAATGTGCGCATCATTTCCCATCATTTTC 2634
Db 2572 CCTGATCTAGATTTGTTCTCGCAGAGATGAGAAAATGTGCGCATCATTTCCCATCATTTTC 2631
QY 2635 TCTTTGATATTTGATTTGGAATGCACAGACTTGCATGAGAATCTAGGCGTGGGTGGTA 2694
Db 2632 TCTTTGATATTTGATTTGGAATGCATGAGAATCTAGGCGTGGGTGGTA 2691
QY 2695 TTCAAGATTTAAGACGCGAGAAAGGTCTATGCAAGACTAGGAACTTTTGAAGAG 2754
Db 2692 TTCAAGATTTAAGACGCGAGAAAGGTCTATGCAAGACTAGGAACTTTTGAAGAG 2751
QY 2755 AAACCATTTATGAGAGAGCACTGCTGCTGTAAGAGAGAGAGAGAGAGAGAGAGAGAC 2814
Db 2752 AAACCATTTATGAGAGAGCACTGCTGCTGTAAGAGAGAGAGAGAGAGAGAGAGAGAC 2811
QY 2815 AAACGTGAAAACACTACAAATTTGAAAACAAACAGGTATATACAGAGGCAAAAAGAGCTGTG 2874
Db 2812 AAACGTGAAAACACTACAAATTTGAAAACAAACAGGTATATACAGAGGCAAAAAGAGCTGTG 2871
QY 2875 GATGCTTTTATTTGATGTTCTCAATATATAGATTTTACAAGCGGATACAAAATTTGGCATG 2934
Db 2872 GATGCTTTTATTTGATGTTCTCAATATGATAGATTTTACAAGCGGATACAAAATTTGGCATG 2931
QY 2935 ATTCAATGGCGAGATAAATCTGTTTCATCGAATTCGAGAGGCTTATCTGTCAGAATTTATCT 2994
Db 2932 ATTCAATGGCGAGATAAATCTGTTTCATCGAATTCGAGAGGCTTATCTTTCAGAAATTTATCT 2991
QY 2995 GTTATCCCGGTGTAAATGCGGAAATTTTTCAGAAATTTAGAGGTGCGCATTTATCACTGCA 3054
Db 2992 GTTATCCCGGTGTAAATGCGGAAATTTTTCAGAAATTTTTCAGAAATTTTATCACTGCA 3051
QY 3055 ATCTCCCTATACGATGCGAGAAATGTCGTTAAAAATGCTGATTTTAAATGGAATTAGCA 3114

Db 3052 ATCTCCCTATACGATGCGAGAAATGTCGTTAAAAATGCTGATTTTAAATGGAATTAGCA 3111
QY 3115 TGCTGGAATGTAAAGGCGCATGTAGATGTACAAACAGAGCCATCACCGTTCCTGCTGTT 3174
Db 3112 TGCTGGAATGTAAAGGCGCATGTAGATGTACAAACAGAGCCATCACCGTTCCTGCTGTT 3171
QY 3175 ATCCAGATGCGGAAGCAGAAAGTGTACAGCAGTTCGCTCTGTCGGGGCGGTGGCTAT 3234
Db 3172 ATCCAGATGCGGAAGCAGAAAGTGTACAGCAGTTCGCTCTGTCGGGGCGGTGGCTAT 3231
QY 3235 ATCCCTCGTGTACAGCGGTACAAAGAGGGATATGAGAGGGTGTGTAACCATCATGAA 3294
Db 3232 ATCCCTCGTGTACAGCGGTACAAAGAGGGATATGAGAGGGTGTGTAACCATCATGAA 3291
QY 3295 ATCCAGAACCAATACAGACGAACTTAAATTTAAAAAATCTGTGAAGAGGAAAGTGTATCCA 3354
Db 3292 ATCCAGAACCAATACAGACGAACTTAAATTTAAAAAATCTGTGAAGAGGAAAGTGTATCCA 3351
QY 3355 AGGATACAGAAACGCTGTAATGATTTATCTGCAACCAAGGTACAGCAGTGTAAATTC 3414
Db 3352 AGGATACAGAAACGCTGTAATGATTTATCTGCAACCAAGGTACAGCAGTGTAAATTC 3411
QY 3415 CGTAACTCTCGATATGAGGATGCATATGAAGTTGATGAAAGTGTATCTAGCATCTGTTAAATTACAA 3474
Db 3412 CGTAACTCTCGATATGAGGATGCATATGAAGTTGATGAAAGTGTATCTAGCATCTGTTAAATTACAA 3471
QY 3475 CCGACTTTATGAAGAAAGAAAGCTATACAGATGTACGAAGAGATAATCATTTGTAATATGAC 3534
Db 3472 CCGACTTTATGAAGAAAGAAAGCTATACAGATGTACGAAGAGATAATCATTTGTAATATGAC 3531
QY 3535 AGGGGTATGTAAATTTACCACTACCACTACCACTGCTGTTATATGACAAAGAAATTTAGAAATC 3594
Db 3532 AGGGGTATGTAAATTTACCACTACCACTACCACTGCTGTTATATGACAAAGAAATTTAGAAATC 3591
QY 3595 TTCCAGAACCCGATAGGTATGATTCAGATTCGAGAAACGGAAGGAAAGTGTATTCGA 3654
Db 3592 TTCCAGAACCCGATAGGTATGATTCAGATTCGAGAAACGGAAGGAAAGTGTATTCGA 3651
QY 3655 GACAGCGTGAATTTACTCTCTTATCGAGGAATAG 3687
Db 3652 GACAGCGTGAATTTACTCTCTTATCGAGGAATAG 3684

RESULT 4
US-09-661-322A-62
; Sequence 62, Application US/09661322A
; Patent No. 6593293
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Ruper, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compos
; FILE REFERENCE: MECO201
; CURRENT APPLICATION NUMBER: US/09/661,322A
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 62
; LENGTH: 3684
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-09-661-322A-62

Query Match 88.4%; Score 3260.2; DB 4; Length 3684;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 3445; Conservative 0; Mismatches 233; Indels 15; Gaps 3;
QY 1 TTGACTTCAATAGAGAAATTTAGAAATTTAAATGCTTTTATCGATTCGAGTCTGTA 60
|||||

Db 1 TTGACTTCAAAATAGGAAAAATCAGAAATGAAATTAATAATGCTTTATCGAATCCAGCTGTA 60
 QY 61 TCGAATCAATCCACACAAATGGATCTATCACCAGATGCTCGTATTTAGGATTTCTTGTGT 120
 Db 61 TCGAATCAATCCGACAAATGAATCTATCAACCGATGCTCGTATTTAGGATAGCTTGTGT 120
 QY 121 ATAGCCGAGGGGAATATATCAATCCACTTGTAGCGCATCAACAGATCCAAACGGGTATT 180
 Db 121 ATAGCCGAGGGGAACATATATCGATCCATTTGTAGCGCATCAACAGATCCAAACGGGTATT 180
 QY 181 AACATAGCTGTAGAAATCTAGGTGTATTTAGCGGTACCGTTTGTGACAAATAGTAGT 240
 Db 181 AACATAGCTGTAGAAATCTAGGTGTATTTAGCGGTACCGTTTGTGACAAATAGTAGT 240
 QY 241 TTTTATAGTTTCTTGTGTGTAATATGCGCGCGCGCGCAGAGATCAGTGGGAATTTTC 300
 Db 241 TTTTATAGTTTCTTGTGTGTAATATGCGCGCGCGCGCAGAGATCAGTGGGAATTTTC 300
 QY 301 CTAGAAATGTCGAACCACTTATAAATCAACAAATTAACAGAAATGCTTAGGAATACGGCA 360
 Db 301 CTAGAAATGTCGAACCACTTATAAAGACAACAGTAACAGAAATCTAGGGATACGGCT 360
 QY 361 CTGCTCGATTAACAGGTTTAGGAGATTCCTTTAGAGCTTACAAAGTCACTTTGAAGAT 420
 Db 361 CTGCTCGATTAACAGGTTTAGGAGATTCCTTTAGAGCTTACAAAGTCACTTTGAAGAT 420
 QY 421 TGGCTAGAAAACCGTGATGTCGAAGACGAGAGTGTCTTTATATACCCCAATATATAGCC 480
 Db 421 TGGCTAGAAAACCGTGATGTCGAAGACGAGAGTGTCTTTATATACCCCAATATATAGCC 480
 QY 481 TTAGAACTTTGATTTTCTTAATGCGATGCGCTTTTCGCAATTAGAAAACCAAGAGTTCCA 540
 Db 481 TTAGAACTTTGATTTTCTTAATGCGATGCGCTTTTCGCAATTAGAAAACCAAGAGTTCCA 540
 QY 541 TTATTAATGTTATGTCGAAGTGCAGAAATTTACACCTATTTATTTAGAGAGTGCCTCT 600
 Db 541 TTATTAATGTTATGTCGAAGTGCAGAAATTTACACCTATTTATTTAGAGAGTGCCTCT 600
 QY 601 CTTTTTCGTAGTGAATTTGGGCTTACATCGCAGAAATTCACCGTATTTATGAGCGCAA 660
 Db 601 CTTTTTCGTAGTGAATTTGGGCTTACATCGCAGAAATTCACCGTATTTATGAGCGCAA 660
 QY 661 GTGGAACAAACAGAGATTTATTCGAGTATTCGCTAGAAATGGTATATACAGGTCTAAAT 720
 Db 661 GTGGAACAAACAGAGATTTATTCGATTTATTCGCAAGATGGTATATACAGGTCTAAAT 720
 QY 721 AGCTTGAGAGGGAACAATGCGCAAGTTGGGTGCTTATATCAATTCGCTAGAGATCTA 780
 Db 721 AATTTGAGAGGGAACAATGCTGAAAGTTGGTTGCGATATATCAATTCGCTAGAGATCTA 780
 QY 781 ACGTTAGGGTATTAGATCTAGTGGCACTATTCGCAAGCTATGACATCGCACTTATCCA 840
 Db 781 ACGTTAGGGTATTAGATCTAGTGGCACTATTCGCAAGCTATGACATCGCACTTATCCA 840
 QY 841 ATAAATACGAGTGTCTAGTTAAACAGGGAAGTTTATACAGCGCAATTTGGAGCAACAGGG 900
 Db 841 ATGAATACCACTGCTCAATTAACAGAGAAATTTATACAGATCCAATTTGGGAGAACAAAT 900
 QY 901 GTAAT-----ATGGCAAGTATGAATGGTATTAATTAATGAATGACCTTGTTCGCT 954
 Db 901 GCACCTTCAGGATTTGCAAGTACGAAATGGTTTAAATTAATGAATGACCACTGTTTCTGCC 960
 QY 955 ATAGAGACTGGGTATTCCGAAGCGCGCATCTACTGATTTTCGAGAACACTTACAAAT 1014
 Db 961 ATAGAGGCTGCGTTATTAGGCTTCGCACTCTGATTTTCGAGAACACTTACAAAT 1020
 QY 1015 TTTAGCACTTCATCAGATGAGGTGCTACTAGGCATATGACTTACTGCGGGGGCACACA 1074
 Db 1021 TTCAGCGTATTAAAGTCGATGAGTAATCTCAATATATGAATTTACTGGTGGGACATAGA 1080
 QY 1075 ATTCAACTTCGGCCAAATAGGAGCGGATTAATACCTCAACGATGGGTCTACCAATACT 1134
 Db 1081 CTTGAATCGCGAACAAATAGGGGGTTCATTAAGTACCTGGACACACCGGAAATACCAATACT 1140

QY 1135 TCTATTAAATCCTGTAAGATTATCATTTCTCTCGACGCGTATATTGCACTGTAATCATAT 1194
 Db 1141 TCTATTAAATCCTGTAAGATTATCATTTCTCGACGCGTATTATAGAACAGAAATCATTT 1200
 QY 1195 GCAGGAGTGTCTTATGCGGAAATTTACCTTTGAACCTTATTCATGTTGCTCCCTACTGTTAGA 1254
 Db 1201 GCAGGATAAATAT-----ACTTCTAACTACTCTCTGTAATGGAGTACCTTGGGCTAGA 1254
 QY 1255 TTTAAATTTTAGGAACCTTCAGAAATATCTTTTGAAGAGGTACTGCTAACTATAGTCAACCC 1314
 Db 1255 TTTAAATTTAGGAATCCCTCTGAATTTCTTT---AGAGGTAGCTTCTCTATCTATATAGG 1311
 QY 1315 TATGAGTCACTCGGCTTCAATTAAGATTCAGAAATCGAAATTTACCACAGAAACAAACA 1374
 Db 1312 TATCTGAGTGGGACACAACTATTTGATTCAGAAATCGAAATTTACCACAGAAACAAACA 1371
 QY 1375 GAACGACCAAAATATGAATCATATAGTATAGGTTATCTCACATAGGGCTCATTTTCAAA 1434
 Db 1372 GAACGACCAAAATATGAATCTTACAGTCAATAGATTTATCTAATAAGACTAATATCAGGA 1431
 QY 1435 TCTAGGCTGATGTACCGATATATTTCTTGACGCGCAGTGTAGTCAGATCGTACAAATACC 1494
 Db 1432 AACACTTTGAGACGACCAAGTATATTTCTTGACGCGCAGTGTAGTCAGATCGTACAAATACC 1491
 QY 1495 ATTAGTTTCAGATAGCATAAACAAATACCATTTGGTAAATTCATTTCAACCTTAATTTCAAGT 1554
 Db 1492 ATTAGTTTCAGATAGCATAAACAAATACCATTTGGTAAATTCATTTCAACCTTAATTTCAAGT 1551
 QY 1555 ACCTCTGATGCTGCGCCAGGATTTACAGGAGGGGATATAATCCGAACTTAAGCTTAAT 1614
 Db 1552 ACCTCTGATGCTGCGCCAGGATTTACAGGAGGGGATATAATCCGAACTTAAGCTTAAT 1611
 QY 1615 GGTAGTCTAATAGTATGGGTCTTTAATTTAATAATACATCATTTACAGCGGTATCGCGTG 1674
 Db 1612 GGTAGTCTAATAGTATGGGTCTTTAATTTAATAATACATCATTTACAGCGGTATCGCGTG 1671
 QY 1675 AGAGTTGCTGCTGCTCTCAAAACAAATGCTCTGAGGGTAACTGTCGAGGGGAGTACT 1734
 Db 1672 AGAGTTGCTGCTGCTCTCAAAACAAATGCTCTGAGGGTAACTGTCGAGGGGAGTACT 1731
 QY 1735 ACTTTTGATCAAGGATTTCCCTAGTATGATGAGTGCAGAAATGAGTCTTTGACATCTCAATCA 1794
 Db 1732 ACTTTTGATCAAGGATTTCCCTAGTATGATGAGTGCAGAAATGAGTCTTTGACATCTCAATCA 1791
 QY 1795 TTTAGATTTTCAGAAATTTCTGTTAGTATTTAGTGCATCTGGCAGTCAAACTGCTGGGAATA 1854
 Db 1792 TTTAGATTTTCAGAAATTTCTGTTAGTATTTAGTGCATCTGGCAGTCAAACTGCTGGGAATA 1851
 QY 1855 AGTATAGTAAATATGAGTGCAGTACAAACCGTTTCACTTTGATATAAATTTGAATTCATTTCCA 1914
 Db 1852 AGTATAGTAAATATGAGTGCAGTACAAACCGTTTCACTTTGATATAAATTTGAATTCATTTCCA 1911
 QY 1915 ATTAAGTCAACCTTCGAAGCAGAAATGAGTTTGAAGAGGGCGCAAGAGGGGTGAATGCT 1974
 Db 1912 ATTAAGTCAACCTTCGAAGCAGAAATGAGTTTGAAGAGGGCGCAAGAGGGGTGAATGCT 1971
 QY 1975 CTGTTTACTAATACGATCCAGAAATTCAGAAACAGATGTGACAGATTTATCATTTGAT 2034
 Db 1972 CTGTTTACTAATACGATCCAGAAATTCAGAAACAGATGTGACAGATTTATCATTTGAT 2031
 QY 2035 CAAGTATCCAAATTTAGTGGGCTGTTTATCGGATGAATTTCTGCTTAGATGAAAGAGAGAA 2094
 Db 2032 GAAGTATCCAAATTTAGTGGGCTGTTTATCGGATGAATTTCTGCTTAGATGAAAGAGAGAA 2091
 QY 2095 TTAAGTGAAGAGTGAATTTAGGAAACGATGATGAGTGAAGAACTTACTTCAAGAT 2154
 Db 2092 TTAAGTGAAGAGTGAATTTAGGAAACGATGATGAGTGAAGAACTTACTTCAAGAT 2151
 QY 2155 CCAAACTTCATCCATCAATAAGCAACAGACTTCAATCTCTAATGAGCAATCGAAT 2214
 Db 2152 CCAAACTTCATCCATCAATAAGCAACAGACTTCAATCTCTAATGAGCAATCGAAT 2211

QY 2215 TTCACTCTATCCATGAACAACTCTGAACATGATGGTGGGAAGTGAGAACATTACAAATC 2274
Db 2212 TTCACTCTATCCATGAACAACTCTGAACATGATGGTGGGAAGTGAGAACATTACAAATC 2271
QY 2275 CAGGAAGGAATGACGTATTTAAAGAGAAATACGTACACATACCGGGGACCTTTTAAATGAG 2334
Db 2272 CAGGAAGGAATGACGTATTTAAAGAGAAATACGTACACATACCGGGGACCTTTTAAATGAG 2331
QY 2335 TGTATCCGAGCTATTTATATCAAAAAATAGAGAGTCCGAAATTTAAAGCTTTATACCTGC 2394
Db 2332 TGTATCCGAGCTATTTATATCAAAAAATAGAGAGTCCGAAATTTAAAGCTTTATACCTGC 2391
QY 2395 TACCAATTTAAGAGGATATTTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGTTAT 2454
Db 2392 TACCAATTTAAGAGGATATTTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGTTAT 2451
QY 2455 AATCGGAAACATGAAACATTTCCAGTGTCCAGGTACCGAGTCCGATGGCCGCTTTTCAGTT 2514
Db 2452 AATCGGAAACATGAAACATTTCCAGTGTCCAGGTACCGAGTCCGATGGCCGCTTTTCAGTT 2511
QY 2515 GAAAGCCCAATCGAAGGTGCGAGAACCCGAATCGATCGCCACCAATTTTGAATGGAAT 2574
Db 2512 GAAAGCCCAATCGAAGGTGCGAGAACCCGAATCGATCGCCACCAATTTTGAATGGAAT 2571
QY 2575 CCTGATCTAGATTTCTTCTCGAGAGATGGAGAAAATGTGCGCATCATTTCCCATCATTTTC 2634
Db 2572 CCTGATCTAGATTTCTTCTCGAGAGATGGAGAAAATGTGCGCATCATTTCCCATCATTTTC 2631
QY 2635 TCTTTGATATTTGATTTGATGACACAGACTTGCATGAGAACTAGGCGTGTGGTGTA 2694
Db 2632 TCTTTGATATTTGATTTGATGACATAGACTTGCATGAGAACTAGGCGTGTGGTGTA 2691
QY 2695 TTCAAGATTTAAGACCGCAGGAAGGTCTGCAAGACTAGGGAATCTGGAATTTTGAAGAG 2754
Db 2692 TTCAAGATTTAAGACCGCAGGAAGGTCTGCAAGACTAGGGAATTTTGAAGAG 2751
QY 2755 AAACCATTTATAGAGAGCTCTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2814
Db 2752 AAACCATTTATAGAGAGAGCTCTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2811
QY 2815 AAACGTGAAACACTACAACTTGGAAACAAACAGGTATATACAGAGGCAAAAGAGAGCTGTG 2874
Db 2812 AAACGTGAAACACTACAACTTGGAAACAAACAGGTATATACAGAGGCAAAAGAGAGCTGTG 2871
QY 2875 GATCTCTTTATTTGATAGTTCTCAATATAATAGATTTACAAGCGGATACAAACATTTGGCATG 2934
Db 2872 GATCTCTTTATTTGATAGTTCTCAATATAGATTTACAAGCGGATACAAACATTTGGCATG 2931
QY 2935 ATTCATCGCGCAGATAAATCTTGTTCATCGAAATTCGAGAGGCTTATCTGTCAGAATTTATCT 2994
Db 2932 ATTCATCGCGCAGATAAATCTTGTTCATCGAAATTCGAGAGGCTTATCTTTCAGAAATTTATCT 2991
QY 2995 GTTATCCGGGTGTAATGCGGAATTTTGAAGAAATTTAGAGGCTTATCTTTCAGAAATTTATCT 3054
Db 2992 GTTATCCAGGTGTAATGCGGAATTTTGAAGAAATTTAGAGGCTTATCTTTCAGAAATTTATCT 3051
QY 3055 ATCTCCCTATACGATGCGAGAAATGTCGTTAAAAATGCTGATTTTAAATGGAATTTAGCA 3114
Db 3052 ATCTCCCTATACGATGCGAGAAATGTCGTTAAAAATGCTGATTTTAAATGGAATTTAGCA 3111
QY 3115 TGCTGGAATGTAAGGGCATGTAGATGTACAAAGAGGCTTGTGTAACGATCATCATGAA 3174
Db 3112 TGCTGGAATGTAAGGGCATGTAGATGTACAAAGAGGCTTGTGTAACGATCATCATGAA 3171
QY 3175 ATCCAGAAATGGGAAGCAGAGATGTCAACAGCTTCCGCTCTCGGGGCGTGGCTAT 3234
Db 3172 ATCCAGAAATGGGAAGCAGAGATGTCAACAGCTTCCGCTCTCGGGGCGTGGCTAT 3231
QY 3235 ATCTCTCGTGTACAGCGGTACAAAGAGGATATGAGAGGCTTGTGTAACGATCATCATGAA 3294
Db 3232 ATCTCTCGTGTACAGCGGTACAAAGAGGATATGAGAGGCTTGTGTAACGATCATCATGAA 3291
QY 3295 ATCGAGAACATACAGAGCAACTAAAAATTTAAAAAATCTGTGAGAGAGGAGAGTGTATCCA 3354

Db 3392 ATCGAGAACATACAGAGCAACTAAAAATTTAAAAAATCTGTGAAGAGAGAAAGTGTATCCA 3351
QY 3355 ACGGATACAGGAACGCTGTAATGATTATCTGCACACCAAGGTACAGCAGTATGTAATTC 3414
Db 3352 ACGGATACAGGAACGCTGTAATGATTATCTGCACACCAAGGTACAGCAGTATGTAATTC 3411
QY 3415 CGTAATCTGATATGAGGATGATATGAAGTTGATGATCTGATCTGTTAATTAACAA 3474
Db 3412 CGTAATCTGATATGAGGATGATATGAAGTTGATGATCTGTTAATTAACAA 3471
QY 3475 CCGACTTATGAAGAGAAACGTTATACAGATCTGACGAAGAGATAATCATTTGTAATATGAC 3534
Db 3472 CCGACTTATGAAGAGAAACGTTATACAGATCTGACGAAGAGATAATCATTTGTAATATGAC 3531
QY 3535 AGAGGATGTGAATTTATCCACCTACCTACCTGTTTATATGACAAAGAAATTAAGATATAC 3594
Db 3532 AGAGGATGTGAATTTATCCACCTACCTACCTGTTTATATGACAAAGAAATTAAGATATAC 3591
QY 3595 TTCCGAGAAACCGATAGGATGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 3654
Db 3592 TTCCGAGAAACCGATAGGATGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 3651
QY 3655 GACAGCGTGAATTTACTCTTATCGAGGAATAG 3687
Db 3652 GACAGCGTGAATTTACTCTTATCGAGGAATAG 3684

RESULT 5
US-08-377-690-1
; Sequence 1, Application US/08377690
; Patent No. 5628995
; GENERAL INFORMATION:
; APPLICANT: PEPEROEN, Marnix
; APPLICANT: JANSENS, Stefan
; APPLICANT: DENOLF, Peter
; TITLE OF INVENTION: CONTROL OF OSTRINIA
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: The George Mason Bldg., Washington & Prince
; STREET: Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/377,690
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/164,781
; FILING DATE:
; APPLICATION NUMBER: US 07/938,362
; FILING DATE: 31-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-039
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4074 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear


```

; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: entomocidus HD 110
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 186..3872
; OTHER INFORMATION: /note= "PROPERTIES: CryIB is toxic to
; OTHER INFORMATION: Ostrinea nubilalis (among others)"
US-08-377-690-1

Query Match      85.0%; Score 3133.6; DB 1; Length 4074;
Best Local Similarity 91.1%; Pred. No. 0;
Matches 3373; Conservative 0; Mismatches 299; Indels 30; Gaps 3;

Qy 1 TTGACTTCAATAGGAAATAGAAATGAAATTAATAATGCTTATCGATCCAGCTGTA 60
Db 186 TTGACTTCAATAGGAAATAGAAATGAAATTAATAATGCTTATCGATCCAGCTGTA 230
Qy 61 TCGAATCATTCACACAAATGATCTATCACCAGATGCTGTTATGAGGATTTCTTGTGT 120
Db 231 TCGAATCATTCGCGACAAATGATCTATCACCAGATGCTGTTATGAGGATGCTTGTGT 290
Qy 121 ATAGCCGAGGGAAATATCAATCCACTTGTGTTAGCGCATCAACAGTCCAAACGGGTATT 180
Db 291 ATAGCCGAGGGAAATATGATCCATTTGTTAGCGCATCAACAGTCCAAACGGGTATT 350
Qy 181 AACATAGCTGTGTAATCTAGTGTGTAATAGGCGTACCGTTTGTGACAAATAGTAGT 240
Db 351 AACATAGCTGTGTAATCTAGGCGTATGCGCGTACCGTTTGTGACAAATAGTAGT 410
Qy 241 TTTTATAGTTTCTGTGTTGTAATGATGCGCGCGCGAGATCAGTGGGAAATTTTC 300
Db 411 TTTTATAGTTTCTGTGTTGTAATGATGCGCGCGCGAGATCAGTGGGAAATTTTC 470
Qy 301 CTAGAAATGTCGAAACAACTTATAAATCAACAAATACAGAAATGCTAGGAATACGGCA 360
Db 471 CTAGAAATGTCGAAACAACTTATAAATCAACAAATACAGAAATGCTAGGAATACGGCT 530
Qy 361 CTTCCTCGATTAAGGTTTAGAGATTCCTTTAGAGCTTATCAACAGTCACTTGAAGAT 420
Db 531 CTTCCTCGATTAAGGTTTAGAGATTCCTTTAGAGCTTATCAACAGTCACTTGAAGAT 590
Qy 421 TGGCTAGAAACCGTGATGTCAGAACGAGAGTGTCTTTATACCCAAATATATAGCC 480
Db 591 TGGCTAGAAACCGTGATGTCAGAACGAGAGTGTCTTTATACCCAAATATATAGCT 650
Qy 481 TTAGAACTTGAATTTCTTAATGCGATGCGCTTTTCGCAATTAGAAACCAAGAGTTCCA 540
Db 651 TTAGAACTTGAATTTCTTAATGCGATGCGCTTTTCGCAATTAGAAACCAAGAGTTCCA 710
Qy 541 TTATTAATGATATGCTCAAGCTGCAAAATTTACACCTATTTATTTAGAGATGCGCTCT 600
Db 711 TTATTAATGATATGCTCAAGCTGCAAAATTTACACCTATTTATTTAGAGATGCGCTCT 770
Qy 601 CTTTTCGTAGTGAATTTGGGCTTACATCGCAGGAAATTCAGCTTATTTAGCGGCCAA 660
Db 771 CTTTTCGTAGTGAATTTGGGCTTACATCGCAGGAAATTCAGCTTATTTAGCGGCCAA 830
Qy 661 GTGGAAACAAACAGAGATTTATTCGACTATTTGCGTAGAATGGTATAATACAGGTCTAAAT 720
Db 831 GTGGAAACAAACAGAGATTTATTCGACTATTTGCGTAGAATGGTATAATACAGGTCTAAAT 890
Qy 721 AGCTTGAGAGGGAACAAATGCGCAAGTTGGGTGCGTTATTAATCAATTCGCTAGAGATCTA 780
Db 891 AGCTTGAGAGGGAACAAATGCGCAAGTTGGGTGCGTTATTAATCAATTCGCTAGAGATCTA 950
Qy 781 ACCTTAGGGTATTAGTCTAGTGGCACTATTTCCCAAGCTATGACATCCGACCTTATCCA 840
Db 951 ACCTTAGGGTATTAGTCTAGTGGCACTATTTCCCAAGCTATGACATCCGACCTTATCCA 1010
Qy 841 ATAAATACGAGTGTCTAGTTAAACAGGGAAGTTTATACAGACGCAATTTGGAGCAACAGGG 900

```

```

1011 ATAAATACGAGTGTCTCAGTTTAAACAGAGAAAGTTTATACAGACGCAATTTGGAGCAACAGGG 1070
Qy
901 GTAAATATGCAAGTATGAAATGCTATTAATAAATGCACTTCCTGTTTTCGCTATATAGAG 960
Db
1071 GTAAATATGCAAGTATGAAATGCTATTAATAAATGCACTTCCTGTTTCTCTGCCATATAGAG 1130
Qy
961 ACTGCGGTTATCGAAGCCCGCATCTACTTGTATTTCTAGAAACAACTTACAAATTTTATGAG 1020
Db
1131 GCTGCGGCTATCGAAGCCCGCATCTACTTGTATTTCTAGAAACAACTTACAAATTTTATGAG 1190
Qy
1021 ACTTCATCAGATGAGTGTCTACTAGGCATATGACTTACTTGGCGGGGGGACACAAATTCAA 1080
Db
1191 GCTTCATCAGATGAGTGTCTACTAGGCATATGACTTACTTGGCGGGGGGACACAGATTCAA 1250
Qy
1081 TCTCGGCAATAGAGCGGATTAATAATACCTCAACGATCGGTCTACCAATACTTCTTATT 1140
Db
1251 TCTCGGCAATAGAGCGGATTAATAATACCTCAACGATCGGTCTACCAATACTTCTTATT 1310
Qy
1141 AATCCTGTAAGATTATCATTTCTCTCGAGAGCTATATTGGAGTGAATCATATGACAGGA 1200
Db
1311 AATCCTGTAAGATTATCATTTCTCGAGAGCTTATATAGGACTGAATCATATGACAGGA 1370
Qy
1201 GTGCTTCTATGGGAAATTTACCTTGAACCTTATTCATGCTGTCCTTACTGTTAGATTTAAT 1260
Db
1371 GTGCTTCTATGGGAAATTTACCTTGAACCTTATTCATGCTGTCCTTACTGTTAGATTTAAT 1430
Qy
1261 TTTAGGAACTCAGATACTTTTGAAGAGTACTGCTAACTATATAGTCAACCTATGAG 1320
Db
1431 TTTAGGAACTCAGATACTTTTGAAGAGTACTGCTAACTATATAGTCAACCTATGAG 1490
Qy
1321 TCACCTGGGCTTCAATTTAAAGATTCAGAAATCGAATTTACACAGAAACAAACAGAACGA 1380
Db
1491 TCACCTGGGCTTCAATTTAAAGATTCAGAAATCGAATTTACACAGAAACAAACAGAACGA 1550
Qy
1381 CCAAATATGAAATCATATAGTCAATAGGTTATCTCAATAGGGCTCATTTCAAACTCTAGG 1440
Db
1551 CCAAATATGAAATCATATAGTCAATAGGTTATCTCATATAGGTTATTTTACAACTCCAGG 1610
Qy
1441 GTGATGATCCAGTATATCTTGGAGCGATGCTAGTGCAGATCGTACAAATACCATTAGT 1500
Db
1611 GTGATGATCCAGTATATCTTGGAGCGATGCTAGTGCAGATCGTACAAATACCATTAGT 1670
Qy
1501 TCAGATAGCAATAACAAATACCAATTCGTTAAATCAATTCACCTTAACTCAGGTAACCTCT 1560
Db
1671 CCAAATAGATACCCCAAAATCCCAATCGTAAAGCATCCGAACTTCTCAAGGTACCACT 1730
Qy
1561 GTAGTCAAGTCCAGGATTTACAGAGGGGATATAATCCGAACTAACGTTAATGTTAGT 1620
Db
1731 GTTGTAGAGGACCGGATTTACTGTTGGGGATATTTCTTCAAGAACCAATACTGTTGGA 1790
Qy
1621 GTACTAAGTATGGGTCTTAAATTTTAAATATACATCATTTACAGGGTATCGCTGAGAGTT 1680
Db
1791 TTTGGACCGGATAGAGTACTGTTTACGGACCATTAACAAAGATATCGTATAGGATTC 1850
Qy
1681 CGTTATGCTCTCTCTCAAAACAAATCGTCTCGAGGGTAACTGTCGGAGGGAGTACTACTTTT 1740
Db
1851 CGCTATGCTTCAACTGTAGATTTTGTATTTCTTGTATCACGTGGAGGTACTACTGTAAAT 1910
Qy
1741 GATCAAGATTTCCCTAGTACTATAGTGCAGAAATGAGTCTTTTGACATCTCAATCAATTTAGA 1800
Db
1911 AAATTTAGATTTCTTACGTAACATGAAACAGTGGAGACGAACTAAATACGGAATTTTGTG 1970
Qy
1801 TTTTCAGAAATTTCTGTAGGTATTTAGTGCATCTGGCAGTCAA --- ACTGCTGGAATAAGT 1857
Db
1971 AGAGCTGCTTTTACTACACCTTTTACTTTTACAAATTCAGAAATTAATTCGAACTCT 2030
Qy
1858 ATAAGTAAATATGAGGTAGACAAACGTTTTCATCTTGTATTTAAATTTGAATTTCAATTTCC 1917
Db
2031 ATTCAGGCGCTTAGTGGAAATGGGAGTGTATATAGATAAATTTGAAATTTATTTCCAGTT 2090
Qy
1918 ACTGCAACCTTCGAGCAGAAATACGATTTTGAAGGGCGGCAAGGGCGGTGAATGCTCTG 1977
Db
2091 ACTGCAACCTTCGAGCAGAAATATGATTTAGAAAGAGCGCAAGAGCGGTGAATGCTCTG 2150

```


QY 1978 TTTACTAATACCAATCCAGAGATTGAAACAGATGTCAGAGATTATCATATTGATCAA 2037
DB |||||
2151 TTTACTAATACCAATCCAGAGATTGAAACAGATGTCAGAGATTATCATATTGATCAA 2210
QY |||||
2038 GTATCCAAATTTAGTGGCGTGTATTCGGATGAATTCCTGTAGATGAAAGAGAGAAATTA 2097
DB |||||
2211 GTATCCAAATTTAGTGGCGTGTATTCGGATGAATTCCTGTAGATGAAAGAGAGAAATTA 2270
QY |||||
2098 CTTTGAAAGTGAATATTCGAAACGACTCAGTGAATGAAAGAACTTACTCCAAGATCCA 2157
DB |||||
2271 CTTTGAAAGTGAATATTCGAAACGACTCAGTGAATGAAAGAACTTACTCCAAGATCCA 2330
QY |||||
2158 AACTTCACATCCATCAATTAAGCAACGACTTCATCTACTAATGAGCAATCGAATTC 2217
DB |||||
2331 AACTTCACATCCATCAATTAAGCAACGACTTCATCTACTAATGAGCAATCGAATTC 2390
QY |||||
2218 ACATCTATCCATGAACATCTGAACATGATGGGGAAGTGAGAACATTAACATCCAG 2277
DB |||||
2391 ACATCTATCCATGAACATCTGAACATGATGGGGAAGTGAGAACATTAACATCCAG 2450
QY |||||
2278 GAAGGAATGACGTATTTAAAGAGAAATTCAGTCACTACCGGGGACTTTTAAATGAGTGT 2337
DB |||||
2451 GAAGGAATGACGTATTTAAAGAGAAATTCAGTCACTACCGGGTACTTTTAAATGAGTGT 2510
QY |||||
2338 TATCGAGCTATTTATATCAAAAATAGAGAGTCGGAATTTAAAGCTTTATCTCGCTAC 2397
DB |||||
2511 TATCGAGCTATTTATATCAAAAATAGAGAGTCGGAATTTAAAGCTTTATCTCGCTAC 2570
QY |||||
2398 CAATTAAGAGGTTATTTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGTTATAT 2457
DB |||||
2571 CAATTAAGAGGTTATTTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGTTATAT 2630
QY |||||
2458 GCGAAACATGAACATTTGGATGTTCCAGGTACCGAGTCCGATGCGCGCTTTTCAGTTGAA 2517
DB |||||
2631 GCGAAACATGAACATTTGGATGTTCCAGGTACCGAGTCCCTATGCGCGCTTTTCAGTTGAA 2690
QY |||||
2518 AGCCCAATCGAAGTGGCGGAGAACCGAATCGATGCGCACCAATTTTGAATGGAATCCT 2577
DB |||||
2691 AGCCCAATCGAAGTGGCGGAGAACCGAATCGATGCGCACCAATTTTGAATGGAATCCT 2750
QY |||||
2578 GATCTAGATGTTCTCTGAGAGATGGAGAAATGTCGCGCATCTTCCCATCATTTCTCT 2637
DB |||||
2751 GATCTAGATGTTCTCTGAGAGATGGAGAAATGTCGCGCATCTTCCCATCATTTCTCT 2810
QY |||||
2638 TTGGATTTGATATTTGGATGCACAGACTTGCATGAGAACTAGGCGTGGGTGGTATTC 2697
DB |||||
2811 TTGGATTTGATATTTGGATGCACAGACTTGCATGAGAACTAGGCGTGGGTGGTATTC 2870
QY |||||
2698 AAGATTAAAGCGCAGGAGGTCATGCAAGACTAGGGAATCTGGAATTTATTTGAAGAGAAA 2757
DB |||||
2871 AAGATTAAAGCGCAGGAGGTCATGCAAGACTAGGGAATCTGGAATTTATTTGAAGAGAAA 2930
QY |||||
2758 CCATTTATAGAGAGCACTCTCTGTTGAAGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2817
DB |||||
2931 CCATTTATAGAGAGCACTCTCTGTTGAAGAGGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 2990
QY |||||
2818 CGTGAAGAACTACAAATTTGGAACAAACGATATATACAGAGGCAAGAGAGAGAGAGAGAGAG 2877
DB |||||
2991 CGTGAAGAACTACAAATTTGGAACAAACGATATATACAGAGGCAAGAGAGAGAGAGAGAG 3050
QY |||||
2878 GCTTTATTTGATGTTCTCAATTAATATAGATTACAGCGGATACAAACATTTGGCATGATT 2937
DB |||||
3051 GCTTTATTTGATGTTCTCAATTAATATAGATTACAAAGCGGATACAAACATCGCATGATT 3110
QY |||||
2938 CATGGCAGATAAATCTGTTTCATGCAATTCAGAGGCTTATCTGTCAAGATTTATCTGTT 2997
DB |||||
3111 CATGGCAGATAAATCTGTTTCATGCAATTCAGAGGCTTATCTTTTCAGAAATTAACCTGTT 3170
QY |||||
2998 ATCCGGGTGTAATTCGGGAAATTTTGAAGAAATTTAGAGAGTTCGATTTATCACTGCAATC 3057
DB |||||
3171 ATCCAGGTGTAATTCGGGAAATTTTGAAGAAATTTAGAGAGTTCATTTATCACTGCAATC 3230

QY 3058 TCCCTATACGATCGAGAAATGTCGTTAAATGCGTGAATTTTAATGATGATTCATGCG 3117
DB |||||
3231 TCCCTATACGATCGAGAAATGTCGTTAAATGCGTGAATTTTAATGATGATTCATGCG 3290
QY |||||
3118 TGGATGTAAGAGGCGATGATAGATGTACAAAGAGCCATCACCGTTCCTGCTTCTGTTATC 3177
DB |||||
3291 TGGATGTAAGAGGCGATGATAGATGTACAAAGAGCCATCATCGTTCGACCTTGTATC 3350
QY |||||
3178 CCAGATGGGAAGCAGAAAGTGTCAAGCAGTTCGCGTCTGTCGCGGCGTGGCTTATATC 3237
DB |||||
3351 CCAGATGGGAAGCAGAAAGTGTCAAGCAGTTCGCGTCTGTCGCGGCGTGGCTTATATC 3410
QY |||||
3238 CTCGCTGTCACAGGCTCAAGAGAGGATATCGAGAGGCTTGTGTAAACCATCCATCAATC 3297
DB |||||
3411 CTCGCTGTCACAGGCTCAAGAGAGGATATCGAGAGGCTTGTGTAAACCATCCATCAATC 3470
QY |||||
3298 GAGAAACATACAGACCAACTAAATTTTAAACCTGTGTAAAGAGAGAGAGAGAGAGAGAG 3357
DB |||||
3471 GAGAAACATACAGACCAACTAAATTTTAAACCTGTGTAAAGAGAGAGAGAGAGAGAGAG 3530
QY |||||
3358 GATACAGAACTGTGTAAATTTATATCTGCAACCAAGGTACAGC-----AGTA 3405
DB |||||
3531 GATACAGAACTGTGTAAATTTATATCTGCAACCAAGGTACAGCTGGATGCGCAGATGCA 3590
QY |||||
3406 TGTAAATCCCGTAAATCTGGATATGAGATGCATATGAAATTTGATCTACAGCATCTGTT 3465
DB |||||
3591 TGTAAATCCCGTAAATCTGGATATGAGATGCATATGAAATTTGATCTACAGCATCTGTT 3650
QY |||||
3466 AATTACAAACCGCTTATGAGAGAGAAACGATATACAGATGTACGAGAGAGAGAGAGAGAG 3525
DB |||||
3651 AATTACAAACCGCTTATGAGAGAGAAACGATATACAGATGTACGAGAGAGAGAGAGAGAG 3710
QY |||||
3526 GAATATGACAGAGGTTATGAAATTTATCCACCATCTACAGCTGGTGTATATGACAAAAGAA 3585
DB |||||
3711 GAATATGACAGAGGTTATGCAATTTATCCACCATCTACAGCTGGTGTATGACAAAAGAA 3770
QY |||||
3586 TTGAATATCTCCAGAAACCGATAGATGATGAGATGAGATTTGAGAGAGAGAGAGAGAGAG 3645
DB |||||
3771 TTGAATATCTCCAGAAACAGATACAGATGAGATTTGAGATTTGAGAGAGAGAGAGAGAG 3830
QY |||||
3646 TTTATTTAGACAGCGTGGAAATTTACTCTTATGAGAGAGATAG 3687
DB |||||
3831 TTTATTTAGATAGCGTGGAAATTTACTCTCTATGAGAGAGATAG 3872

RESULT 6

US-08-100-709-3

; Sequence 3, Application US/08100709

; Patent No. 5322887

; GENERAL INFORMATION:

; APPLICANT: Donovan, William P.

; APPLICANT: Tan, Yuping

; APPLICANT: Jany, Christine S.

; APPLICANT: Gonzalez Jr., Jose M.

; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5

; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.

; ADDRESSEE: Nadel

; STREET: 1601 Market Street, 36th Floor

; CITY: Philadelphia

; STATE: Pennsylvania

; COUNTRY: U.S.A.

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/100,709

; FILING DATE: 19930729

:	CLASSIFICATION:	514			
:	ATTORNEY/AGENT INFORMATION:				
:	NAME:	Egolf, Christopher			
:	REGISTRATION NUMBER:	27633			
:	REFERENCE/DOCKET NUMBER:	7205-49			
:	TELECOMMUNICATION INFORMATION:				
:	TELEPHONE:	215-757-1590			
:	INFORMATION FOR SEQ ID NO:	3:			
:	SEQUENCE CHARACTERISTICS:				
:	LENGTH:	3934 base pairs			
:	TYPE:	nucleic acid			
:	STRANDEDNESS:	double			
:	TOPOLOGY:	circular			
:	MOLECULE TYPE:	DNA (genomic)			
:	FEATURE:				
:	NAME/KEY:	CDS			
:	LOCATION:	67..3756			
:	FEATURE:				
:	NAME/KEY:	misc feature			
:	LOCATION:	2253..2272			
:	US-08-100-709-3				
Query Match 72.9%; Score 2687.2; DB 1; Length 3934;					
Best Local Similarity 83.5%; Pred. NO. 0;					
Matches 3088; Conservative 0; Mismatches 593; Indels 15; Gaps 3					
Qy	1	TTGACTTCAAATAGCAAAATAACGAAATTCGAATTAATAAATCTTATCGATTCAGGTCCAGCTGTA	60		
Db	67	TTGACTTCAAATAGCAAAATAACGAAATTCGAATTAATAAATCTTATCGATTCCAACGGTA	126		
Qy	61	TGGAATCATTTCCACAATAATGGATCTATCACAGATGCTCGTATTGAGGATTCCTTTGTCT	120		
Db	127	TGGAATCCTTCCACGCAATGAATCTATCACAGATGCTCGTATTGAGATAGCTTGCT	186		
Qy	121	ATAGCGAGGGGAATTAATATCAATCCACTGTTTAGCGCATCAACAGTCCAACGGGTATT	180		
Db	187	GTAGCGAGGTGAACAATATTGATCCATTTGTTAGCGCATCAACAGTCCAACGGGTATA	246		
Qy	181	AACATAGCTGGTAGAATACTAGGTGTTATTAGGCCTACCGTTGCTGGACAATAAGTACTG	240		
Db	247	AACATAGCTGGTAGAATAATTGGCGTATTAGTGTGCCGTTGCTGGACAATAAGTACTG	306		
Qy	241	TTTTATAGTTTTCTTTGGTGAATTAATATGCCCCGCGCAGAGATCAGTGGGAAAATTTTC	300		
Db	307	TTTTATAGTTTTCTTTGGGGAAATTATGGCCTAGTGGCAGAGATCCATGGGAAAATTTTC	366		
Qy	301	CTAGAACATGTCGAACAATTTATAAATCAACAATACAGAATACTAGGATACGGCA	360		
Db	367	CTGGAACATGTAGAACAATCTATAGACAACAAGTAACAAGAAATACTAGGAATACGGCT	426		
Qy	361	CTTGCTTCGATTAACAAGTTTAGGAGATTCTTTTAGAGCCTTATCAACAGTCACTTGAAGAT	420		
Db	427	ATTGCTTCGATTAGAAGTCTAGGAAGAGGCTATAGATCTTTACCAGCAGGCTCTTGAACCT	486		
Qy	421	TGCGTAGAAAAACCGTGATGATGCAAGAACGAGAAGTGTCTTTATACCCNATATATAGCC	480		
Db	487	TGCTTAGATAACCGGAAATGATGCAAGATCAAGAAGCAATATTCTTGAGCGCTATGTTGCT	546		
Qy	481	TTAGAACTTGATTTTTCTTAATCCGATCCGCTTTTCGCAATTAGAAACCAAGAAGTTCCA	540		
Db	547	TTAGAACTTGCAATTACTACTGCTATACCGCTTTTCAGAAATACGAATGAAGNAGTTCCA	606		
Qy	541	TTATTAATGGTATATGCTCAAGCTGC AAAATTAC CTTATATATATGAGAGATGCTCT	600		
Db	607	TTATTAATGGTATATGCTCAAGCTGC AAAATTAC CTTATATATGAGAGATGCTCT	666		
Qy	601	CTTTTTGGTAGTGAATTTTGGGCTTACATCGCAGGAAATTC AAGTATTATATGAGCGCAA	660		
Db	667	CTTTTTGGTAGTGAATGGGGATGGCATCTCCGATGTTAACCAATATTATCCNAGAACAA	726		
Qy	661	GTGGAACAAACGAGAGATTTATCCGACTATTTCGGTAGAATGGTATATATACAGTCTTAAT	720		
Db	727	ATCAGATATACAGAGGAATTTCTAACCATTTGGTCAATATGGTATATATACAGGCTTAAT	786		

QY 1792 TCATTTAGATTTGAGATTTCTCTAGTATTAGTGCATCTGGCAGTCAAACTGCTGGA 1851
 Db 1861 AGTTTTAGAACTGCGAGGATTTAGTACTCTCTTTTAAATTTTAAATGCCCCAAGCACATTC 1920
 QY 1852 ATAAGTATAAGTAATAATGCGAGGTAGACAAAGTTTCACTTTGATAAAATTTGAATTCATT 1911
 Db 1921 ACATTTGGGTGCTCAGAGTTTTCATCAATCAGAAATTTATATAGATAGAGTCAATTTGTT 1980
 QY 1912 CCAATTTACTGCAACTTCGAAGCAGAAATACGATTTAGAAAGGCGCGCAAGAGCGGTGAAT 1971
 Db 1981 CCAGCAGAGGTAAACATTTGAGCGCAGAAATATGATTTAGAAAGAGCACAAAGCGGTGAAT 2040
 QY 1972 GCTCTGTTTACTAATACGAATCCAAAGAGATGAAAACAGATGTGACAGATTTATCATTT 2031
 Db 2041 GCTCTGTTTACTTCTACAAATCCAAAGAGATTTGAAAACAGATGTGACAGATTTATCATTT 2100
 QY 2032 GATCAAGTATCAATTTAGTGGCGTGTTCCTGATGAATTTCTGCTTAGATGAAAGAGA 2091
 Db 2101 GACCAAGTGTCAATATGCTGGCATGTTTATCAGATGAAATTTGCTTGGATGAGAGCGA 2160
 QY 2092 GAATTTACTTGAGAAAGTGAATATGCGAAACGACTCAGTGATGAAAGAACTTACTCCAA 2151
 Db 2161 GAATTTATTTGAGAAAGTGAATATGCGAAAGCAGTCACTGATGAAAGAACTTACTCCAA 2220
 QY 2152 GATCCAACTTTCATCATCAATCAATGAACCAACGACTTCATCTACTAATGAGCAATCG 2211
 Db 2221 GATCCAACTTTCATCATCACTGGGCAATTAAGTTTCGATCCATCGATGGAACAATCA 2280
 QY 2212 AATTTTCATCATCTATCTCAATGAACATCTGAACATGATGCTGGGGAAGTGAGAACATTACA 2271
 Db 2281 AACTTCCCTCTATTAATGAGCTATCTGAACATGATGCTGGGGAAGTGCGAATGTTTACC 2340
 QY 2272 ATCCAGGAAGGAAATGAGCTATTTAAAGAGAAATACGTCACACTACCGGGGACTTTTAAAT 2331
 Db 2341 ATTCCAGGAAGGAAATGAGCTATTTAAAGAGAAATACGTCACACTACCGGGTACTTTTAAAT 2400
 QY 2332 GAGTGTATCCAGCTATTTATATCAAAATATAGAGAGTGGAAATTAAGAGCTTTACT 2391
 Db 2401 GAGTGTATTCACAAATTTATTTATCAAAATATAGAGAGTGGAAATTTAAAGCTTTATACG 2460
 QY 2392 CGCTACCAATTTAAGAGGATTTATGAGATAGTCAAGATTTAGAGATATATTTGATTCGT 2451
 Db 2461 CGCTATCAATTTAAGAGGATTTATGAGATAGTCAAGATCTAGAGATTTATTTAATTCGT 2520
 QY 2452 TATTAATCGAAACATGAAACATTTGGATGTTCCAGGTACCGAGTCCGATGCGCGCTTTCA 2511
 Db 2521 TACATGCAAGAGATGAAACATTTGGATGTTCCAGGTACCGATTTCCCTATGCGCGCTTTCA 2580
 QY 2512 GTTGAAAGCCCAATCGGAAGTGGGAGAACCGAATCGATCGGCAACCAATTTTGAATGG 2571
 Db 2581 GTTGAAAGCCCAATCGGAAGTGGGAGAACCAAAATCGATCGGCAACCAATTTTGAATGG 2640
 QY 2572 AATCTGATCTAGATTTGTTCTGTCAGAGATGAGAAATGTCGCACTCATTTCCCATCAT 2631
 Db 2641 AATCTGATCTAGATTTGTTCTGTCAGAGATGAGAAATGTCGCACTCATTTCCCATCAT 2700
 QY 2632 TTCTCTTTGATATTTGATTTGATGTCACAGACTTTGCATGAGAAATCTAGGCGTGTGGGTG 2691
 Db 2701 TTCACTTTGGATATTTGATTTGGTGGCAGACTTTGCATGAGAAATCTAGGCGTGTGGGTG 2760
 QY 2692 GTATTTCAAGATTAAGACGCAAGAGGTTCATCAAGATCTAGGAAATCTGGAATTTATGAA 2751
 Db 2761 GTATTTCAAGATTTAAGACGCAAGAGGTTCATCAAGATTTAGGAAATCTGGAATTTATGAA 2820
 QY 2752 GAGAAACATTTATGAGAGAGCTCTGCTGTTGAGAGAGCAGAGAGAGAGAGAGAGAGAGAG 2811
 Db 2821 GAGAAACATTTATTTGAGAGAGCTCTGCTGTTGAGAGAGCAGAGAGAGAGAGAGAGAGAG 2880
 QY 2812 GACAAACCTGAAAACTACAATTTGAAACAAACCGAGTATATACAGAGGCAAAAGAGCT 2871
 Db 2881 GACAAACGGAAGAACTACAATTTGAAACAAACCGAGTATATACAGAGGCAAAAGAGCT 2940
 QY 2872 GTGGATGCTTTATTTGTAGATTTCTCAATATAATAGATTTACAAGCGGATACAAACATTTGGC 2931

Db 2941 GTGGATGCTTTATTTGATGATTTCTCAATATGATCAATTTACAAGCGGATACAAACATTTGGC 3000
 QY 2932 ATGATTCATGCGGCGAGATAAACTTTGTTTCATGCAATTTGAGAGGCTTATCTGTCAGAAATTA 2991
 Db 3001 ATGATTCATGCGGCGAGATAAACTTTGTTTCATGCAATTTGAGAGGCTTATCTTTCAGAAATTA 3060
 QY 2992 TCTGTTATCCCGGTGTAATGCGGAAATTTTGAAGAAATTTAGAGGTCGCAATTTACT 3051
 Db 3061 CTTGTTATCCCGGTGTAATGCGGAAATTTTGAAGAAATTTAGAGGTCGCAATTTACT 3120
 QY 3052 GCATTCCTCTATACGATGCGGAGAAATGTCGTTAAAAATGCTGATTTTAAATGGAATTA 3111
 Db 3121 GCATGTCCTTTATACGATGCGGAGAAATGTCGTTAAAAATGCTGATTTTAAATGGAATTA 3180
 QY 3112 GCATGTCGGAATGTTAAAAAGGCGATGTAGATGTACAAACAGAGCCATCACCGTTCCTGCTT 3171
 Db 3181 ACATGTTGGAATGTTAAAAAGGCGATGTAGATGTACAAACAGAGCCATCATCGTTCGACCTT 3240
 QY 3172 GTTATCCAGAAATCGGAAGCAGAAAGTGTCAACAGAGTTCGCGTCTGTCGCGGGCGTGGC 3231
 Db 3241 GTTATCCAGAAATCGGAAGCAGAAAGTGTCAACAGAGTTCGCGTCTGTCGCGGGCGTGGC 3300
 QY 3232 TATATCCTCTGTCACAGCGTACAAAGAGGATATGAGAGGGTGTGTGAACGATCCAT 3291
 Db 3301 TATATCCTCTGTCACAGCGTACAAAGAGGATATGAGAGGGTGTGTGAACGATCCAT 3360
 QY 3292 GAAATCCAGAAACATACAGAGCAATTAATAATTTAAAACTGTGAAGAGAGAGAGTGTAT 3351
 Db 3361 GAAATCCAGAAACATACAGAGCAATTAATAATTTAAAACTGTGAAGAGAGAGAGTGTAT 3420
 QY 3352 CCACCGGATACAGAACTGTAATGATTTATATCTCACACCAAGGTACAGAGTATGTAAT 3411
 Db 3421 CCACCGGATACAGAACTGTAATGATTTATATCTCACACCAAGGTACAGAGTATGTAAT 3480
 QY 3412 TCCCGTAACTGCTGATATGAGGATGCATATGAAGTGTGATACAGCATCTGTTAAATTTAC 3471
 Db 3481 TCCCGTAACTGCTGATATGAGGATGCATATGAAGTGTGATACAGCATCTGTTAAATTTAC 3540
 QY 3472 AAACCGACTTATGAAGAGAAACGATATACAGATGTACAGAGAGATAATCATTTGTAATAT 3531
 Db 3541 AAACCGACTTATGAAGAGAAACGATATACAGATGTACAGAGAGATAATCATTTGTAATAT 3600
 QY 3532 GACAGAGGATATGTAATTTATCCACCTACCTGCTGTTATATGACAAAAAGAAATTAGAA 3591
 Db 3601 GACAGAGGATATGTAATTTATCCACCTACCTGCTGTTATGACAAAAAGAAATTAGAA 3660
 QY 3592 TACTTCCAGAAACCGATAGGATGAGATTTGAGATTTGAGAAACGGAAGGAAAGTTTAT 3651
 Db 3661 TACTTCCAGAAACCGATAGGATGAGATTTGAGATTTGAGAAACGGAAGGAAAGTTTAT 3720
 QY 3652 GTAGACAGCGTGAATTTACTCTTTATGAGGAATAG 3687
 Db 3721 GTAGTACGCTGGAACTACTCTCTCATGGAAGATAG 3756

RESULT 7
 US-08-176-865-3
 ; Sequence 3, Application US/08176865
 ; Patent No. 5616319
 ; GENERAL INFORMATION:
 ; APPLICANT: Donovan, William P.
 ; APPLICANT: Tan, Yiping
 ; APPLICANT: Jany, Christine S.
 ; APPLICANT: Gonzalez Jr., Jose M.
 ; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
 ; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
 ; ADDRESSEE: Nadel
 ; STREET: 1601 Market Street, 36th Floor
 ; CITY: Philadelphia

```

STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk.
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176.865
FILING DATE: 30-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/100,709
FILING DATE: 29-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Egolf, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3934 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 67..3756
FEATURE:
NAME/KEY: misc feature
LOCATION: 2253..2272
US-08-176-865-3

Query Match 72.9%; Score 2687.2; DB 1; Length 3934;
Best Local Similarity 83.5%; Pred. No. 0;
Matches 3088; Conservative 0; Mismatches 593; Indels 15; Gaps 3;

Qy 1 TTGACTTCAAATAGAGAAATGAGAATGAAATTAATAATGCTTTTATCGATTCAGCTGTA 60
Db 67 TTGACTTCAAATAGAGAAATGAGAATGAAATTAATAATGCTTTTATCGATTCAGCTGTA 126

Qy 61 TCGAATCAATCCACAAATGGATCTATCACCAGATGCTGTATGAGGATCTTTGT 120
Db 127 TCGAATCCTTCCACGCAATGAATCTATCACCAGATGCTGTATGAGGATCTTTGT 186

Qy 121 ATAGCCGAGGGGAATAATATCAATCCACTTGTAGCGCATCAACAGTCCAAACGGGTAT 180
Db 187 GTAGCCGAGGGGAATAATATGATCCATTTGTTAGCGCATCAACAGTCCAAACGGGTATA 246

Qy 181 AACATAGCTGTAGAAATCTAGGTGTATAGGCGGTACCGTTTGTCTGGACAAATAGTAGT 240
Db 247 AACATAGCTGTAGAAATCTAGGTGTATAGGCGGTATAGGTGCGGTGTTGCTGGACAAATAGTAGT 306

Qy 241 TTTTATAGTTTTCTTTGTTGGTAATATATGGCCCGCGCGCAGAGATCAGTGGGAATTTTC 300
Db 307 TTTTATAGTTTTCTTTGTTGGGAATATATGGCCTAGTGGCAGAGATCCATGGGAAATTTTC 366

Qy 301 CTAGAACATGTCGAACAACTTATAATCAACAAATAACAGAAAATGCTAGGAATACGCA 360
Db 367 CTGAAACATGTAACAACTTATAGACAAAGTAAACAGAAATATCTAGGAAATACGGCT 426

Qy 361 CTTGCTCGAATTAAGGTTTATAGGAGATTCCTTTAGAGCCTATCAACAGTCACTTGAAGAT 420
Db 427 ATTGCTCGAATTAAGGTTCTAGGAAGAGGCTATAGATCTTACCAGCGGCTCTTGAAGT 486

Qy 421 TGGCTAGAAAACCGTGATGATGCAAGAACGAGAGATGTTCTTTTATACCAATATATAGCC 480
Db 487 TGGTTAGATAACCGAAATGATGCAAGATCAAGAGCAATTTCTTTGAGCGCTATGTTGCT 546

Qy 481 TTAGAACTTGATTTCTTTAATGCGATGCGGCTTTTTCGCAATTAGAAAACCAAGAGTTCCA 540

```

```

Db 547 TTAGAACTTGACATTACTACTGCTATACCGCTTTTCAGAAATACGAAATGAAGAAGTTCCA 606
Qy 541 TTATTAAATGTTATGCTCAAGCTGCAAAATTTACACCTATATTTATTGAGAGATGCTCT 600
Db 607 TTATTAAATGTTATGCTCAAGCTGCAAAATTTACACCTATATTTATTGAGAGATGCTCT 666
Qy 601 CTTTTTGTAGTGAATTTGGGCTTTACATCGCAGGAAATTCACGTTATTATTAGCGGCAA 660
Db 667 CTTTTTGTAGTGAATTTGGGGAATGCGCATCTTCGATGTTAACCAATATACCAAGAACAA 726
Qy 661 GTGGAACAAACGAGAGATTTATTCGACTATTGCGTAGAATGGTATAATACAGGTTTAAAT 720
Db 727 ATCAGATATACAGAGGAATATTTCAACCAATGCGTACAAATGGTATAATACAGGCTAAAT 786
Qy 721 AGCTTGAGAGGACAAATGCGCAAGTTGGTGGCTTATATCAATTTCCGTAGAGATCTA 780
Db 787 AACTTAAGAGGGACAAATGCTGAAAGTTGGTGGCTTATATCAATTTCCGTAGAGATCTA 846
Qy 781 ACGTTAGGGGTATTAGATCTAGTGGCACTATTCGCAAGCTATGACACTCGCACCTTATCCA 840
Db 847 ACGTTAGGGGTATTAGATTTAGTAGCCCTATTTCCGAGCTATGATCTCGCACTTATCCA 906
Qy 841 ATAAATACGAGTGTCTCAGTTTAAACAGGGAAGTTTATACAGCGCAATTTGGAGCAACAGG 900
Db 907 ATCAATACGAGTGTCTCAGTTTAAACAGGGAATTTATACAGATCCAAATGGGAGAACAAAT 966
Qy 901 GTAAT-----ATGGCAAGTATGAATGGTATAATTAATGACACCTTGTTCGCT 954
Db 967 GCACCTTCAGGATTTGCAAGTACGAAATGGTTAAATTAATGACCATCGTTTTCTGCCC 1026
Qy 955 ATAGAGACTCGGTTATCCGAAGCCCGCATCTACTTCAATTTCTAGAACAACTTACAAAT 1014
Db 1027 ATAGAGCTGCCATTTTCAGGCTCCGCATCTACTTGAATTTCCAGAACAACTTACAAAT 1086
Qy 1015 TTTAGCACTTTCATCAGCATGAGTGTCTACTAGGCATATGACTTACTCGCGGGGCAACACA 1074
Db 1087 TACAGTGCATCAAGCCGTTGGAGTAGCACTCAACATATGAATTTATTTGGTGGGACATAGG 1146
Qy 1075 ATTCAATCTCGGCAATAGGAGCGGATTAATACCTCAACGCGATGGTCTTACCA---AT 1131
Db 1147 CTTAACTTCGCGCAATAGGAGGGACATAAATAACCTCAACACAGGACTTACTTAATAAT 1206
Qy 1132 ACTTCTAATTAATCCTGTAAGATTAATCATCTCTCTCGAGACGTATATTTGGACTGAATCA 1191
Db 1207 ACTTCAATTAATCCTGTAAGATTAATCATCTCTCTCGAGACGTATTAAGAACAGATCA 1266
Qy 1192 TATGACGAGTGTCTTCTATGGGAAATTTA CTTTGAACCTTATTCATGTTGCTCCCTACTGTT 1251
Db 1267 AATGACGGGACAAATAT-----ACTATTTACTACTCTCTGTAATGAGTACCTTGGGCT 1320
Qy 1252 AGATTTAAATTTTAGGAACCCCTCAGAACTACTTTTGAAGAGGTACTGCTTAATATAGTCAA 1311
Db 1321 AGATTTAAATTTTAAACCCCTCAGAAATTTATGAAAGAGCGCCACTACCTACAGTCAA 1380
Qy 1312 CCCTATCAGTCACCTCGGCTTCAATTAAGAAATTCAGAACTGAATTTACCAACAGAAACA 1371
Db 1381 CCGTATCAGGAGTTGGGATTCATTTATTTGATTCAGAACTGAATTTACCAACAGAAACA 1440
Qy 1372 ACAGAACGACCAATTAATGAATCATATAGTATCATAGGTTATCTCATAGGGCTCATTTCA 1431
Db 1441 ACAGAACGACCAATTAATGAATCATATAGTATCATAGGTTATCTCATAGGACTAATCATA 1500
Qy 1432 CAATCTAGGGTGCATGTATCCAGTATATTTCTTGGAGCGACCGTAGTCGATCGTACAAAT 1491
Db 1501 GGAAACACTTTTGAAGACCGACGCTATTTCTTGGACGCTATGTTGAGATCGTACGAAAT 1560
Qy 1492 ACCAATTAAGTTTCAGATAGCAATAACAAATACCATTTGGTAAATCATTTCAACCTTAAATCA 1551
Db 1561 ACGATTGCAACCAATAGAAATTTACAAATACCATTTGGTAAAGACCTGAATCTTCAATCA 1620
Qy 1552 GGTAACCTCTGTAGTTCAGTGGCCAGGATTTACAGGAGGGGATATAATTCGGAACCTAACGTT 1611

```

Db 1621 GGTGTTACTGTTGGAGGCCAGGATTTACAGTGGGATATCCTTCGTAGAACAAAT 1680
Qy 1612 AATGGTAGTACTAAGTATGGCTCTTAATTTTAAATAATACATCATACAGCGGTATCGC 1671
Db 1681 ACGGTTACATTTGGAGATATACGATTAATATTAATGTGCAATTTATCCCAAAGATATCGC 1740
Qy 1672 GTGAGAGTTGCTTATGCTGCTTCTCAACAATGCTCGGAGGTAACCTGCGGGGAGT 1731
Db 1741 GTAAGGATTCGTATGCTTCTACTACAGATTTACAAATTTTCAAGAGAAATTAATGGAAACC 1800
Qy 1732 ACTACTTTTGTATCAAGGATTCCTTAGTACTAGTGCATAATGAGTCTTTGACATCTCAA 1791
Db 1801 ACTGTTAATATTTGTTAAATTTCTCAAGACTATGATAGCGGGGATAAITTAGAATATAGA 1860
Qy 1792 TCATTTAGATTTGAGAAATTTCTGTTAGGATTAATGTCAGTCTGGCAGTCAAACTGCTGGA 1851
Db 1861 AGTTTTAGAACTGCGAGGATTTAGTACTCTTTTAAATTTTTTAAATGCCCAAAGCACATTC 1920
Qy 1852 ATAGTATAAGTAATATGCGAGGTAGACAAACGTTTCACTTTGTATATAAATTTGAATTCAT 1911
Db 1921 ACATGGGTGCTCAGAGTTTTCAAATCAGGAAGTTTATATAGATAGAGTCGAAATTTGTT 1980
Qy 1912 CCAATTTACTGCAACTTCGAAGCAGAAATACGATTTAGAAAGCGCGCAAGCGCGTGAAT 1971
Db 1981 CCAGCAGGTAAATTTGAGCGCAGATATGATTTAGAAAGCAGACAAAGCGCGTGAAT 2040
Qy 1972 GCTCTGTTTACTAATACGAATCCAAAGAGATTTGAAACAGAGATGTGACAGATTTATCAT 2031
Db 2041 GCTCTGTTTACTCTACAAATCCAAAGAGATTTGAAACAGAGATGTGACAGATTTATCAT 2100
Qy 2032 GATCAAGTATCCAAATTTAGTGGCGTGTATTCGATGAAATTTCTGTTAGATGAAAGAGA 2091
Db 2101 GACCAAGTGTCCAAATATGTTGGCATGTTTATCAGATGAATTTTGTGATGAGAAGCGA 2160
Qy 2092 GAATTTACTTGAAGAGTGAATATGCGAAAGAGTCTCAGTGAATGAAGAACTTACTCTCAA 2151
Db 2161 GAATTTTGAAGAGTGAATATGCGAAGCAGTCTCAGTGAATGAAGAACTTACTCTCAA 2220
Qy 2152 GATCCAACTTACATCCATCAATGAAGCAACAGAGTCTCATATCTACTAATGAGCAATCG 2211
Db 2221 GATCCAACTTACATTCAGTGGGCAATTAAGTTTTCGCATCCATCGATGGACAAATCA 2280
Qy 2212 AATTTACATCTATCCATGAACATCTGAACATGGATGGTGGGAGTGGAGAACATTACA 2271
Db 2281 AACTTCCCTCTATTAATAGCTATCTGAACATGGATGGTGGGAGTGGAGATTTTACC 2340
Qy 2272 ATCCAGGAAGGAATGAGTATTTAAAGAGAAATTTACGTCACTACCGGGACCTTTTAAAT 2331
Db 2341 ATTCAGGAAGGAATGAGTATTTAAAGAGAAATTTACGTCACTACCGGGTACTTTTAAAT 2400
Qy 2332 GAGTGTATCCGAGTATTTATATCAAAAAATAGGAGTGGGAATTTAAAGCTTATACT 2391
Db 2401 GAGTGTATCCAAATTTATATCAAAAAATAGGAGTGGGAATTTAAAGCTTATACG 2460
Qy 2392 CGTTACCAATTAAGAGGTATTTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGT 2451
Db 2461 CGCTATCAATTAAGAGGTATTTGAAGATAGTCAAGATTTAGAGATATATTTTAAATTCGT 2520
Qy 2452 TATAATCGGAACATGAACATTTGGATTTCCAGGTACCGAGTCCGATGCGCGCTTCA 2511
Db 2521 TACAATGGAAGCATGAACATTTGGATTTCCAGGTACCGAGTCCCTATGCGCGCTTCA 2580
Qy 2512 GTTGAAGCCCAATCGGAAGGTGCGGAGAACCGAATCGATCGGCACACATTTTGAATGG 2571
Db 2581 GTTGAAGCCCAATCGGAAGGTGCGGAGAACCAATCGATCGGCACACATTTTGAATGG 2640
Qy 2572 AATCCTGATCTAGATTTGTTCTGAGAGATGAGAGAAATTTGCGCATCATTTCCCATCAT 2631
Db 2641 AATCCTGATCTAGATTTGTTCTGAGAGATGAGAGAAATTTGCGCATCATTTCCCATCAT 2700
Qy 2632 TTCTCTTTGATATTTGATTTGATGATGACAGACTTGCATGAGATCTAGCGGTGCGGTG 2691
Db 2701 TTCACTTTGATATTTGATTTGGGTGCGACAGACTTGCATGAGAACCTTAGCGGTGCGGTG 2760

RESULT 8

US-08-474-038-3

; Sequence 3, Application US/08474038

Qy 2592 GTATTCAAGATTAAGACGCGAGGAAGGTCACTGCAAGACTAGGGAATCTCGAAATTTATTGAA 2751
Db 2761 GTATTCAAGATTAAGACGCGAGGAAGGTATGCAAGATTTAGGAAATCTGGAATTTATCGAA 2820
Qy 2752 GAGAAACCATTTATTAGGAGAGCACTGCTCGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 2811
Db 2821 GAGAAACCATTTATTGGAGAGCACTGCTCGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 2880
Qy 2812 GACAAACGTTGAAAACTCAATTTGAAACAAAGCGAGTATATACAGAGGCAAAAGAACT 2871
Db 2881 GACAAACGGAAGAACTACAAATTTGAAACAAAGCGAGTATATACAGAGGCAAAAGAACT 2940
Qy 2872 GTGATGCTTTATTGTTAGATTTCTCAATATATATATATATATATATATATATATATATAT 2931
Db 2941 GTGATGCTTTATTTCGTAGATTTCTCAATATATATATATATATATATATATATATATAT 3000
Qy 2932 ATGATTCATGCGGAGAGTAACATTTGTTTCATCGAATTCGAGAGGCTTATCTCTCGAAATTA 2991
Db 3001 ATGATTCATGCGGAGAGTAACATTTGTTTCATCGAATTCGAGAGGCTTATCTTTTCAGAAATTA 3060
Qy 2992 TCTGTTATCCCGGTGTAATTCGGAATTTTGAAGAAATTTAGAGGTCGCAATTTACT 3051
Db 3061 CTTGTTATCCAGGTGTAATTCGGAATTTTGAAGAAATTTAGAGGTCACATTTACT 3120
Qy 3052 GCAATCTCCTTATACGATGCGAGAAATGTCGTTAAAAATGCTGATTTTAAATGGAATTA 3111
Db 3121 GCAATGCTTATACGATGCGAGAAATGTCGTTAAAAATGCTGATTTTAAATGGAATTA 3180
Qy 3112 GCATGCTGGAATGTAAGAGGCACTGATAGTGTACAAAGAGGCTTATCTCTGCTCT 3171
Db 3181 ACATTTGGAATGTAAGAGGCACTGATAGTGTACAAAGAGGCTTATCTCTGACCTT 3240
Qy 3172 GTTATCCAGAAATGCGGAAGCAGAGTGTCAAGCAGTTCGCGTCTGTCGCGGGCGTGGC 3231
Db 3241 GTTATCCAGAAATGCGGAAGCAGAGTGTCAAGCAGTTCGCGTCTGTCGCGGGCGTGGC 3300
Qy 3232 TATATCTCCTGTCACAGCGTCAAGAGGGATATGAGAGGGTGTGTTAAACGATCAT 3291
Db 3301 TATATCTCTGTCACAGCGTCAAGAGGGATATGAGAGGGTGTGCGTAAACGATCAT 3360
Qy 3292 GAATCCAGAACATACAGAGCACTAAATTTAAAACTGTGAAGAGAGAGAGTGTAT 3351
Db 3361 GAATCCAGAACATACAGAGCACTAAATTTAAAACTGTGAAGAGAGAGAGTGTAT 3420
Qy 3352 CCAAGGATACAGGAACGTTAATGATTTATCTGCAACCAAGGTACAGAGATGTAAT 3411
Db 3421 CCAAGGATACAGGAACGTTAATGATTTATCTGCAACCAAGGTACAGAGATGTAAT 3480
Qy 3412 TCCGTTAATGCTGGATATGAGGATGCAATATGAAGTTGATATCTACAGCATCTGTTAAATPAC 3471
Db 3481 TCCGTTAATGCTGGATATGAGGATGCAATATGAAGTTGATATCTACAGCATCTGTTAAATPAC 3540
Qy 3472 AAACCGATTTAGAAAGAAACGTTATACAGATGTACAGAGATATATCATTTGTAATAT 3531
Db 3541 AAACCGATTTAGAAAGAAACGTTATACAGATGTACAGAGATATATCATTTGTAATAT 3600
Qy 3532 GACAGAGGTATGTGAATTTCCACCACTACCGAGTGTATATGACAAAGAAATTAAGAA 3591
Db 3601 GACAGAGGTATGTGAATTTCCACCACTACCGAGTGTATATGACAAAGAAATTAAGAA 3660
Qy 3592 TACTTCCAGAAACCGAATTAAGGTATGGAATTTGAGATTTGAGAAACCGAAGGGAAGTTTATT 3651
Db 3661 TACTTCCAGAAACCGAATTAAGGTATGGAATTTGAGATTTGAGAAACCGAAGGGAAGTTTATT 3720
Qy 3652 GTAGACAGGTGGAATTTACTCTTTATGAGAGAAATAG 3687
Db 3721 GTAGATAGCGTGGAACTACTCTCTCATGGAAGAAATAG 3756

[illegible]

Qy	2452	TATTAATCGGAAA	CATGAAA	CATTGGATGTTCC	AGGTACCGAGTCCG	TATCGCCGCTTTCA	2511
Db	2521	TACAATGCAAGCAT	GAAACATTTGGATGTTCC	AGGTACCGGATTTCCCT	TATCGCCGCTTTCA	2580	
Qy	2512	GTTCAAGGCCNAT	CGAAGGTCGGG	AGAACCGAATCGATCGCCACAC	CAATTTTGAATGG	2571	
Db	2581	GTTGAAAGCCCAAT	CGGAAGGTCGGG	AGAACCAATTCGATCGCGACAC	CAATTTTGAATGG	2640	
Qy	2572	AACTCCTGATCT	TAGATTGTTCT	CTGCAGAGATGGG	AAAAAATGTGCGCATCAT	TCCCATCAT	2631
Db	2641	AACTCCTGATCT	TAGATTGTTCT	CTGCAGAGATGGG	AAAAAATGTGCGCATCAT	TCCCATCAT	2700
Qy	2632	TTCTCTTTTGATAT	TGATATTTGGATGC	ACAGACTTGTGCATGAGAAAT	CTPAGCGGTGTGGGTG	2691	
Db	2701	TTCACTTTTGGATAT	TGATATTTGGGTGC	ACAGACTTGTGCATGAGAAAT	CTPAGCGGTGTGGGTG	2760	
Qy	2692	GTATTTCAAGATT	TAAGACGCAAGG	AGGTCATGCAAGCTTAGGGAAT	CTGGGAATTTTATGAA	2751	
Db	2761	GTATTTCAAGATT	TAAGACGCAAGG	AGGTTATGCAAGATTTAGGAAAT	CTGGGAATTTTATGCA	2820	
Qy	2752	GAGAAACCATTA	TATTTAGGAGAAG	CACCTGTCGTGTGAAGAGAG	CAGAGAAAAAATGGAGA	2811	
Db	2821	GAGAAACCATTA	TATTTAGGAGAAG	CACCTGTCGTGTGAAGAGAG	CAGGAAAAAATGGAGA	2880	
Qy	2812	GACAAACGCTG	AAAAACTTACAAT	TTGGAAAAAACGAGTATATAC	GAGGCAAAAGAGCT	2871	
Db	2881	GACAAACGCGAA	AAAAACTTACAAT	TTGGAAAAAACGAGTATATAC	GAGGCAAAAGAGCT	2940	
Qy	2872	GTGGATGCTTTAT	TTTGTAGATTCT	CAATATAATAGATTACA	ACGCGGATACAAACATTTGGC	2931	
Db	2941	GTGGATGCTTTAT	TTTGTAGATTCT	CAATATGATCAAT	TACAACGCGGATACAAACATTTGGC	3000	
Qy	2932	ATGATTCATCG	CGGAGATAA	CTTGTTTCATCGAATTCG	CAGAGCTTATCTGT	CAGAAATTA	2991
Db	3001	ATGATTCATCG	CGGAGATAA	CTTGTTTCATCGAATTCG	CAGAGCGGTATCTTT	CAGAAATTA	3060
Qy	2992	TCTGTTATCC	GGGTGTAAAT	TGCGGAAATTTTGAAGAAAT	TAGAAGCTCGCAT	TATTCACCT	3051
Db	3061	CCTGTTATCC	AGGTGTAAAT	TGCGGAAATTTTGAAGAAAT	TAGAAGCTCACAT	TATTCACCT	3120
Qy	3052	GCAATCTCCT	TATACGATCG	CAGAAATGTCGTTTAAAAAT	TGGTGATTTTAAAT	TGGAATTA	3111
Db	3121	GCAATGCTCTT	TATACGATCG	CAGAAATGTCGTTTAAAAAT	TGGTGATTTTAAAT	TGGAATTA	3180
Qy	3112	GCATGCTGGAAT	GTTAAAGGCGAT	GTAGATGTAACACAGAGCC	CATCACGTTCTGTCTCTT	3171	
Db	3181	ACATGTTTGSAA	TGTAAAAGGCGAT	GTAGATGTAACACAGAGCC	CATCATGCTTCTGACCTT	3240	
Qy	3172	GTTATCCGAAAT	TGGGAAGCAGAA	GTGTCAAGCAGTTTCGCGTCTGT	TCGGGGCGTGGC	3231	
Db	3241	GTTATCCGAAAT	TGGGAAGCAGAA	GTGTCAAGCAGTTTCGCGTCTGT	TCGGGGCGTGGC	3300	
Qy	3232	TATATCCTCT	CGTGTCA	CAGCGTACAAAGAGGG	ATATGGAGAGGTTGTGT	TAAACGATCCAT	3291
Db	3301	TATATCCTCT	CGTGTCA	CAGCGTACAAAGAGGG	ATATGGAGAGGCTCGGT	TAAACGATCCAT	3360
Qy	3292	GAAATCGAAG	CAANTACAGAC	CGAACTTAAATTTAAAACTGT	CAAGAGAGGAGTG	TAT	3351
Db	3361	GAAATCGAAG	CAANTACAGAC	CGAACTTAAATTTAAAACTGT	CAAGAGAGGAGTG	TAT	3420
Qy	3352	CCAAAGGAT	CAGGAACG	TGTATGATTTACTTGC	ACACCAAGGTACAG	CAGTATCTGAAT	3411
Db	3421	CCAAAGGAT	CAGGAACG	TGTATGATTTACTTGC	ACACCAAGGTACAG	CAGTATCTGAAT	3480
Qy	3412	TCCCGTAA	TGCTGGATAT	TGAGGTG	CATATGAAGTTG	ATACACGATCTGT	3471
Db	3481	TCCCGTAA	TGCTGGATAT	TGAGGTG	CATATGAAGTTG	ATACACGATCTGT	3540
Qy	3472	AAACCGG	ACTTATGA	AGAGAAACG	TATACAGATG	TACGAAGATTAAT	3531
Db	3541	AAACCGG	ACTTATGA	AGAGAAACG	TATACAGATG	TACGAAGATTAAT	3600

QY 1132 ACTTCTATTAATCCTGTGAAGATTATCACTTCTCTCGAGACGTATATTGGACCTGAATCA 1191
 Db 1207 ACTTCAATTAATCCTGTGAACATTAACAGTTTACGTCTCGAGACGTTTATAGAACAGAAATCA 1266
 QY 1192 TATGCAGGAGTCTTCTATGGGAAATTTACCTTGAACCTATTTCTATGGTGTCCCTACTGTT 1251
 Db 1267 AATGCAGGACAAATAT-----ACTATTACTACTCTCTGTGAATGGAGTACCTTGGGCT 1320
 QY 1252 AGATTTAATTTTAGAACCCCTCAGAAATACCTTTTGAAGAGGTACTGCTTAATATAGTACAA 1311
 Db 1321 AGATTTAATTTTATAAACCCCTCAGAAATATTTATGAAGAGGCGCACTTACCCTACAGTCAA 1380
 QY 1312 CCCTATGAGTCACCTGGGCTTCAATTAAGAAATTCAGAACTGGAATACCAACCAAGAAC 1371
 Db 1381 CCGTATCAGGAGTGGGATTTCAATTTATTGATTCAGAACTGAATTACCAACCAAGAAC 1440
 QY 1372 ACAGAACCAAAATTAATGAATCATATAGTATAGGTTTATCTCATAAGGGCTCATTTCA 1431
 Db 1441 ACAGAACCAAAATTAATGAATCATATAGTATAGTATTTCTCATATAGGACTAATCAT 1500
 QY 1432 CAATCTAGGGTGCAATACCAAGTATATTCTTGGACGCCAGCTAGTGCAAGATCGTACAAAT 1491
 Db 1501 GGAACACCTTTGAGAGCACCACTCTATTCTTGGACGCATCGTAGTGCAAGATCGTACGAAT 1560
 QY 1492 ACCATTAGTTCAGATAGCATTAACAAATACATTTGTTAAATCATTTCAACCTTAATTTCA 1551
 Db 1561 ACGATTGACCAAAATAGAAATTTACAAATACATTTGTTAAAGCACTGAATCTTTCAATTTCA 1620
 QY 1552 GGTACCTCTGTAGTCAGTGGCCAGGATTTTACAGAGGGGATATAATCCGAACTTAAAGT 1611
 Db 1621 GGTGTTACTGTGTTGGAGGCCAGGATTTACAGTGGGGATATCCCTCGTAGAACAAAT 1680
 QY 1612 AATGGTAGTGTACTAAGTATGGGCTTTAATTTTAAATTAATCATCATTTACAGCGGTATCGC 1671
 Db 1681 ACGGTACATTTGGAGATATACGATTAATTAATTAATGTCCTATTTCCAAAGATATCGC 1740
 QY 1672 GTGAGAGTTCGTTATGCTGCTTCTCAAAACAAATGTCCTGAGGGTAACTGTGCGAGGAGT 1731
 Db 1741 GTAAGGATTCGTTATGCTTCTACTACAGATTTTACAAATTTTTCACGAGAAATTAATGGAACC 1800
 QY 1732 ACTACTTTTGTATCAAGGATTCCTAGTACTAGTGCATAATGAGTCTTTGACATCTCAA 1791
 Db 1801 ACTGTTAATATGTTAAATTTCTCAAGAACTATGATAGGGGGGATTAATTTAGAAATATAGA 1860
 QY 1792 TCATTTAGATTTGCAGAAATTTCTGTAGGTATAGTGCACTGTGGCAGTCAAACTGCTGGA 1851
 Db 1861 AGTTTATAGAACTGCAGGATTTAGTACTCTCTTTAATTTTAAATGCCAAAGCACATTC 1920
 QY 1852 ATAAGTATAAGTATAATAGCAGGTAGACAAACGTTTCACTTTGTATGATAAAATTTCAAT 1911
 Db 1921 ACATTTGGGTGCTCAGAGTTTTTCAAATCAGGAAGTTTATATAGATAGAGTTCGAATTTGTT 1980
 QY 1912 CCAATTACTGCAACCTTCGAGGCAAGTATACGATTTAGAAAGGCGCAGAGCGGTGAAT 1971
 Db 1981 CCAGCAGAGGTAAATTTGAGGCGAAGTATGATTTAGAAAGAGCACAAAGGCGGTGAAT 2040
 QY 1972 GCTCTGTTTACTTAATACGAATTCGAAGAGATTTGAAACAGAGTGTGACAGATTTATCATATT 2031
 Db 2041 GCTCTGTTTACTTCTACAAATTCGAAGAGATTTGAAACAGAGTGTGACAGATTTATCATATT 2100
 QY 2032 GATCAAGTATCCAAATTTAGTGGCGTGTATCGGATGAATTTCTGCTTAGATGAAAGAGA 2091
 Db 2101 GACCAAGTGTCCAATATGTTGGCATGTTTATACAGATGAATTTTGTGTTGATGAGAGCGA 2160
 QY 2092 GAATTAATTGAGAAAGTGAATATGCGAAACGACTCAGTGTATGAAAGAACTTACTCCAA 2151
 Db 2161 GAATTAATTGAGAAAGTGAATATGCGAAAGGCACTCAGTGTATGAAAGAACTTACTCCAA 2220
 QY 2152 GATCCAAATTTTCAATCATCAATAAGCAACAGACTTTTCAATCTTACTTAATGAGCAATCG 2211
 Db 2221 GATCCAAATTTTCAATCATCAGTGGGCAATTAAGTTTCGATCCATCGATGGCAATCA 2280
 QY 2212 AATTTTCAATCTATCCATGAACAATCTGAACATGGATGGTGGGAAAGTGAGAACATTTACA 2271

Db 2281 AACTTCCCTCTTAATTAAGCTATCTGAACATCGATGGTGGGAGAGTGCGAATGTTACC 2340
 QY 2272 ATCCAGGAAGAAATGACGTATTTAAAGAGAAATTTACGTCACTACCGGGACCTTTTAAAT 2331
 Db 2341 ATTCCAGGAAGGAAATGACGTATTTAAAGAGAAATTTACGTCACTACCGGGTACTTTTAAAT 2400
 QY 2332 GAGTGTATTCCGACGTATTTATATCAAAATATAGAGAGTCCGAATTTAAAGAGCTTATACT 2391
 Db 2401 GAGTGTATTCCAAATTTATATCAAAATATAGAGAGTCCGAATTTAAAGAGCTTATACG 2460
 QY 2392 CGCTACCAATTTAAGAGAGTATTTGAAGATAGTCAAGATTTAGAGATATATTGATTCGT 2451
 Db 2461 CGCTATCAATTTAAGAGAGTATTTGAAGATAGTCAAGATCTAGAGATTTATTTAATTCGT 2520
 QY 2452 TATAATCGAAACATGAACATTTGGATGTTTCCAGGTACCGAGTCCGTATGCGCTTTTCA 2511
 Db 2521 TACAATGCAAGCATGAACATTTGGATGTTTCCAGGTACCGATTTCCCTATGCGCGCTTTCA 2580
 QY 2512 GTTGAAGCCCAATCGGAAGGTGCGGAGAACCGAATCGATCGGCACCAATTTTGAATGG 2571
 Db 2581 GTTGAAGCCCAATCGGAAGGTGCGGAGAACCAATCGATCGGCACCAATTTTGAATGG 2640
 QY 2572 AATCCTCATCTAGATGTTCTCTGAGAGATGAGAAATTTGTCGCGCATCTTCCCATCAT 2631
 Db 2641 AATCCTCATCTAGATGTTCTCTGAGAGATGAGAAATTTGTCGCGCATCTTCCCATCAT 2700
 QY 2632 TTCTCTTTGGATTTGATTTATTTGGATGTCACAGACTTGCATGAGAAATCTAGGGGTGCGGTG 2691
 Db 2701 TTCACTTTGGATTTGATTTGTTGGTGCACAGACTTGCATGAGAACCTAGGGGTGCGGTG 2760
 QY 2692 GTATTCAAGATTTAAGACGCGAAGGTCTGCAAGATCTGAGGAAATCTGGAATTTTATGAA 2751
 Db 2761 GTATTCAAGATTTAAGACGCGAAGGTCTGCAAGATTTAGGAAATCTGGAATTTTATCGAA 2820
 QY 2752 GAGAAACCATTTATTAGGAGAGCACTCTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 2811
 Db 2821 GAGAAACCATTTATTGAGAGAGCACTCTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 2880
 QY 2812 GACAAACGTTGAAACCTCAATTTGGAACCAAAACGAGTATATACAGAGGCGCAAAAGAGCT 2871
 Db 2881 GACAAACGTTGAAACCTCAATTTGGAACCAAAACGAGTATATACAGAGGCGCAAAAGAGCT 2940
 QY 2872 GTGATGCTTTATTTGTAGATTTCAATTAATAGATTTACAAGCGGATACAAACATTTGGC 2931
 Db 2941 GTGATGCTTTATTTCTGTAGATTTCTCAATATGATCAATTTACAAGCGGATACAAACATTTGGC 3000
 QY 2932 ATGATTTATGCGGCGAGATAAATTTGTTTCATCGAATTTGAGAGGCTTATCTGTCAGAAATTA 2991
 Db 3001 ATGATTTATGCGGCGAGATAAATTTGTTTCATCGAATTTGAGAGGCTTATCTTTTCAGAAATTA 3060
 QY 2992 TCTGTTATCCCGGTGTAAATGCGGAAATTTTGAAGAAATTTAGAGGTCGCAATTTATCACT 3051
 Db 3061 CCGTGTATCCAGGTGTAAATGCGGAAATTTTGAAGAAATTTAGAGGTCACATTTATCACT 3120
 QY 3052 GCAATCTCCCTTATACGATGCGAGAAATTTCTGTTAAAAATGCTGATTTTAAATTAATGGAATTA 3111
 Db 3121 GCAATGCTCTTATACGATGCGAGAAATTTCTGTTAAAAATGCTGATTTTAAATTAATGGAATTA 3180
 QY 3112 GCATGCTGGAATGTAAAAAGGCGATGTAGATGTACAAACAGGCCATCACCGTTCTGTCTCTT 3171
 Db 3181 ACATGTTGGAATGTAAAAAGGCGATGTAGATGTACAAACAGGCCATCACCGTTCTGTCTCTT 3240
 QY 3172 GTTATCCAGAAATGCGGAGAGAGAGTGTCAACAGCTTTCGCTGTCGCGGGCGTGGC 3231
 Db 3241 GTTATCCAGAAATGCGGAGAGAGAGTGTCAACAGCTTTCGCTGTCGCGGGCGTGGC 3300
 QY 3232 TATATCTCTCGTGTCAACAGGCTTACAAAGAGGAGTATGAGAGGCTTGTGTAAACGATCCAT 3291
 Db 3301 TATATCTCTCGTGTCAACAGGCTTACAAAGAGGAGTATGAGAGGCTTGTGTAAACGATCCAT 3360
 QY 3292 GAAATCGAGAACCAATACAGAGAACTTAAAAATTTAAAACTGTGAAGAGAGAGAGAGTGTAT 3351

```

Db 3361 GAAATCGAGAACAAATACAGACGAACTAAAAATTTAAAAAATGTGTAAGAGGAAAGTGTAT 3420
Qy 3352 CCAACGGATACAGGAACGTGTAATGATTATATCTGCACACCAAGGTACAGCAGTATGTAAT 3411
Db 3421 CCAACGGATACAGGAACGTGTAATGATTATATCTGCACACCAAGGTACAGCAGTATGTAAT 3480
Qy 3412 TCCCGTAAATGCTGGATATGAGGATGCATATGAAATTTGATATCTACAGCATCTGTTAAATTAC 3471
Db 3481 TCCCGTAAATGCTGGATATGAGGATGCATATGAAATTTGATATCTACAGCATCTGTTAAATTAC 3540
Qy 3472 AAACCGCATTTAGAAAGAAACGTATACAGATGTACAGAGATATCATTTGTGAATAT 3531
Db 3541 AAACCGCATTTAGAAAGAAACGTATACAGATGTACAGAGATATCATTTGTGAATAT 3600
Qy 3532 GACAGAGGTATGTGAATATCCACCACTACCACTGCTTATATGACAAAGAAATTAAGAA 3591
Db 3601 GACAGAGGTATGTGAATATCCACCACTACCACTGCTTATATGACAAAGAAATTAAGAA 3660
Qy 3592 TACTTCCAGAAACCGATAGGATGATGATTTGAGATTGGAGAAACGGAAGGAAGTTTATT 3651
Db 3661 TACTTCCAGAAACCGATAGGATGATGATTTGAGATTGGAGAAACGGAAGGAAGTTTATT 3720
Qy 3652 GTAGACAGCGTGGAAATTTACTCTTATGGAGGAATAG 3687
Db 3721 GTAGATAGCGTGGAAATTTACTCTTATGGAGGAATAG 3756

RESULT 10
US-08-881-340-3
; Sequence 3, Application US/08881340
; Patent No. 5942658
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jan, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/881.340
; FILING DATE: 24-JUN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3934 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; FEATURE:

```

```

; NAME/KEY: CDS
; LOCATION: 67..3756
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 2253..2272
US-08-881-340-3

Query Match 72.9%; Score 2687.2; DB 2; Length 3934;
Best Local Similarity 83.5%; Pred. No. 0;
Matches 3088; Conservative 0; Mismatches 593; Indels 15; Gaps 3;

Qy 1 TTGACTTCAAATAGGAAAAATGAGAAATGAAATATATAAATGCTTTATCGATTTCCAGCTGTA 60
Db 67 TTGACTTCAAATAGGAAAAATGAGAAATGAAATATATAAATGCTTTATCGATTTCCAAACGTA 126
Qy 61 TCGAATCATTTCCACACAAATGGAATCTATCACAGATGCTCGTATTTAGAGGATTTCTTCTGT 120
Db 127 TCGAATCTTTCCACGCAAAATGAATCTATCACAGATGCTCGTATTTAGAGGATTTCTTCTGT 186
Qy 121 ATAGCCGAGGGGAATATATCAATCCACTTTGTTAGCGCATCAACAGTCCAAACGGGTATT 180
Db 187 GTAGCCGAGGTGAACAATATTGATCCATTGTTAGCGCATCAACAGTCCAAACGGGTATA 246
Qy 181 AACATAGCTGGTAGAATACCTAGGTGTATTTAGGCGTACCGTTTGTCTGACAAAATAGCTAGT 240
Db 247 AACATAGCTGGTAGAATATTGGGCGTATTAGGTGTGCGGTTTGTCTGACAACTAGCTAGT 306
Qy 241 TTTTATAGTTTTCTTTGTTGTTGTAATTTATGCGCGCGGCGAGAGATCAGTGGGAAATTTTC 300
Db 307 TTTTATAGTTTTCTTTGTTGTTGTTGTAATTTATGCGCGTATTAGGCGTATCATGGGAAATTTTC 366
Qy 301 CTAGAACATGTGAAACAACTTATAAAATCAACAAATAACAGAAAATGCTAGGAAATACGGCA 360
Db 367 CTGGAACATGTAGAACAACTTATAAGACAAACAGTAACAGAAAATCTAGGAAATACGGCT 426
Qy 361 CTGCTCGATTACAAGTTTAGGAGATTCCTTTAGAGCCTATCAAGTCACTCATTGAGAGAT 420
Db 427 ATTGCTCGATTAGAAAGTCTAGGAAGAGGCTATAGATCTTTACCAGCAGGCTCTTGAAC 486
Qy 421 TGCTGAGAAACCGTGTATGATGCAAGAACGAGAGTGTCTTTATATACCAATATATAGCC 480
Db 487 TGGTTAGATAACCGAAATGATGCAAGAGCAATTAATCTTTGAGCGCTATGTTGCT 546
Qy 481 TTAGAACTTCAATTTCTTTAATGCGATGCCCTTTTCGAAATTAGAAACCAAGAGTTCCA 540
Db 547 TTAGAACTTGACATTACTACTGCTATACCGCTTTTCAGAAATACGAAATGAAGATTCCA 606
Qy 541 TTATTAATGTTATGCTCAAGCTGCAAAATTTACCTATTATTATTGAGAGATGCCTCT 600
Db 607 TTATTAATGTTATGCTCAAGCTGCAAAATTTACACCTATTATTATTGAGAGAGCATCC 666
Qy 601 CTTTTGGTAGTGAATTTGGCTTACATCGCAGGAATTTCAAGTTTATTTATGAGCGCAA 660
Db 667 CTTTTGGTAGTGAATTTGGGGATGCGCATCTTCGATGTTAACCAATATTACCAGAACAA 726
Qy 661 GTGGAACAAACGAGAGATTTATCCGACTATTGCGTAGAATGCGTATATATACAGGTTAAAT 720
Db 727 ATCAGATATACAGAGGAATTTCTAACCAATGCGTACAAATGTTATATACAGGCTAAAT 786
Qy 721 AGCTTAGAGGGAACAATGCCGAAGTTGGGTGCTTATTAATCAATTTCCGTAGAGATCTA 780
Db 787 AACCTTAAGAGGGAACAATGCTGAAAGTTGGTTGCGGTATTAATCAATTTCCGTAGAGCTA 846
Qy 781 ACGTTAGGGGTATTAGATCTAGTGCGCACTATTTCCAGCTATGACACTCGCAGCTTATCCA 840
Db 847 ACGTTAGGGGTATTAGATTTAGTAGCCCTATTCCCAAGCTATGATATCTCGACCTTATCCA 906
Qy 841 ATAAATACGAGTCTCAGTTTAAACAAAGGAAGTTTATACAGACGCAATTTGGAGCAACAGG 900
Db 907 ATCAATACGAGTCTCAGTTTAAACAGAGAAATTTATACAGATCCAAATTTGGAGAACAAAT 966
Qy 901 GTAAAT-----ATGGCAAGTATGAATTGGTATTAATTAATGACACCTTGTGTTTCGCT 954

```

Db	967	GCACCTTCAGGATTTGCAAGTACGAATTTGGTTTAAATAATAATGACCAATCGTTTTCTGCC	1026
Qy	955	ATAGAGACTGCGGTTATCCGAAGCCCGCATCTACTTGAATTTTCTAGAACAACTTACAAAT	1014
Db	1027	ATAGAGGCTGCCATTTTCAGGCTCCGCATCTACTTGAATTTTCAGAAACAACCTTACAAT	1086
Qy	1015	TTTAGCATTCTATCAGCATGAGTGTCTACTAGGCATATGACTTACTTGGCGGGGACACACA	1074
Db	1087	TACAGTGATCAAGCCGTTGGAGTAGCACTCAACATATGAATTAATTTGGGTGGGACATAGG	1146
Qy	1075	ATTCAATCTCGGCCAATAGGAGGGGATTAATACTCTCAACGCGATGGGTCTACCA--AT	1131
Db	1147	CTTAATCTCGGCCAATAGGAGGGACATTAATACCTCAACACAGGACTTACTAATAAT	1206
Qy	1132	ACTTCTATTAATCTGTGAAGATTATCATTTCTCTCGAGACGTATATTTGGAGCTGAATCA	1191
Db	1207	ACTTCAATTAATCTGTGAACATTAACAGTTAGCTCGAGAGCTTTATAGAACAGATCA	1266
Qy	1192	TATGAGGAGTGTCTTATGGGAAATTTACCTTGAACCTATTCATGTGGTGCCTACTGTT	1251
Db	1267	AATGCGGGACAAATAT-----ACTATTTACTCTCCTGTGAATGGAGTACCTTGGGCT	1320
Qy	1252	AGATTTAATTTTAGGAACCTCAGAACTATTTTGAAGAGGTACTGTCTAACTATAGTCAA	1311
Db	1321	AGATTTAATTTTAAACCTCAGAAATATTTATGAAGAGGCGCACCTACCTACAGTCAA	1380
Qy	1312	CCCTATGAGTCACTGGGCTTCAATTAAGAGATTGAGAACTGAAATTAACCAACCAAGAA	1371
Db	1381	CGGTATCAGGGAGTTGGGATTTCAATTTATTTGATTGAGAACTGAAATTAACCAACCAAG	1440
Qy	1372	ACAGAACCAACAAATTAATGAATCATATAGTCAATAGGTTATCTCATAGGGCTCAATTTCA	1431
Db	1441	ACAGAACCAACAAATTAATGAATCATATAGTCAATAGTATCTCATATAGGACTAATCATA	1500
Qy	1432	CAATCTAGGGTGCATGATACCAAGTATTTCTTGGAGCGCACCGTAGTGAGATCGTACAAAT	1491
Db	1501	GGAAACCTTTGAGAGCACCGAGTCTATTTCTTGGAGCGCATCTGTAGTGCAAGTCGACGAAT	1560
Qy	1492	ACCATTAGTTCAGATAGCATAAACAATAACATTTGGTAAATCAATCAACCTTAATTTCA	1551
Db	1561	ACGATTGCAACCAATAGAAATTAACAATAACATTTGGTAAAGCACTGAATCTTCAATTTCA	1620
Qy	1552	GGTACCTCTGTAGTACGTCGAGGATTTACAGAGGGGATATAATCCGAACCTAACGTT	1611
Db	1621	GGTGTACTGTGTGGAGGCGCAGGATTTACAGGTGGGATATCCTTTCGTAGAACAAAT	1680
Qy	1612	AATCGTAGTACTAAGTATGGGCTTAAATTTTAATAATCATCATATACACGCGGTATCGC	1671
Db	1681	ACGGGTACATTTGGAGATATACGATTAATAATTAATGTGCCATTTATCCCAAGATATCGC	1740
Qy	1672	GTGAGAGTTCTGTATGCTGCTTCTCAACAATGGTCTCTGAGGGTAACTGTGAGGGAGT	1731
Db	1741	GTAAGGATTCGTTATGCTTCTACTACAGATTTCAATTTTTCACAGAAATTAATGGAACC	1800
Qy	1732	ACTACTTTTGTCAAGGATTCCTTAGTACTATGAGTGCAATGAGTCTTTGACATCTCAA	1791
Db	1801	ACTGTTAATATTTGTAATTTCTCAAGAACTATGAATAGGGGGGATAATTTAGAAATAGA	1860
Qy	1792	TCATTTAGATTTGAGAAATTTCTGTAGGTATAGTGCACTGGCAGTCAAACTGCTGGA	1851
Db	1861	AGTTTGAAGTTCGAGGATTTAGTACTCTCTTTTAAATTTTTTAAATGGCCCAAGCACATTC	1920
Qy	1852	ATAAGTATAAGTAAATGACAGGTAGACAAACGTTTCACTTTTGATATAAAATGAATTCAT	1911
Db	1921	ACATTTGGTGTCTAGAGTTTTCATACAGAAATTTTATATAGATAGAGTCAATTTGTT	1980
Qy	1912	CCAATTTACTGCAACCTTCGAAGCAGAAATACGATTTTGAAGAGGGCGCAAGGCGGTGAAT	1971
Db	1981	CCAGCAGAGGTAAACATTTGAGCAGAAATATGATTTAGAAAGAGCACAAAGCGGTGAAT	2040
Qy	1972	GCTCTGTTTACTAATACGAATCCAGAGATTTGAAACAGATGTGACAGATTTATCATTT	2031
Db	2041	GCTCTGTTTACTTCTCAAAATCCAGAGATTTGAAACAGATGTGACAGATTTATCATATT	2100
Qy	2032	GATCAAGTATCCAAATTTAGTGGCGTGTATTATCGGATGAATTTCTGCTTAGATGAAAGAGA	2091
Db	2101	GACCAAGTGTCCAATATGGTGGCATGTTTATCAGATGAATTTTCTGCTGATGAGAAGCGA	2160
Qy	2092	GAATTAATTTGAGAAAGTCAATATGCGAAACGACTCAGTGATGAAGAACTTACTCCAA	2151
Db	2161	GAATTAATTTGAGAAAGTCAATATGCGAAACGACTCAGTGATGAAGAACTTACTCCAA	2220
Qy	2152	GATCAAACTTCAATCCATCAATAAGCAACAGACTTCAATCTATCTATTAATGAGCAATCG	2211
Db	2221	GATCAAACTTCAATCCATCAATGAGTGGCAATTAAGTTTTCGATCCATCGATGGCAATCA	2280
Qy	2212	AATTTCACTCTCTCATGAAACAATCTGAACATGGATGGTGGGAAAGTGAGAACATTAACA	2271
Db	2281	AATTTCCCTCTAATTAATGAGTATCTGAACATGGATGGTGGGAAAGTGCGAATGTTACC	2340
Qy	2272	ATCAGGAAGAAATGAGTATTTAAAGAGAAATTAACGTCACTACACACCGGGACTTTTAAT	2331
Db	2341	ATTGAGGAAGGAAATGAGTATTTAAAGAGAAATTAACGTCACTACACACCGGGACTTTTAAT	2400
Qy	2332	GAGTGTATCCGAGCTATTTATATCAAAATAAGAGAGTCCGAAATTAAGAGCTTATACT	2391
Db	2401	GAGTGTATCCAAATTTATATCAAAATAAGAGAGTCCGAAATTAAGAGCTTATAGG	2460
Qy	2392	CGTCAACAAATTAAGAGGTTATTTGAAGATAGTCAAGATTTTAGAGATATATTTGATTCGT	2451
Db	2461	CGCTATCAATTTAAGAGGTTATTTGAAGATAGTCAAGATCTAGAGATTTATTTAATTCGT	2520
Qy	2452	TATTAATCGGAAACATGAAACATTTGGATGTTTCCAGGTACCGAGTCCGTATGCGCGTTTCA	2511
Db	2521	TACAATCGAAGCATGAAACATTTGGATGTTTCCAGGTACCGAATTTCCCTATGCGCGTTTCA	2580
Qy	2512	GTTCAAAGCCCAATCGGAAGGTGGAGAACCGAATCGATCGGCACACCATTTTGAATGG	2571
Db	2581	GTTCAAAGCCCAATCGGAAGGTGGAGAACCGAATCGATCGGCACACCATTTTGAATGG	2640
Qy	2572	AATCCTGATCTAGATTTGCTCTGAGAGATGAGAGAAATTTGGGCACTCATTTCCCATCAT	2631
Db	2641	AATCCTGATCTAGATTTGCTCTGAGAGATGAGAGAAATTTGGGCACTCATTTCCCATCAT	2700
Qy	2632	TTCTTTTGGATATTTGATTTGATGTCACAGACTTGCATGAGAACTTAGGGGTGGGTG	2691
Db	2701	TTCACTTTGGATATTTGATTTGGGTGTCACAGACTTGCATGAGAACTTAGGGGTGGGTG	2760
Qy	2692	GTATTTCAAGATTAAGACGCGAGAGGTCTATGAGACTTAGGGAATCTGGAATTTATTCGA	2751
Db	2761	GTATTTCAAGATTAAGACGCGAGAGGTCTATGAGAACTTAGGAAATCTGGAATTTATTCGA	2820
Qy	2752	GAGAAACCATTTATGAGAGAGCACTGCTCTGTTGAGAGAGAGAGAGAGAGAGAGAGAG	2811
Db	2821	GAGAAACCATTTATTTGAGAGAGCACTGCTCTGTTGAGAGAGAGAGAGAGAGAGAGAG	2880
Qy	2812	GACAAACGTGAAACCTACAAATTTGAAACAAACAGATATATACAGAGGCAAAAGAGCT	2871
Db	2881	GACAAACGTGAAACCTACAAATTTGAAACAAACAGATATATACAGAGGCAAAAGAGCT	2940
Qy	2872	GTGATGCTTTATTTGATGATTTCTCAATATATAGATTTACAGCGGATACAAACATTTGGC	2931
Db	2941	GTGATGCTTTATTTGATGATTTCTCAATATATAGATTTACAGCGGATACAAACATTTGGC	3000
Qy	2932	ATGATTCATGCGGAGATTAATTTGTTTCACTGGAATTCGAGAGGCTTATCTGTCAGAAATTA	2991
Db	3001	ATGATTCATGCGGAGATTAATTTGTTTCACTGGAATTCGAGAGGCTTATCTTTTCAAGATTA	3060
Qy	2992	TCGTTATCCGGGTGTAATTTGCGGAAATTTTGAAGAAATTTGAGAGGTTCGATTCACAT	3051
Db	3061	CTGTTATCCAGGTGTAATTTGCGGAAATTTTGAAGAAATTTGAGAGGTTCATTCATCACT	3120
Qy	3052	GCAATCTCCCTATACGATGCGGAAATGTCGTTAAAAATGCTGATTTTAAATGGAATTA	3111
Db	3121	GCAATGCTTCTATACGATGCGGAAATGTCGTTAAAAATGCTGATTTTAAATGGAATTA	3180

3112	GCATGCTGGAATGTA	AAAGGCGCATGTA	GTATCAACAGAGCC	NATCACCGTTCTGTCTT	31171
3181	ACATGTTGGAAATGT	AAAGGCGCATGTA	GTATCAACAGAGCC	NATCATCGTTCTGACCTT	3240
3172	GTTATCCGAATGGG	AAGCAGAAAGTGT	CACAAGCAGTTCCG	GTCTCTCGGGGCGTGGC	3231
3241	GTTATCCGAATGGG	NAGCAGAAAGTGT	CACAGCAGTTCCG	GTCTCTCGGGGCGTGGC	3300
3232	TATATCCTCCGTGT	CACAGCGTCAAA	AGAGGGGATATGG	AGAGGGTTGTGTAA	CGATCCAT 3291
3301	TATATCCTCTGT	CACAGCGTCAAA	AGAGGGGATATGG	AGAGGGCTCGGTAA	CGATCCAT 3360
3292	GAAATCGAGAAACA	ATACAGACGAACT	TAATAATTTAAACA	CTGTGAGAAAGGAG	AGTGTAT 3351
3361	GAAATCGAGAAACA	ATACAGACGAACT	TAATAATTTAAACA	CTGTGAGAAAGGAG	AGTGTAT 3420
3352	CCAAAGGATACAG	GAAGCTGTATGATT	TACTGACACCAAG	GTACAGACAGATGT	GAAT 3411
3421	CCAAAGGATACAG	GAAGCTGTATGATT	TACTGACACCAAG	GTACAGACAGATGT	GAAT 3480
3412	TCCCGTAATCTCG	ATATGAGGATGCA	TATGAAGTTGATAC	TACTACAGCATCTG	TTAATTAC 3471
3481	TCCCGTAATCTCG	ATATGAGGATGCA	TATGAAGTTGATAC	TACTACAGCATCTG	TTAATTAC 3540
3472	AAACCGACTTTAT	GAAGAAGAAACG	TATACAGATGTAC	GAAAGATATCAAT	GTGGAATAT 3531
3541	AAACCGACTTTAT	GAAGAAGAAACG	TATACAGATGTAC	GAAAGATATCAAT	GTGGAATAT 3600
3532	GACAGAGGGTATG	TGAATTTACCA	CCACTACCACTGG	TTATATGACAAAG	GAATTAGAA 3591
3601	GACAGAGGGTATG	TGAATTTACCA	CCACTACCACTGG	TTATATGACAAAG	GAATTAGAA 3660
3592	TACTTCCGAAACC	CGATAAGTATG	GAATTTGAGATTG	GAGAAACGGAAG	CGGAAGTTTATT 3651
3661	TACTTCCGAAACC	CGATAAGTATG	GAATTTGAGATTG	GAGAAACGGAAG	CGGAAGTTTATT 3720
3652	GTAGACAGCGTGA	ATTTACTTCCTT	ATGGAGGAATAG		3687
3721	GTAGATAGCGTGA	AATCTACTCCT	CATGGAAGATAG		3756

RESULT 11

US-080-040-751-A
Sequence 4, Application US/08040751
Patent No. 5407825
GENERAL INFORMATION:
APPLICANT: Payne, Jewel M
APPLICANT: Sick, August J
TITLE OF INVENTION: No. 5407825el Bacillus thuringiensis isolates
active against Lepidopteran Pests and Genes Encoding No. 5407825el
Lepidopteran-active Toxins
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID R. SALIWANCHIK
STREET: 2421 N.W. 41st STREET, SUITE A-1
CITY: GAINESVILLE
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
'COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/040,751
FILING DATE: 19930329
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SALIWANCHIK, DAVID R.
REFERENCE/DOCKET NUMBER: MA39.C1.D3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100

Db	843	TTTCGAGAGTATCGAAANTCAGCTATTAGAAAGTCCCCATCTTATGGATTTCTTAAATAAA	902
Qy	1005	ACTTTACAAATTTTATAGCACTTCATCAGCATGAGTGTCTACTAGGCATATGACTTACTCGCG	1064
Db	903	TATAAATTATTGACACTGATTTA-----ATTAGAGCGGTTCATTATGGCG	947
Qy	1065	GGGGCACAAATTCAAATCTCGGCCAATAGAGAGCGGATTAATAATCCTCAACGATGGGT	1124
Db	948	GGGGCATCGTGTAACTTCTCATTTTACCGGTAGTTCGCAAGTGAAGAAGTCCCTCAATA	1007
Qy	1125	TACCAATACTTCTAATTAATCCTGTAAGATTATCATTTCTCTCGAGACGTATATTGGAC	1184
Db	1008	CGGGATTAATCTCAAAACGAGAACCGAGTCGAACATATTGCTCCTAGCACTTTTCCAGGTCT	1067
Qy	1185	TGAATCATATGACGAGTGTCTTATGGGGAATTTTACCTTGAACCTTATTCATGTGTCCC	1244
Db	1068	TAACTCTATTTTATAGACACTATCAGACCCCTTTCTTCGAAGATCCGATAATATTATGCC	1127
Qy	1245	TACTGTTAGATTAAATTTTATAGGAACCTCTCAGAACTACTTTTGAAGAGGTACTGCTAACTA	1304
Db	1128	AACATTAGGAATAAATGTAGTGCAGGGGTAGGATTCATTCAACCAAAATATGCTGAAGT	1187
Qy	1305	TAGTCAACCCCTATGAGTCACTCGGTGGCTTCAATTAAAGATTTCAGAACTGNAATTACCACC	1364
Db	1188	TCTATATAGAAGGAGAGAACAGTAGATTCTCTTGATGAGTTGCCAATTGA-----CGG	1241
Qy	1365	AGAAACAACAGAACGACCAAAATTATGAATCATATAGTCATAGGTTATCTCACATAGGGCT	1424
Db	1242	TGAGAAATTCATTAGTTGGATATAGTCATAGATTAAAGTCACTGTTACNTAACAGGTCTGT	1301
Qy	1425	CATTTCAAATCTAGGTGTCATGTACAGTATATTTCTTGGACGCCGTAGTCAGATCG	1484
Db	1302	ATATAACTAAATAAATACTAGCTTGGCCAAACATTTGTTGGACATCACAGTGTACTGA	1361
Qy	1485	TACAAATACCAATTAGTTTCAGATAGCATAAACAAATACCATTTGTTAAATTCATTCAACCT	1544
Db	1362	TCGAAATATTAATCTATCCGATGTAATTTACAAATACCAATGGTAAATTCATTCTCCCT	1421
Qy	1545	TAATTCAGGTACCTCTCTAGTTCAGTGGCCAGGATTTTACAGGAGGGGATATAATCCGAAC	1604
Db	1422	TACTTCAGGTACCTCTGTAGTCAGAGCCCGAGATTTTACAGGAGGGATATCATCCGAC	1481
Qy	1605	TAACTGTTAAATGGTATGTACTAAGTATGGGTCTTAAATTTTAAATAATACATTCACGCG	1664
Db	1482	TAACTGTTAAATGGTAAATGTACTAAGTATGAGTCTTAAATTTTATGTAATACATTCACGCG	1541
Qy	1665	GTATCGCGTGAGAGTTCGTTATGCTGCTTCTCAAAACAATGGTCTCTGAGGTAACTGTGCG	1724
Db	1542	GTATCGCGTGAGAGTTCGTTATGCTGCTTCTCAAAACAATGGTCTATGAGAGTAATGTGTG	1601
Qy	1725	AGGAGTACTACTTTTTCATCAAGGATTTCCCTAGTACTATGAGTGCAAATGAGTCTTTTGAC	1784
Db	1602	AGGAGTACTACTTTTTCATCAAGGATTTCCCTAGTACTATGAGTGCAAATGGTCTTTTGAC	1661
Qy	1785	ATCTCAATCAATTTAGATTTTCAGAAATTTCCCTGTAGGTATTTAGTGCATCTGGCAGTCAAAC	1844
Db	1662	ATCTCAATCAATTTAGATTTTCAGAAATTTCCCTGTAGGCATTTAGTACATCTGGCAGTCAAAC	1721
Qy	1845	TGCTGGAAATAGTATAAGTATAAATAGAGGTAGACAAACGTTTCACTTTGATATAAATTTGA	1904
Db	1722	TGCTGGAAATAGTATAAGTATAAATAGAGGTAGACAAACGTTTCACTTTAGTAGAATTTGA	1781
Qy	1905	ATTTCATTCCAAATTAATCGAACCCTTCGAGCAGATACGATTTTGAAGGGCGCAAGGCG	1964
Db	1782	ATTTCATCCCAAGTTGATCGAATTTGAAGCAGAAATATGATTTAGAAAGGCACAAAAGGC	1841
Qy	1965	GGTGAATGCTCTGTTTACTAATACGAATCCAAAGAGATTGAAAACAGATGTGACAGATTA	2024
Db	1842	GGTGAATTCGCTGTTTACTTCTTCCATCAATCGAGTTTAAACAGATGTGACGATTA	1901
Qy	2025	TCATATTGATCAAGTATCCAAATTTAGTGGCGTGTTTATTCGGATGGAATTCCTGCTTAGATGA	2084

Db	1902	TCATATTGATCAAGTATCCAAATTTTAGAGANTGTTTATCCGATGAAATTTTGTCTCGATGA	1961
Qy	2085	AAAGAGAGAAATTACTTTGAGAAAGTGAAATATATGCGAAACGACTCAGTGATCAAGAAACATT	2144
Db	1962	AAAGCGAGAAATGTGCGAGAAAGTCAAAATGCGAAGCGACTCAGTGATGAGCGGAATTT	2021
Qy	2145	ACTCCAAGATCCAAACTTTCAATCATCTCAATTAAGCAACCGAGACTTCATATCTACTAATGA	2204
Db	2022	ACTTTCAAGATCCAAACTTTCAAGAGGGATCAATAGGCAACCAGAC-----	2064
Qy	2205	GCAATCGAAATTTACATCTATTCATCAATCTGAACAATCTGAACATGATGCTGGGGAAGTGAGAA	2264
Db	2065	-----CGTGGCTGGAGAGGAATGACGA	2087
Qy	2265	CATTACAATCCAGGAAGGAATGACGTATTTAAAGAGAATTTACGTCACTACCGGGGAC	2324
Db	2088	TATTTACCATCCAAGGAGGAGTACGCTATTCAAAGAGAAATTAAGTCACTACCAAGGTAC	2147
Qy	2325	TTTTTAATGAGTGTATCCGACGTATTTATATCAAATAATAGGAGAGTCCGAATTTAAAGC	2388
Db	2148	CTTTTGATGAGTGTATCCCAACGTATTTTGATCAAAATAATAGATGAGTCGAAATTTAAAGC	2207
Qy	2385	TTATACTCGCTCCCAATTAAGAGGGTATATTGAAGATAGTCAAGATTTAGAGATATATTT	2444
Db	2208	CTATAACCGTTTCAATTTAAGAGGGTATATCGAAGATAGTCAAGACTTAGAATCTATTT	2267
Qy	2445	GATTCGTTTAAATGCGAAACATCAAAACATTTGGAATGTTCCAGGTACCGAGTCCGTATGGCC	2504
Db	2268	AAATTCGCTACAATGCAAAACACGAAACAGTAAATGTACCAGGTACGGGTTCCTATGGCC	2327
Qy	2505	GCCTTCAGTTGAAAGCCCAATCCGAAGGTGCGGAGAACCGAATPCGATGCGCACCAATTT	2564
Db	2328	GCCTTCAGTCCAAAGTCCAAATTCGAAGGTGTGAGAAACCGAATCCGGTGTGTGCCACACCT	2387
Qy	2565	TGAATGGAATCCTGATCTAGATTGTTTCCTGCGAGAGATGGAGAAATAATGTGCCATCATTC	2624
Db	2388	TGAATGGAATCCTGATTTAGATTGTTTCCTGCGAGACGGGGAAAAATGTGCATCATTTTC	2447
Qy	2625	CCATCATTTCTCTTTGGATATTGATATTGGATGCACAGACTTGCATGAGAAATCTAGGCGT	2684
Db	2448	CCATCATTTCTCTTTGGACATTTGATGTTGGATGCCACAGACTTGCAGAGGATCTAGGCGT	2507
Qy	2685	GTGGGTGGTATTCAAGATTAAAGACGCAAGAGGTCAATGCAAGACTAGGGAATCTGGAATTT	2744
Db	2508	GTGGGTGTGATTCAAGATTAAAGACGCAAGAGGTATTGCAAGATTAGGAAATCTGGAATTT	2567
Qy	2745	TATTTGAAGAAACCAATTTATTAGGAGACCACTGCTCGTGTCAAGAGAGCAGAGAAATA	2804
Db	2568	TATCGAAGAAACCAATTAATTGGAGAGCACTGCTCTGTGTGAAGAGAGCGGAAAAAA	2627
Qy	2805	ATGGAGAGACAAACGTGAAAACTACAATTTGAAAAACAAACAGAGTATATACAGAGGCAAA	2864
Db	2628	ATGGAGAGACAAACGGGAAAACTACAAATTTGNAACAAACGAGTATATACAGAGGCAAA	2687
Qy	2865	AGAAGCTGTGGATGCTTTTATTGTAGATTCTCAATATAATAGATTACAAGCGGATACAAA	2924
Db	2688	AGAAGCTGTGGATGCTTTTATTCGTAGATTCTCAATATGATAGATTACAAGCAGATACAAA	2747
Qy	2925	CATTGGCATGATTCATGCGGCAGATAAACTTGTTCATCGAAATTCGAGAGGCTTATCTGTC	2984
Db	2748	CATTGGTATGATTTCATGCGCGAGATAGACTTGTTCATCAGNTCCAGAGGCTTATCTCTCC	2807
Qy	2985	AGAATTATCTGTTATCCCGGGTGAATGCGGAAATTTTTTGAAGAAATTAGAAGGTCCGAT	3044
Db	2808	AGAACTTACCTTTTCATTTCCAGGAATAAATGTGGTGATTTTTTGAAGAAATTAGAAAAA	2867
Qy	3045	TATCACTGCAATCTCCCTATACGATCGGAGAAATGTGCTTAAAAATGGTGATTTTTTAATAA	3104
Db	2868	TTCTACTGCAATTATCCCTATATGATCGGAGAAATGTCAATTAATAATGGCGATTTCAATAA	2927
Qy	3105	TGGAATTAGCATGCTGGAATGTAAAGGGCATGTAGAT---GTACAACAGAGCCATCACCG	3161
Db	2928	TGGCTTATCATGCTGGAACTGTGAAGGGATGTAGATGTAGTAGAAACAAACACACCG	2987

Db	843	 TTTCGAGGATTTGAAAATTCAGCTATTAGAAGTCCCATCTTATGATTTCTTAAATAA	902
Qy	1005	ACTTACAAATTTTAGCACTTTCATCACGATGGAGTGCTACTAGGCATATGACTTACTCGGC	1064
Db	903	TATAATTTATTGACACTGATTTA-----ATTAGAGCGGTTCACTATTGGC	947
Qy	1065	GGGGCACACAATTCOAATCTCGGCCAATAGGAGGCGGATTAATACTCAAGCATGGGTC	1124
Db	948	GGGGCATCGTGTAACTTCTCATTTTACCGGTAGTTCGCAAGTGATAAGCTCCCTCAATA	1007
Qy	1125	TACCAATACTTCTATTAACTCTGTAAAGATTATCATTTCTTCTCTCGAGAGCTATATTGGAC	1184
Db	1008	CGGGATAACTGCAAAACGAGAACCGAGTCGAACCTATTGCTCTTAGCACTTTTCCAGGTCT	1067
Qy	1185	TGAATCATATGCGAGGAGTCTTCTATGGGGAATTTACTCTTGAACCTATTCAATGCTGTCCC	1244
Db	1068	TAATCTATTTTATAGAACATCATACGACCCTTCTTCCGAAGATCCGATTAATTATGTC	1127
Qy	1245	TACTGTTAGATTTAAATTTTATAGGAACCTCAGAAATACTTTTGAAAGAGGTACTGCTAACTA	1304
Db	1128	AACATTAGGAATAAATGTAGTGCAGGGGTAGGATTCATTCAACCAATAATGCTGAAGT	1187
Qy	1305	TAGTCAACCCCTATGAGTCACTCGGGCTTCAATTAAAGATTTCAGAACTGAAATTACACC	1364
Db	1188	TCTATATAGAAGGAGAGAAACAGTAGAATCTCTTGATGAGTTGCCAATTGA-----CGG	1241
Qy	1365	AGAAACAACAGAACGACCAAAATTATGAATCATATAGTCATAGGTTATCTCACATAGGGCT	1424
Db	1242	TGAGAATTCATTAGTTGGATATAGTCATAGNTAAAGTCACGTTACATTAACCAAGTCGTT	1301
Qy	1425	CATTTCAAATCTAGGGTGCATGPAACAGTATATTTCTTGGACGCCGCTAGTCAGATCG	1484
Db	1302	ATATAACTAAATATAACTAGCTAGCTGGCCAAACATTTGTTTGGACACATCACAGTGTACTGA	1361
Qy	1485	TACAAATACCAATTAGTTTCAGATAGCATAAACAAATACCAATTGGTAAATTCATTCAACCT	1544
Db	1362	TCGAAATATAATCTATCCGATGTAAATTACACAAATACCAATGGTAAATTCATTCTCCCT	1421
Qy	1545	TAATTCAGGTACCTCTGTAGTCAGTGCCACAGGATTTTACAGGAGGGGATATAATCCGAAC	1604
Db	1422	TACTTCAGGTACCTCTGTAGTCAGAGCCACAGGATTTTACAGGAGGGGATATCATCCGAC	1481
Qy	1605	TACGTTTAAATGGTAGTGTACTTAAGTATGGGTCTTAAATTTTAAATAATACATTTACAGCG	1664
Db	1482	TAAAGTTAAATGGTAAATCTACTAAGTATGAGTCTTAAATTTTAGTAAATACATTTACAGCG	1541
Qy	1665	GTATCGCGTGAGAGTTTCGTTATGCTCTTCTCAAAACAATGGTCTGAGGGTAACTGTGCG	1724
Db	1542	GTATCGCGTGAGAGTTTCGTTATGCTGTTCTCTCAAAACAATGGTCTATGAGAGTAAATGTGG	1601
Qy	1725	AGGAGTACTACTTTTTCATCAAGGATTTCCCTAGTACTATCGAGTGCAATAGTCTTTTGAC	1784
Db	1602	AGGAGTACTACTTTTTCATCAAGGATTTCCCTAGTACTATCGAGTGCAATAGGTTCTTGAC	1661
Qy	1785	ATCTCAATCATTTAGATTTTCAGAAATTTCCCTGTAGGTATTAGTGCATCTGGCAGTCAAAC	1844
Db	1662	ATCTCAATCATTTAGATTTTCAGAAATTTCCCTGTAGGCATTAGTACATCTGGCAGTCAAAC	1721
Qy	1845	TGCTGGAAATAGGTATAAGTATAATAGCGGTAGACAAACGTTTTCATCTTTGATTAATAATGA	1904
Db	1722	TGCTGGAAATAGTATAAGTATAATATCAGGTAGACAAACGTTTTCATCTTAGTAGAATTTGA	1781
Qy	1905	ATTTCATTTCCAAATTACTCAACCTTCGAAGCAGAAATACGATTTAGAAAGGCGCAAGGC	1964
Db	1782	ATTTCATTTCCCAAGTTGATGCACATTTGAAGCAGAAATATGATTTAGAAAGACAAAGGC	1841
Qy	1965	GGTGAATTCCTCTGTTTACTAATACGAATCCAAAGAAAGTTGAAACAGATGTGACAGATTA	2024
Db	1842	GGTGAATTCGCTGTTTACTTCTTCCANTCAAATCGAGTTAAAAACAGATGTGACGATTA	1901
Qy	2025	TCAATTATGATCAAGTATCCAAATTTAGTGGCGGTGTTTATCGGATGAAATTCCTGCTTAGATGA	2084

Db	1902	TCATATTGATCAAGTATCCAAATTTAGTAGATTGTTTATCCGATGAATTTTGTCTCGATGA	1961
Qy	2085	AAAGAGAGAATTACTTCAGAAAGTGAAATATGCGAAACGACTCAGTGATGAAAGAACTT	2144
Db	1962	AAAGCGAGAAATGTCCGAGGAAAGTCAAACATGCGAAGCACTCAGTGATGAGCGGAATTT	2021
Qy	2145	ACTCCAAGATCCAAACTTCACATCCATCAATAAGCAACACAGACTTCATATCTACTAATGA	2204
Db	2022	ACTTCAAGATCCAAACTTCAGAGGGATCAATAGCCAAACAGAC-----	2064
Qy	2205	GCAATCGAATTTACATCTATCCATGNAACATCTGAACATGATGCTGGGAGTGCAGAA	2264
Db	2065	-----CGTGGCTGAGAGGAAGTACGGA	2087
Qy	2265	CAATTACAATCCAGGAAGGAAATGACGTATTTAAAGAGAAATTACGTCACTACCGGGGAC	2324
Db	2088	TATTAACCATCCAGGAGGAGATGACGTATTCAAAGAGAAATTAGTCTCACATACCAGGTAC	2147
Qy	2325	TTTTAATGAGTGTATCCCGACGTATTTATATCAAAAAAATAGGAGAGTTCGGAAATTAAAAAGC	2384
Db	2148	CTTTTGATGAGTCTATCCAAACGTATTTGTTATCAAAAAAATAGATGAGTCGAAATTTAAAAAGC	2207
Qy	2385	TTTACTCGCTCCCAATTAAGAGGGTATATTGAAGATAGTCAAGATTTTAGAGATATATTT	2444
Db	2208	CTATAACCGGTTTCAATTTAAGAGGGTATATCGAAGATAGTCAAGACTTAGAAATCTATTT	2267
Qy	2445	GATTCGGTTATAATGCGAAACATCAAAACATTTGGATGTTCCAGGTACCCAGTCCCGTATGGCC	2504
Db	2268	AAATCGCTACAATGCAAAACACGAAACAGTAAATGTACCAGGTACGGGTTCTTATATGGCC	2327
Qy	2505	GCTTTTCAGTTGAAGGCCAATCGGAAGGTGCGAGAAACCGAATTCGATGCGCACCACATTT	2564
Db	2328	GCTTTTCAGTCGAAAGTCCAATTCGGAAGGTGCGAGAAACCGAATCCGGTGTGCGCACACCT	2387
Qy	2565	TGAATGGAATCCTGATCTAGATTTGTTCTGCAGAGATGGAAGAAATGTGCGCATCATTTTC	2624
Db	2388	TGAATGGAATCCTGATTTAGATTTGTTCTGCAGAGACGGGGAAAAATGTGCACATCATTTTC	2447
Qy	2625	CCATCATTTCTCTTTGGATATTGATATTGATGCAACAGACTTGTCATGAGAATCTAGGCGT	2684
Db	2448	CCATCATTTCTCTTTGGACNTTGAATGTTGGATGCAACAGACTTGCAGAGAGATCTAGGCGT	2507
Qy	2685	GTGGTGGTATTCAAGATTAAAGACGAGGAAGGTCAATCAAGACTTAGGAAATCTGGAAATTT	2744
Db	2508	GTGGTGGTATTCAAGATTAAAGACGAGGAAGGTATTCAAGATTAGGAAATCTGGAAATTT	2567
Qy	2745	TATTTGAAGAGAAACCAATTATTAGGAGAGCACTGCTCTCGTGTGAAGAGACGAGAGAAAA	2804
Db	2568	TATTCGAAGAGAAACCAATTAATTGGGAAGCACTGCTCTCGTGTGAAGAGACGAGAGAAAA	2627
Qy	2805	ATGAGAGACAAACGTGAAAACTCAATTTGGAACAAACACAGTATATACAGAGGCAAA	2864
Db	2628	ATGAGAGACAAACGGGAAAAACTACANTTGGNAACAAACGNGTATATACAGAGGCAAA	2687
Qy	2865	AGAAGCTGTGGATGCTTTATTTGTAGATTTCTCAATATAATAGATTACAAGCGGATACAAA	2924
Db	2688	AGAAGCTGTGGATGCTTTATTTCTAGATTTCTCAATATGATAGATTACAAGCAGATACAAA	2747
Qy	2925	CATTTGGCATGATTCATGCGGCAGATAAACTTGTTTCATCGAATTCGAGAGGCTTATCTGTC	2984
Db	2748	CATTTGGTATGATTCATGCGGCAGATAGACTTGTTTCATCAGATCCACAGGCTTATCTCTCC	2807
Qy	2985	AGAAATATCTGTTATCCCGGCTGTAATGCGGAAATTTTTGAAGAAATTAGAAGTCCGCAT	3044
Db	2808	AGAACTACCTTTTCATTTCCAGGAATAAATGTGTGTGATTTTTGAAGAAATTAGAAAAACGATAT	2867
Qy	3045	TATCACTGCAATCTCCCTATACGATCCGAGAAATGTCGTTAAAAAATGGTGAATTTTAATAAA	3104
Db	2868	TTCTCTACTGCAATTCCTCTATATGATCCGAGAAATGTCTTAAAAATGGCGATTTTCAATAA	2927
Qy	3105	TGAATTAGCATGCTGGAATGTAAAAAGGGCATGTAGAT----GTACAACAGAGCCATCACCG	3161
Db	2928	TGGCTTATCATGCTGGAACGTGAAAGGCACTGTAGATGTAGTAGAAACAAACACACACCG	2987


```

QY 3162 TTCTGTCCTTCTTATCCAGAAATGGGAAGCAGAAAGTGTCACAAAGCAGTTCCGCTGCTGCC 3221
DB 2988 TTCCGTCCTTCTTATCCCGGAATGGGAAGCAGAAAGTGTCACAAACAAATTCGTGCTGCTGCC 3047
QY 3222 GGGCGTGGCTATATCTCTCCGTGTCACAGCTGACAAAGAGGATATGGAGAGGTTGTTGTT 3281
DB 3048 GGGCGTGGCTATATCTCTCCGTGTCACAGCTGACAAAGAGGATATGGAGAGGTTGTTGTT 3107
QY 3282 AACGATCCATCAATCCGAGACAAATACAGACGAACTAAATTTAAACCTGTGAGGAGA 3341
DB 3108 AACGATCCATCAATCCGAGACAAATACAGACGAACTAAATTTAAACCTGTGAGGAGA 3167
QY 3342 GGAAGTGTATCCAAACGAGATACAGAACTGTAATGATTTATCTGCACACCAAGGTACAGC 3401
DB 3168 GGAAGTGTATCCAAACGAGATACAGAACTGTAATGATTTATCTGCACACCAAGGTACAGC 3227
QY 3402 AG-----TATGTAATCCCGTAATGCTGGATATGAGGATGATATGAAGTTGA 3449
DB 3228 AGGATCCACAGATTCATGTAATCCCGTAATGCTGGATATGAGGATGATATGAAGTTGA 3287
QY 3450 TACTACAGCATCTGTAATTAACAACCGACTTATGAAGAGAAACGATATACAGATGTACG 3509
DB 3288 TACTACAGCATCTGTAATTAACAACCGACTTATGAAGAGAAACGATATACAGATGTACG 3347
QY 3510 AAGAGATAATCATCTGTAATGACAGAGGCTATGTAATTTATCCACACTTACCAGCTGG 3569
DB 3348 AGGAGATAATCATCTGTAATGACAGAGGCTATGTAATTTATCCACACTTACCAGCTGG 3407
QY 3570 TTATATGACAAAGAAATAGAAATCTTCCAGAAACCGATTAAGTATGATGATGATGG 3629
DB 3408 TTATGTCACAAAGAAATAGAGTACTTCCAGAAACCGATTAAGTATGATGATGATGG 3467
QY 3630 AGAAACGGAAGGAAGTTATTTAGACAGCGTGGAAATTAATCTCTTATGAGGAA 3684
DB 3468 AGAAACGGAAGGAAGTTATTTAGACAGCGTGGAAATTAATCTCTTATGAGGAA 3522

RESULT 13
US-08-962-190-1
; Sequence 1, Application US/08962190
; Patent No. 5985267
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel M.
; APPLICANT: Sick, August J.
; TITLE OF INVENTION: No. 5985267el Bacillus thuringiensis Isolates
; TITLE OF INVENTION: Active Against Lepidopteran Pests
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/962.190
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/291.368
; FILING DATE:
; APPLICATION NUMBER: 07/597.607
; FILING DATE: 15-OCT-90
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA50.C1

```

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904)375-8100
; TELEFAX: (904)372-5800
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3522 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: aizawai
; INDIVIDUAL ISOLATE: PS81A2
; IMMEDIATE SOURCE:
; LIBRARY: LambdaGem - 11 (tm) Library of August Sick
; CLONE: 81A2
; US-08-962-190-1

Query Match 48.6%; Score 1793.4; DB 2; Length 3522;
Best Local Similarity 71.9%; Pred. No. 0;
Matches 2497; Conservative 0; Mismatches 861; Indels 117; Gaps 7;

QY 228 ACAATAGCTAGTATTTTATAGTATTTCTTGTGGTGAATATGCGCCCGCGCAGAGATCA 287
DB 147 ACTAGGGGATTTTATAGTATTTCTTGTGGTGAATATGCGCCCGCGCAGAGATCA 206
QY 288 GTGGGAAATTTTCTAGAACATGTCGAAACAACTTATAAATCAACAATACAGAAATGC 347
DB 207 ATGGGATATATTTTATAGCAAAATTCAGCTATTTGATCGGCAAAAGATAGAGGAATTCG 266
QY 348 TAGGATACCGCACTTCTCGATTTACAGGTTTAGAGGATTCCTTTAGAGCCTATCAACA 407
DB 267 TAGGAATCAGGCAATTTCTAGATTTACAGGGCTTAAGCAATCTTTACCGAATTTACACAA 326
QY 408 GTCACCTTGAAGATTTGGCTAGAAAACCGTGATGATGCAAGAACGAGAGAGTGTCTTTATAC 467
DB 327 TGCTTTTAAAACTGGGAAGTAGATCTCTACTAATCCAGCATTTAAGAGAGAGATCGGTAT 386
QY 468 CCAATATATAGCCCTTAGAACCTGATTTCTTAAATGCGATCGCGCTTTTCGCAATAGAAA 527
DB 387 TCAATTTAATGACATGAACAGCTGCTCTTACACAGCTATTTCTCTTTTTCAGTTCGAAG 446
QY 528 CCAAGAGTTCCATTTAATATGATGATGATGCTCAAGCTGCAAAATTTACACCTATTTATT 587
DB 447 TTATGAATTCCTTTTATCAGTATATGTTCAAGCTGCAAAATTTACATTTATTCGGTTTT 506
QY 588 GAGAGATGCTCTCTTTTGGTAGTGAATTTGGGCTTTACATCGCAGGAAATTCACCGTTA 647
DB 507 GAGAGATGTTTCAGTGTTCGACAAACGTTGGGATTTGATGTAGCAACAATCAATAGTCG 566
QY 648 TTATGAGGCCAAGTGAACAAACGAGAGATTTTCGACTATTCGTAAGATGGGTATTA 707
DB 567 TTATATGATTTAACTAGGCTTTATGCGCAATATCTGATTTATGCTGCTAGCTGGTTATA 626
QY 708 TACAGGCTTAAATAGCTTTGAGAGGCAAAATCCG---CAAGTTGGGTGGTGTATATCA 764
DB 627 TAGGGGTTAAATCGTTTACCAAGTATGAGGGGTACGAGGATGGCAAGATTTAATAG 686
QY 765 ATTCCGTAGAGATCTAACGTTAGGGGTATTTAGATCTAGTGGCACTATTTCCCAAGCTATGA 824
DB 687 GTTTAGAAAGAGAGTTAACAATATCAGTATTTAGATATTTATTTCTTTTTCAAAATTAACA 746
QY 825 CACTCGCACTTATCCAAATAAATACGAGTGTCTAGTTAAACAGGGAGTTTATACAGACGC 884
DB 747 TTCTAGATTTATCCAAATTCGCAATCTATCAATTAACCGCGGAAGATATATACAGATCC 806
QY 885 AATTGGAGCAACAGGGGTAATATGCAAGTATGGAATTTGGTATATAATAATAATGACACCTTC 944
DB 807 -----GGTAATTAATAACTGATTTATAGATTACCCCAAG 842

```


QY 945 GTTTTCGCTATAGAGACTCGGTTATCCGAAGCCCGCATCTACTTCTGATTTTCTAGAAC 1004
DB 843 TTTTCGAGATTTGAAATTCAGCTATTAGAGTCCCCATCTTATGATTTCTTAAATA 902
QY 1005 ACTTACAAATTTTACGACTTTCATCAGCATGGAGTCTACTAGGCATATGACTTACTGGCG 1064
DB 903 TATAATTTATTGACACTGATTTA-----ATTAGAGCGGTTCACATTATGGCG 947
QY 1065 GGGGCACACAAATTCATCTGGCCCAATAGAGGGCGGATTAATACCTCAAGCATGGGTC 1124
DB 948 GGGGCATCGTGTAACTTCTCATTTTACCGGTAGTTCGCAAGTGATAAGCTCCCCCTCAATA 1007
QY 1125 TACCAATACTTCTAATTAATCTCTGAAGATTATCATCTCTCTCGAGACGTATATTCGAC 1184
DB 1008 CGGATTAATCGCAACCGAGAACCGAGTTCGAACATATTGCTCTTAGCACTTTTCCAGGTCT 1067
QY 1185 TGAATCATATGCGAGGAGTCTTCTATGGGAAATTTACCTTTGAACCTATTTCATGTGTCCC 1244
DB 1068 TAATCTATTTATAGACACTATCAGACCCTTCTCTCGAAGATCCGATATATATATGCC 1127
QY 1245 TACTGTTAGATTTTAATTTTAGGAACCTCAGAAATPACTTTTGAAGAGGTACTGCTAACTA 1304
DB 1128 AACATTAGGAATAAATCTAGTGCAGGGGGTAGGATTCAATCAACCAAAATAATGGTGAAGT 1187
QY 1305 TAGTCAACCTATAGAGTCACTGGGCTTCAATTAAGAGATTCAGAACTGAATTAACACC 1364
DB 1188 TCTATATAGAAGGAGAGGAACAGTAGATTCTTTGATGAGTTGCCAATTGA-----CGG 1241
QY 1365 AGAAACAACAGACGACAAATTAATGAATCATATAGTATAGTATCTCACATAGGGCT 1424
DB 1242 TGAGAATTCATTTAGTGGATATAGTCAATAGATTAAGTTCAGCTTACATTAACAGGTCTT 1301
QY 1425 CATTTCAATCTAGGTTGATGATGACAGTATATTTCTTGGACGCCCGTATGCGAGATCG 1484
DB 1302 ATATAATTAATAATACTAGTTGCCAACAATTTGTTTGGACACATCACAGTGTCTACTGA 1361
QY 1485 TACAAATACCATTTAGTTAGATGACATTAACAATAACCATTTGTAATAATCAATTCACCT 1544
DB 1362 TCGAAATATAATCTATCCGATGTAATTAACAATAACCATTTGTAATAATCAATTCCTCC 1421
QY 1545 TAATTAGGTACCTCTGTAGTTCAGTGGCCAGAGTTTACAGGAGGGGATATAATCCGAAC 1604
DB 1422 TACTTCAGGTACCTCTGTAGTTCAGAGCCGAGGATTTACAGGAGGGGATATCATCCGAC 1481
QY 1605 TAACGTTTAATGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1664
DB 1482 TAACGTTTAATGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1541
QY 1665 GTATCGCGTGAGAGTTCGTTATGCTGCTTCTCAACAAATGCTGCTGAGGTAATCTGTCGG 1724
DB 1542 GTATCGCGTGAGAGTTCGTTATGCTGCTTCTCAACAAATGCTGCTGAGAGTAAATGTTGG 1601
QY 1725 AGGAGTACTACTTTTTCATCAAGGATTTCCCTAGTACTATGATGATGATGATGATGATGATG 1784
DB 1602 AGGAGTACTACTTTTTCATCAAGGATTTCCCTAGTACTATGATGATGATGATGATGATGATG 1661
QY 1785 ATCTCAATCAATTTAGATTTCAGAAATTTCTGTAGGTAATGATGATGATGATGATGATGATG 1844
DB 1662 ATCTCAATCAATTTAGATTTCAGAAATTTCTGTAGGTAATGATGATGATGATGATGATGATG 1721
QY 1845 TGCTGGAATAAGTATAAGTATAATAGCAGGTAGACAAACGTTTTCATTTGATATAAATTTGA 1904
DB 1722 TGCTGGAATAAGTATAAGTATAATAGCAGGTAGACAAACGTTTTCATTTAGATAGAAATTTGA 1781
QY 1905 ATTCATTTCCAAATTTACTGCAACCTTCGAAGCAGATAGATTTAGAAAGGGCGGAGAGGC 1964
DB 1782 ATTTATCCCAAGTTGATGCAACATTTGAAGCAGAAATATGATTTAGAAAGAGCACAAGAGGC 1841
QY 1965 GGTGAATGCTCTGTTTACTAATAGCAATCCAAAGAGATTTGAACACAGATGTGACAGATTA 2024
DB 1842 GGTGAATGCTCTGTTTACTTCTCCATCAATCAATCGAGTTAAACACAGATGTGACGATTA 1901
QY 2025 TCATATTGATCAAGTATCCAAATTTAGTGGCGGTGTTTATCGGATGAAATTTCTGCTTAGATGA 2084

DB 1902 TCATATTGATCAAGTATCCAAATTTAGTAGATTGTTTATCCGATGAATTTGTCTGGATGA 1961
QY 2085 AAAGAGAGAATTTACTTTGAGAAAGTGAATAATGCGAAACGACTCAGTGATGAAAGAACTTT 2144
DB 1962 AAAGCGAGAATTTGTCGAGAAAGTCAAAATGCGAAGCGACTCAGTGATGAGCGGAATTT 2021
QY 2145 ACTTCAAGATCCAACTTTCACATCCATCAATAGCAACCGAGACTTCATATCTACTAATGA 2204
DB 2022 ACTTCAAGATCCAACTTTCAGAGGATCAATAGGCAACCGAG----- 2064
QY 2205 GCAATCGAATTTTCACATCTATCCATGAACAATCTGAACATGGATGGTGGGGAAGTGAGAA 2264
DB 2065 -----CGTGGCTGGAGAGGAGTACGGA 2087
QY 2265 CATTTCAATCCAGGAAGAAATGACGTATTTAAAGAGAAATTTACGTCACTACCTACCGGGAC 2324
DB 2088 TATTACCATCCAGGAGGAGATGACGTATTTCAAAGAGAAATTAACGTCACTACCGAGTAC 2147
QY 2325 TTTTATGAGTGTATCCGAGCGTATTTATATCAAAAATAGGAGAGTCGGAATTTAAAGC 2384
DB 2148 CTTTGTAGTGTCTATCCAACTGTTTGTATCAAAAATAGTGAAGTTCGAAATTTAAAGC 2207
QY 2385 TTATACTCGCTACCAATTAAGAGGGTATATTGAAGATAGTCAAGATTTAGAGATATATTT 2444
DB 2208 CTATAACCGTTTCAATTTAAGAGGGTATATCGAAGATAGTCAAGACTTAGAAATCTATTT 2267
QY 2445 GATTCGTTTAAATGCGAAACATGAAACATTTGGATGTTTCCAGGTACCGAGTCCGATGGCC 2504
DB 2268 AATTCGCTCAATGCAAAACACGAAACAGATAATGTACAGGTACCGGTCTCTTTATGGCC 2327
QY 2505 GCTTTCAGTTGAAAGCCCAATCCGAGAGTCCGAGAGAACCGAATCGATGCGCACACATTT 2564
DB 2328 GCTTTCAGTCCAAAGTCCAAATTCGAGAGTGTGAGAGAACCGAATCGGTGTGTGCCACACCT 2387
QY 2565 TGAATGAATCTCTGATCTAGATTTCTCTCGAGAGATGAGAAATAATGTGCGCATCATTC 2624
DB 2388 TGAATGAATCTCTGATTTAGATTTCTCTCGAGAGCGGGAATAATGTGCAATCATTC 2447
QY 2625 CCATCATTTCTCTTTGGATTTGATATTGGATGACACAGCTTGATGAGAAATCTAGGCGT 2684
DB 2448 CCATCATTTCTCTTTGGACATTTGATTTGGATGACACAGCTTGCAAGAGGATCTAGGCGT 2507
QY 2685 GTGGTGGTATTCAGATTAAGACCGAGAGAGGTGATGCAAGACTAGGAAATCTGGAATTT 2744
DB 2508 GTGGTGGTATTCAGATTAAGACCGAGAGAGGTGATGCAAGACTAGGAAATCTGGAATTT 2567
QY 2745 TATTGAAGAGAAACCATTTATTAGGAGAGCACTGCTCTGTTGAGAGAGCAGAGAGAGAAA 2804
DB 2568 TATCGAAGAGAAACCATTTATTGGAGAGCACTGCTCTGTTGAGAGAGCGGAAAGAAA 2627
QY 2805 ATGGAGAGACAAACGCTGAAATACTCAATTTGGAAACAAACCGAGTATATACAGAGGCAAA 2864
DB 2628 ATGGAGAGACAAACGCGGAAATACTCAATTTGGAAACAAACCGAGTATATACAGAGGCAAA 2687
QY 2865 AGAAGTGTGGATGCTTTTATTGTAGATTTCTCAATATAATAGATTAACAGCGGATACAAA 2924
DB 2688 AGAAGTGTGGATGCTTTTATTGTAGATTTCTCAATATAATAGATTAACAGCGAGATACAAA 2747
QY 2925 CATTTGGCATGATTCATGCGGCAGATAAATGTTGTTTCATCGAATTCGAGAGGCTTATCTGTC 2984
DB 2748 CATTTGGTATGATTCATGCGGCAGATAGACTGTTGTTTCATCGATCCAGGCGCTTATCTTCC 2807
QY 2985 AGAATTTATCTGTTATCCCGGTGTAAATGCGGAAATTTTGAAGAAATTAGAAGTCCGAT 3044
DB 2808 AGAATTTATCTGTTATCCAGGAAATAATGTTGTTGATTTTGAAGAAATTAGAAGTCCGAT 2867
QY 3045 TATCACTGCAATCTCCCTATACGATGCGAGAAATGTCGTTTAAATAATCGTGTATTTAATAA 3104
DB 2868 TTCTACTGCAATTTCCCTATATGATGCGAGAAATGTCATTTAAATAATGCGGATTTCAATAA 2927
QY 3105 TGAATTTAGCATGCTGGAAATGTAAAGGGCATGTAGAT---GTACAAACAGAGGCGATCCCG 3161

```

Db 2928 TGGCTTATCATGCTGGAAACGCTGAAGGCGCATGTAGATGTAGTAGACAAACACCCCG 2987
Qy 3162 TTCTGCTCTCTGTATCCAGAAATGGGAAGCAGAGAGTGTCAACAGCAGTTCCGCTCTGTCC 3221
Db 2988 TTCCGCTCTGTGTCTCCGGAATGGGAAGCAGAGAGTGTCAACAAATTCGTGTCTGTCC 3047
Qy 3222 GGGCGGTGGCTATATCTCTCCGTGTACAGCGGTACAAAGAGGGATATGGAGAGGGTGTGT 3281
Db 3048 GGGCGGTGGCTATATCTCTCCGTGTACAGCGGTACAAAGAGGGATATGGAGAGGGTGTGT 3107
Qy 3282 AACGATCCATGAATTCGAGAACATACAGAGCACTAAATTTAAACCTGTGAAGAAGA 3341
Db 3108 AACCATCCATGAGATCGAGAACATACAGAGCACTAAATTTAAACCTGTGAAGAAGA 3167
Qy 3342 GGAAGTGTATCCACGGATACAGAACTGTGAATGATTATCTCCACCAAGGTACAGC 3401
Db 3168 GGAAGTGTATCCACGGATACAGAACTGTGAATGATTATCTCCACCAAGGTACAGC 3227
Qy 3402 AG-----TATGTAATTCCTGTAATGCTGGATATGAGGATGCATATGAAGTTGA 3449
Db 3228 AGGATCCACAGATTCATGTAATTCCTGTAATGCTGGATATGAGGATGCATATGAAGTGA 3287
Qy 3450 TACTACAGCATCTCTTAATTAACACCGACTTATGAAGAGAAACGTTATACAGATGTACG 3509
Db 3288 TACTACAGCATCTCTTAATTAACACCGACTTATGAAGAGAAAGGTATACAGATGTACA 3347
Qy 3510 AAGAGATAATCATTTGTAATGATACAGAGGTTATGTAATTTATCCACCACTACCACTGG 3569
Db 3348 AGGAGATAATCATTTGTAATGATACAGAGGTTATGTAATTTATCCACCACTACCACTGG 3407
Qy 3570 TTATATGACAAAAGAAATAGAAATCTTCCAGAAACCGATAAGGTATGGAATGAGATGG 3629
Db 3408 TTATGTGACAAAAGAAATAGAGTACTTCCAGAAACCGATAAGGTATGGAATGAGATGG 3467
Qy 3630 AGAACCGAGGAGGAGTTATTTAGACAGCGTGAATTTACTCTTATGAGGAA 3684
Db 3468 AGAACCGAGGAGGAGTTATTTAGACAGCGTGAATTTACTCTTATGAGGAA 3522

```

```

RESULT 14
PCT-US95-10310-1
; Sequence 1, Application PC/TUS9510310
; GENERAL INFORMATION:
; APPLICANT: MYCOGEN CORPORATION
; APPLICANT: STREET ADDRESS: 5501 Oberlin Drive
; APPLICANT: CITY: San Diego
; APPLICANT: STATE/PROVINCE: California
; APPLICANT: COUNTRY: US
; APPLICANT: POSTAL CODE/ZIP: 92121
; APPLICANT: PHONE NUMBER: (619) 453-8030
; APPLICANT: FAX NUMBER: (619) 453-6991
; TITLE OF INVENTION: Protein Toxins Active Against Lepidopteran Pests
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/10310
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/597,607
; FILING DATE: 15-OCT-90
; CLASSIFICATION:

```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA50.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904)375-8100
; TELEFAX: (904)372-5800
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3522 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: aizawai
; INDIVIDUAL ISOLATE: P881A2
; IMMEDIATE SOURCE:
; LIBRARY: Lambdaagem - 11 (tm) Library of August Sick
; CLONE: 81A2
; PCT-US95-10310-1

Query Match 48.6%; Score 1793.4; DB 5; Length 3522;
Best Local Similarity 71.9%; Pred. No. 0;
Matches 2497; Conservative 0; Mismatches 861; Indels 117; Gaps 7;

Qy 228 ACAAATAGCTAGTGTATTTTATAGTGTCTTTTGTGGTAATATGCCCCCGCGCAGAGATCA 287
Db 147 ACTAGGGGATTTTATATCTTGGCTTGTGTGATTAATATGGGGGCTATAGTCTCTTCACA 206
Qy 288 GTGGGAAATTTCTAGAACATGTCGAACAACTTATAAATCAACAATAACAGAAATGC 347
Db 207 ATGGGATATATTTTATAGGCAATTTAGCTATTTGATCGGCCAAGAAATAGGAATTCG 266
Qy 348 TAGGAATACGGCACTTGTCTCGATTACAAGGTTTAGGAGATTCTCTTTAGAGCCCTATCAACA 407
Db 267 TAGGAATACGGCAATTTCTAGATTACAAGGGCTAAGCAATCTTTACCGAATTTACACAAA 326
Qy 408 GTCACTTGAAGATTTGGCTAGAAAACCGTATGATGCAAGAACGAGAGAGTGTCTTTATATAC 467
Db 327 TGCCTTTTAAAACTGGGAGTAGATCCTACTAATCCAGCAATTAAGAGAGAGATGCGTAT 386
Qy 468 CCAATATATAGCTTAGAACTTCTGATTTCTTAATGCGATCGCGCTTTTCGCAATTAGAAA 527
Db 387 TCAATTTAATGACATGAACAGTGTCTTTACAACAGCTATTTCTCTTTTTCAGTTCAAGG 446
Qy 528 CCAAGAGTTTCCATTTATTAATGGTATATGCTCAAGCTGCAAAATTTACACCTATTTATT 587
Db 447 TTATGAAATTTCTCTTTTATCAGTATATGTTCAAGCTGCAAAATTTACATTTATCGGTTT 506
Qy 588 GAGAGATGCTCTCTTTTGGTAGTAATTTGGGCTTACATCGCAGGAAATTCACAGTTA 647
Db 507 GAGAGATGTTTCACTGTTTGGCAACCGTTGGGATTTGATGTAGCAACAATTAATAGTCG 566
Qy 648 TTATGAGCGCAAGTGGAAACAAACGAGAGATTATTCGACTATTTGCTAGCAATGTTATAA 707
Db 567 TTATATGATTTAATAGGCTTATTGGCGAATATCTGATTTGCTGCTGTTGGTATAA 625
Qy 708 TACAGGTCTAAATAGCTTTAGAGGGGCAAAATCGCG---CAAGTTGGGTGGTTATATATCA 764
Db 627 TACGGGGTTAAATCGTTTACCACTAATGAAGGGGTACGAGGATGGCAAGATTTAATAG 686
Qy 765 ATTCCGTAGAGATCTAACGTTAGGGGTATTAGATCTAGTGGCACTATTTCCCAAGCTATGA 824
Db 687 GTTTAGAAGAGAGGTAAACAATATCAGTATTAGATATTTTCTTTTTCAAAATATACGA 746
Qy 825 CACTCGCACTTATCCCAATTAATACGAGTGTCTCAGTTAAACAGGGAAGTATTATACAGACGC 884
Db 747 TTCTAGATTATATCCCAATTCGCAATCTATCAATTAACGGGGAGTATATACAGATCC 806

```

QY 885 AATTGGAGCAACAGGGTAATATGCGAAGTATGAATTGGTATTAATAATATGCACCTTC 944
Db 807 -----GGTAAATTAATAACTGATTATAGATTACCCCAAG 842
QY 945 GTTTTCGCTATAGAGACTGGGTTATCCGAAGCCCGCATCTACTTGATTTTCTAGAAC 1004
Db 843 TTTTCGAGAGTATCGAAATTCAGCTATTAGAGTCCCCATCTTATGGAATTTCTTAATA 902
QY 1005 ACTTACAAATTTTACGACTTCATCAGCATGAGTGCTACTAGGCATATGACTTACTGGCG 1064
Db 903 TATAAATTATTGACACTGATTTA-----ATTAGAGCGGTTCACTATTGGGC 947
QY 1065 GGGGCACACAATTCAACTCCGCCAATAGGAGCGGATTAATACTCAAGCGATGGTC 1124
Db 948 GGGGCATCGTGAATCTCTCAATTTTACCGGTAGTTCCGAAGTATAGCTCCCTCAATA 1007
QY 1125 TACCAATACTTCTAATTAATCTGTAAGATTAATCTTCTCTCGAGACGTATATTGGAC 1184
Db 1008 CGGATTAACGCAACGAGACCGAGTCGAACTATTGCTCCTAGCACTTTTCCAGGTCT 1067
QY 1185 TGAATCATATGACAGAGTGCTTCTATGGGGAATTTAGCTTGAACCTATTCAATGGTGCCC 1244
Db 1068 TAATCTATTTTATAGAACACATATCAGACCCCTTCTTCGGAAGATCCGATTAATAATTATGCC 1127
QY 1245 TACTGTTAGATTAATTTTAGAACCCCTCAGAATACTTTTGAAGAGGACTGCTAATA 1304
Db 1128 AACATTAGGAATAATAGTAGTGCAGGGGGTAGGAATTCATTCAACCAATAATGTGGAAGT 1187
QY 1305 TAGTCAACCCCTATGAGTCACCTGGCTTCAATTAAGAGATTCAGAACTGAATTAACCACC 1364
Db 1188 TCTATATAGAGGAGAGAACAGTAGAATCTCTTGATGAGTTGCCAATTGA-----CGG 1241
QY 1365 AGAAACAACAGAACGCCAAATTAATGATCATATAGTCATAGGTTATCTCAATAGGGCT 1424
Db 1242 TGAGAAATTCATTAGTTGGATATAGTCATAGATTAAGTCAAGTACATTAACCAAGTCTGT 1301
QY 1425 CATTTCAAACTAGGTGCGATGTACCGATATTTCTTGGAGCGACCGTAGTGAGATCG 1484
Db 1302 ATATAAATACTAATAAATACTAGTTGCCAACAAATTTGTTTGGACACATCACAGTGTACTGA 1361
QY 1485 TACAAATACCAATAGTTAGTACATACATAACAAATACCAATGTTGTAATAATCAATCAACCT 1544
Db 1362 TCGAAATATAATCTATCCGATGTAAATTACACAAATACCAATGTTGTAATAATCAATCTCCCT 1421
QY 1545 TAATTCAGGTACCTCTGTAGTCAGTGGCCAGGATTTTACAGAGGGGATATAATCCGAAC 1604
Db 1422 TACTTCAGGTACCTCTGTAGTCAGAGCCAGGATTTTACAGAGGGGATATCATCCGAC 1481
QY 1605 TAACGTTAATGGTAGTGTACTAAGTATGGGTCTTAATTTTAAATAATACATCATACAGCG 1664
Db 1482 TAACGTTAATGGTAAATGTACTAAGTATGAGTCTTAAATTTTAAATAATACATCATACAGCG 1541
QY 1665 GTATCGCGTGAGAGTCTGTTATGCTGCTTCAACCAATGGTCTGAGGGTAACTGTCGG 1724
Db 1542 GTATCGCGTGAGAGTCTGTTATGCTGCTTCAACCAATGGTCTGAGAGTAAATGTTGG 1601
QY 1725 AGGAGTACTACTTTTGTATCAAGGATTCCTGTAGTACTATGAGTGCAAAATGAGTCTTTGAC 1784
Db 1602 AGGAGTACTACTTTTGTATCAAGGATTCCTGTAGTACTATGAGTGCAAAATGGTCTTTGAC 1661
QY 1785 ATCTCAATCATTTAGATTTGAGAAATTTCTGTAGGTATGATGATGATGATGATGATGATGAT 1844
Db 1662 ATCTCAATCATTTAGATTTGAGAAATTTCTGTAGGCAATTTAGTACATCTGGCAGTCAAA 1721
QY 1845 TGCTGGATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAG 1904
Db 1722 TGCTGGAAATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAG 1781
QY 1905 ATTCATTTCCAAATTAATCTCGAAGCAAGTATAGTATAGTATAGTATAGTATAGTATAGTATAG 1964
Db 1782 ATTTATCCAGTTCATGCAATTTTGAAGCAAGTATAGTATAGTATAGTATAGTATAGTATAG 1841
QY 1965 GGTGAATGCTCTGTTTACTAATACGAATCCAAAGAGATTGAAACAGATGTGACAGATTA 2024

Db 1842 GGTGAATTCGCTGTTTACTTCTTCCAATCAAATCGAGTTAAAAACAGATGTGACGGATTA 1901
QY 2025 TCATATTGATCAAGTATCCAAATTTAGTGGCGTGTTTATCGGATGAATTTCTCTTAGATGA 2084
Db 1902 TCATATTGATCAAGTATCCAAATTTAGTATAGTATGTTTATCCGATGAATTTCTCTGATGA 1961
QY 2085 AAAGAGAGATTTACTTTCGAGAAAGTGAATATGCGAAACGACTCAGTGTATGAAGAACTT 2144
Db 1962 AAAGCGAGAAATTTGTCGAGAAAGTCAACCATGCGAAGCGACTCAGTGTATGAGCGGAATTT 2021
QY 2145 ACTCCAGATCCAAACTTTCATCATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 2204
Db 2022 ACTTCAAGATCCAAACTTTCAGAGGATCAATAGGCAACAGAC----- 2064
QY 2205 GCAATCGAATTTTCAATCTATCCATGAACAATCTGAAACATCTGAAACATCTGAAACATCTGAA 2264
Db 2065 -----CGTGGCTGGAGAGGAGTACGGA 2087
QY 2265 CATTAACAATCCAGAGAAATGACGTATTTAAAGAGAAATTAACGTACACTACCGGGAC 2324
Db 2088 TATTACCATCCAGAGGAGATGACGTATTTCAAAAGAGAAATTTACGTACACTTACCGAGTAC 2147
QY 2325 TTTTAAATGAGTGTATCCGACGTATTTATATCAAAAATAGGAGAGTGGAAATTTAAAGC 2384
Db 2148 CTTTGTAGTGTCTATCCACGTATTTGTATCAAAAATAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 2207
QY 2385 TTATACTCGCTTACCAATTAAGAGGGTATATTGAAGATAGTCAAGATTTAGAGATATATTT 2444
Db 2208 CTATACCGTTCACCAATTAAGAGGGTATATCGAAGATAGTCAAGACTTGAAGATCTATTT 2267
QY 2445 GATTTCGTTAATAATGCGAAACATGAAACATTTGGATGTTTCCAGGTACCGAGTCCGTATGGCC 2504
Db 2268 AATTTCGCTCAATGCAAAACACGAAACAGTAAATGTACCAAGTACGGGTCTCTTATGGCC 2327
QY 2505 GCTTTCAAGTTGAAGCCCAATCGGAGGTCGGAGAACCGAATCGATCGACACACATTT 2564
Db 2328 GCTTTCAAGTCCAAATTTGGAAGTGTGGAGAACCGAATCGGTGTGTGTGTCACACCT 2387
QY 2565 TGAATGAAATCTCTGATCTAGATTTCTCTCGAGAGATGGAGAAATTTGTGGCATCATTT 2624
Db 2388 TGAATGAAATCTCTGATTTAGATTTCTCTCGAGAGACGGGAAATTTGTGCACATCATTT 2447
QY 2625 CCATCATTTCTTTTGGATATGATTTGATGACACAGCTTGCATGAGAAATCTAGGCGT 2684
Db 2448 CCATCATTTCTCTTGGACATTTGATTTGGATGACACAGCTTGCAGAGGATCTAGGCGT 2507
QY 2685 GTGGTGTATTTCAAGATTAAGACGAGGAGGTTCATGCAAGACTAGGATCTGGAAAT 2744
Db 2508 GTGGTGTATTTCAAGATTAAGACGAGGAGGTTCATGCAAGATTTGGAAATCTGGAAAT 2567
QY 2745 TATTGAAGAGAAACCATTTATTAGGAGAACACTGCTCTGTTGAAAGAGAGAGAGAGAGAGAGAG 2804
Db 2568 TATCGAAGAGAAACCATTTATTGGAGAACACTGCTCTGTTGAAAGAGAGAGAGAGAGAGAGAG 2627
QY 2805 ATGAGAGACAAACGCGTGAATAACTTCAATTTGGAAACAAACGAGTATATACAGAGGCAAA 2864
Db 2628 ATGAGAGACAAACGCGTGAATAACTTCAATTTGGAAACAAACGAGTATATACAGAGGCAAA 2687
QY 2865 AGAAGCTGTGATGCTTTTATTTGTAGATTTCTCAATATAATAGATTTACAGCGGATACAAA 2924
Db 2688 AGAAGCTGTGATGCTTTTATTTGTAGATTTCTCAATATAATAGATTTACAGCGGATACAAA 2747
QY 2925 CATTTGGCATGATTCATCGGCAGATAAATTTGTTTCATCGAATTCGAGAGGCTTATCTGTCT 2984
Db 2748 CATTTGGTATGATTCATCGGCAGATAGACTTGTTCATCAGATCCAGAGGCTTATCTTCC 2807
QY 2985 AGAATTTATCTGTTATCCCGGTTGTAATGCGGAAATTTTGAAGAAATTTAGAGGTCGAT 3044
Db 2808 AGAATTTATCTGTTTTCATTTCCAGGAATAATGTTGGTGTATTTTGAAGAAATTTAGAAACCGTAT 2867
QY 3045 TATCAGTGTCAATCTCTCCCTATACGATGCGAGAAATGTGCTTTAAAAATCGTGTATTTTATATA 3104

Db 1302 ATATACTAATAATACTAGCTGCCAACATTTGTTGGACACATCACAGTGTCTACTGA 1361
Qy
1485 TACAAATACCAATTAGTTTCAGATAGCATAPACACAAATACCAATGTTGTAATAATCATTTCAACCT 1544
Db
1362 TCGAAATATAATCTATCCGATGTAAATACACAAATACCAATGTTGTAATAATCATTTCCCT 1421
Qy
1545 TAATTCAGGTACCTCTAGTTCAGTGGCCAGAGATTTACAGGGGGATATAATCCGAAC 1604
Db
1422 TACTTCAGGTACCTCTAGTTCAGAGGCCAGAGATTTACAGGGGGATATCATCCGAAC 1481
Qy
1605 TAACTTAATAGGTAGTCTACTAAGTATGGGTCTTAAATTTAAATAATACATCATTTACAGCG 1664
Db
1482 TAAGTTAATGGTAATGCTACTAAGTATGAGTCTTAAATTTAGTAATACATCATTTACAGCG 1541
Qy
1665 GTATCGCGTGAGAGTTCTGTATGCTCTCTCAACCAATGGTCTGAGGGTAATCTGCGG 1724
Db
1542 GTATCGCGTGAGAGTTCTGTATGCTCTCTCAACCAATGGTCTATGAGAGTAAATGTTGG 1601
Qy
1725 AGGAGTACTACTTTTTCATCAAGATTTCCCTAGTACTATGAGTGCATATGAGTGCATATGAGTGC 1784
Db
1602 AGGAGTACTACTTTTTCATCAAGATTTCCCTAGTACTATGAGTGCATATGAGTGCATATGAGTGC 1661
Qy
1785 ATCTCAATCATTTAGATTTGAGATTTGAGATTTCCCTAGTACTATGAGTGCATATGAGTGCATATGAGTGC 1844
Db
1662 ATCTCAATCATTTAGATTTGAGATTTGAGATTTCCCTAGTACTATGAGTGCATATGAGTGCATATGAGTGC 1721
Qy
1845 TGCTGGAATAAGTATAAGTATAATAGTACAGGTAGACAAACGTTTCACATTTGATATAAATTTGA 1904
Db
1722 TGCTGGAATAAGTATAAGTATAATAGTACAGGTAGACAAACGTTTCACATTTAGATATAAATTTGA 1781
Qy
1905 ATTCAATTCGAATTTACTGGAACCTTCGAAGCGAATAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAG 1964
Db
1782 ATTATCCAGTTGATGCAACATTTGAAGCAGAAATATGATTTAGAAAGGCGGCAAGAGGC 1841
Qy
1965 GGTGAATGCTGTTTACTAATACGAATCCGAAGAATTTGAACAGATGTGACAGATTA 2024
Db
1842 GGTGAATGCTGTTTACTTCTTCAATCAATCGAGTTTAAACAGATGTGACAGATTA 1901
Qy
2025 TCATATTGATCAAGTATCCAAATTTAGTGGGTGTTTATCGGATGAATTTCTGCTTAGATGA 2084
Db
1902 TCATATTGATCAAGTATCCAAATTTAGTGGGTGTTTATCGGATGAATTTCTGCTTAGATGA 1961
Qy
2085 AAAGAGAAATTTACTTGAGAAAGTGAATATGCGAAACGACTCAGTGCATGAAGAACTT 2144
Db
1962 AAAGCGAGAAATTTGTCGAGAAAGTCAACCAATGCGAAGCGACTCAGTGCATGAGCGGAAATTT 2021
Qy
2145 ACTCCAAGATCCAACTTTCAATCCATCAATTAAGCAACAGACTTCATATCTACTAATGA 2204
Db
2022 ACTTCAAGATCCAACTTTGAGGGATCAATGAGCAACAGAC----- 2064
Qy
2205 GCAATCGAATTTTCATCTATCCATGAACAACTCTGAACATGGATGGTGGGGAAGTGAGAA 2264
Db
2065 -----CGTGGCTGGAGAGGAAGTACGGA 2087
Qy
2265 CATTACAATCCAGGAAGAAATGACGTATTTAAAGAGAAATTTAGTCACTACCTACCGGGGAC 2324
Db
2088 TATTACCATCCAGGAGGAGATGACGTATTTCAAAGAGAAATTTACGTCACACTACCGAGTAC 2147
Qy
2325 TTTTAAATGAGTGTATCCGAGTATTTATATCAAAAATAGGAGAGTCGGAATTTAAAGC 2384
Db
2148 CTTTGTAGTGTCTATCAACGTATTTGTATCAAAAATAGTATGAGTCGGAATTTAAAGC 2207
Qy
2385 TTATACTCGCTTACCAATTAAGAGGGTATATTGAAGATAGTCAAGATTTAGAGATATATTT 2444
Db
2208 CTATAAACGTTTACCAATTTAGAGGGTATATCGAAGATAGTCAAGACTTAGAATCTATTT 2267
Qy
2445 GATTCTGTTAATGCGAAACATGAAACATTTGGATGTTCCAGGTACCGAGTCCGATGCGC 2504
Db
2268 AATTCTGCTACAAATGCGAAACACAGTAAATGTACCAAGGTACCGGTTCTTTATGCGC 2327
Qy
2505 GCTTTTCAGTTCAAGCCCAATTCGAAGGTGCGGAGAACCGAATCGATGCGCACCACTTT 2564
Db
2328 GCTTTTCAGTCCAAATTTGGAAGGTGTGGAGAACCGAATCGGTGTGTGTCACACCT 2387

Qy 2565 TGAATGGAATCTGTAGTCTAGATTTGTTCTCCAGAGATGGAGAAAATGTGGCATCTTC 2624
Db 2388 TGAATGGAATCTGTAGTCTAGATTTGTTCTCCAGAGATGGAGAAAATGTGGCATCTTC 2447
Qy 2625 CCATCATTTCTCTTTGGATATTGATATTGATGTCACAGACTTTGTCATGAGAAATCTTAGCGT 2684
Db 2448 CCATCATTTCTCTTTGGACATTTGATTTGATGTCACAGACTTTGTCAGAGGATCTTAGCGT 2507
Qy 2685 GTGGGTGGTATTCAAGATTAAAGACGCGAGGAAGTCTATGCAAGACTAGGGAAATCTGGAATT 2744
Db 2508 GTGGGTGGTATTCAAGATTAAAGACGCGAGGAAGTCTATGCAAGATTAGGAAATCTGGAATT 2567
Qy 2745 TATTGAAGAGAAACCATTTATTAGGAGAACACTGTCTCGTGTGAGAGAGCAGAGAAA 2804
Db 2568 TATCGAAGAGAAACCATTTATTGGAGAAGCACTGTCTCGTGTGAGAGAGCAGGAAAAA 2627
Qy 2805 ATGAGAGACAAACGTCGAAAACTTACAATTTGAAAAAAGAGTATATACAGAGGCAAA 2864
Db 2628 ATGAGAGACAAACGCGGAAAACTCAATTTGAAAAAAGAGTATATACAGAGGCAAA 2687
Qy 2865 AGAAGCTGTGGATGCTTTTATTGTAGATTCTCAATATAATAGATTACAAGCGGATACAAA 2924
Db 2688 AGAAGCTGTGGATGCTTTTATTGTAGATTCTCAATATAATAGATTACAAGCAGATACAAA 2747
Qy 2925 CATTGGCATGATTCACTCGGCAGATAAATTTGTTTCATCGAATTCGAGAGGCTTATCTGTC 2984
Db 2748 CATTGGTATGATTCACTCGGCAGATAGACTTTGTTTCATCGATCCACGAGGCTTATCTTCC 2807
Qy 2985 AGAATATCTGTTATCCCGGTGTAAATCGGAAAAATTTTGAAGAAATTAGAAGTTCGCAT 3044
Db 2808 AGAATACCTTTTCATTTCCAGGAATAAATGTTGGTGAATTTTGAAGAAATTAGAAGTTCGCAT 2867
Qy 3045 TATCACTGCAATCTCCCTATACGATCGGAAATGTCGTTAAAAATGGTGAATTTAATAA 3104
Db 2868 TTCTACTGCAATCTCCCTATATGATCGGAAATGTCATTTAAAAATGCGATTTCAATAA 2927
Qy 3105 TGAATTAGCATGCTGGAAATGTAAGGGCATGTAGAT---GTACACAGAGCCATCACCG 3161
Db 2928 TGGCTTATCATGCTGGAACTGTAAGGGCATGTAGATGTAGTAGAACAAACCAACCG 2987
Qy 3162 TTCTGCTCTGTTATCCCAATGGGAAGCAGAAAGTGTCAACAGCAGTTCGCGTCTGTCC 3221
Db 2988 TTGCTCTCTGTTGTCGCGAATGGGAAGCAGAAAGTGTCAACAAATTTGTTGCTGTCC 3047
Qy 3222 GGGCGGTGGCTATATCTCTCGTGTCAAGCGGTACAAAGAGGATATGAGAGGGTGTGT 3281
Db 3048 GGGCGGTGGCTATATCTCTCGTGTACAGCGTACAAAGAGGATATGAGAGGGTGTGT 3107
Qy 3282 AAGATCCATGAAATCGAGAAACAAATACAGAGCAACTAAAAATTTAAAACTGTGAAGA 3341
Db 3108 AACCATCCATGAGATCGAGAAACAAATACAGAGCAACTAAAAATTTAAAACTGTGAAGA 3167
Qy 3342 GGAAGTGTATCCCAACGGATACAGAACTGTAAATGATTACTGCACACCAAGGTACAGC 3401
Db 3168 GGAAGTGTATCCCAACGGATACAGAACTGTAAATGATTACTGCACACCAAGGTACAGC 3227
Qy 3402 AG-----TATGTAATTTCCCGTAAATGCTGGATATGAGGATGCATATGAAGTTGA 3449
Db 3228 AGGATCCACAGATTCATGTAATTTCCCGTAAATATATCAGATATGAGGATGCATATGAAGTGA 3287
Qy 3450 TACTACAGCATCTGTTAAATTAACAAACCGACTTATGAAGAGAAACGATATACAGATGTACG 3509
Db 3288 TACTACAGCATCTGTTAAATTAACAAACCGACTTATGAAGAGAAACGATATACAGATGTAC 3347
Qy 3510 AAGAGTAATCATTTGTAATATGACAGGGTATGTAATTTATCCACACTTACCAGCTGG 3569
Db 3348 AGGAGTAATCATTTGTAATATGACAGCGTATGTAATTTATCGACAGTACCAGCTGG 3407
Qy 3570 TTATATCAAAAAGAAATTAGAATACTTTCCAGAAAAACCGAATGATGGAATTTGAGATTTGG 3629
Db 3408 TTATGTCAGAAAGAAATTAGAGTACTTTCCAGAAACCGAATAAGGTATGGAATTTGAGATTCG 3467

Qy 3630 AGAAACGGAGGGAAGTTTATTGTAGACGCGTGGAATTACTCTTATCGAGGAA 3684
|||||
|||||
Dd 3468 AGAAACGGAGGGAAGTTTATTGTAGACAATGTCGAATTACTCTTATCGAGGAA 3522
|||||
|||||

Search completed: April 21, 2005, 03:37:49
Job time : 635 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 20, 2005, 19:48:34 ; Search time 1933 Seconds
(without alignments)
11571.632 Million cell updates/sec

Title: US-10-614-524-1
Perfect score: 3687
Sequence: 1 ttgactcaaataggaaaa.....tactcttattggagggaatag 3687

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5622541 seqs, 3033355566 residues

Total number of hits satisfying chosen parameters: 11245082

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3687	100.0	3687	17 US-10-614-524-1	Sequence 1, Appli
2	3666.2	99.4	4173	17 US-10-428-961-37	Sequence 37, Appl
3	3260.2	88.4	3684	17 US-10-428-961-62	Sequence 62, Appl
4	3133.6	85.0	3687	17 US-10-809-953-9	Sequence 9, Appli
5	1581.6	42.9	3558	9 US-09-826-660-22	Sequence 22, Appl
6	1495.6	40.6	3624	10 US-09-988-462-6	Sequence 6, Appli
7	1408.4	38.2	3522	9 US-09-826-660-5	Sequence 5, Appli
8	1408.4	38.2	3522	11 US-09-837-961-7	Sequence 7, Appli
9	1408.4	38.2	3522	18 US-10-825-751-7	Sequence 25, Appl
10	1402	38.0	3534	9 US-09-873-873-25	Sequence 25, Appl
11	1402	38.0	3534	10 US-09-916-956A-25	Sequence 25, Appl

12	1402	38.0	3534	10 US-09-997-914-25	Sequence 25, Appl
13	1402	38.0	3534	16 US-10-365-645-25	Sequence 25, Appl
14	1402	38.0	3534	17 US-10-672-163-25	Sequence 25, Appl
15	1402	38.0	3534	18 US-10-739-482-25	Sequence 25, Appl
16	1402	38.0	3534	18 US-10-817-182-25	Sequence 25, Appl
17	1400.6	38.0	3531	9 US-09-873-873-9	Sequence 9, Appli
18	1400.6	38.0	3531	9 US-09-873-873-11	Sequence 11, Appl
19	1400.6	38.0	3531	9 US-09-873-873-13	Sequence 13, Appl
20	1400.6	38.0	3531	10 US-09-916-956A-9	Sequence 9, Appli
21	1400.6	38.0	3531	10 US-09-916-956A-11	Sequence 11, Appl
22	1400.6	38.0	3531	10 US-09-916-956A-13	Sequence 13, Appl
23	1400.6	38.0	3531	10 US-09-997-914-9	Sequence 9, Appli
24	1400.6	38.0	3531	10 US-09-997-914-11	Sequence 11, Appl
25	1400.6	38.0	3531	10 US-09-997-914-13	Sequence 13, Appl
26	1400.6	38.0	3531	16 US-10-365-645-9	Sequence 9, Appli
27	1400.6	38.0	3531	16 US-10-365-645-11	Sequence 11, Appl
28	1400.6	38.0	3531	16 US-10-365-645-13	Sequence 13, Appl
29	1400.6	38.0	3531	17 US-10-672-163-9	Sequence 9, Appli
30	1400.6	38.0	3531	17 US-10-672-163-11	Sequence 11, Appl
31	1400.6	38.0	3531	17 US-10-672-163-13	Sequence 13, Appl
32	1400.6	38.0	3531	18 US-10-739-482-9	Sequence 9, Appli
33	1400.6	38.0	3531	18 US-10-739-482-11	Sequence 11, Appl
34	1400.6	38.0	3531	18 US-10-739-482-13	Sequence 13, Appl
35	1400.6	38.0	3531	18 US-10-817-182-9	Sequence 9, Appli
36	1400.6	38.0	3531	18 US-10-817-182-11	Sequence 11, Appl
37	1400.6	38.0	3531	18 US-10-817-182-13	Sequence 13, Appl
38	1392.4	37.8	3534	9 US-09-873-873-27	Sequence 27, Appl
39	1392.4	37.8	3534	10 US-09-916-956A-27	Sequence 27, Appl
40	1392.4	37.8	3534	10 US-09-997-914-27	Sequence 27, Appl
41	1392.4	37.8	3534	16 US-10-365-645-27	Sequence 27, Appl
42	1392.4	37.8	3534	17 US-10-672-163-27	Sequence 27, Appl
43	1392.4	37.8	3534	18 US-10-739-482-27	Sequence 27, Appl
44	1392.4	37.8	3534	18 US-10-817-182-27	Sequence 27, Appl
45	1390	37.7	3567	10 US-09-972-175-58	Sequence 58, Appl

ALIGNMENTS

RESULT 1
US-10-614-524-1
; Sequence 1, Application US/10614524
; Publication No. US20040016020A1
; GENERAL INFORMATION:
; APPLICANT: Arnaut, Greta
; APPLICANT: Boets, Annemie
; APPLICANT: Damme, Nicole
; APPLICANT: Mathieu, Eva
; APPLICANT: Vanneste, Stijn
; APPLICANT: Van Rie, Jeroen
; TITLE OF INVENTION: Insecticidal proteins from Bacillus thuringiensis.
; FILE REFERENCE: NEWBTSUS2
; CURRENT APPLICATION NUMBER: US/10/614,524
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US/09/739,243
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/173387
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 1
; LENGTH: 3687
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3687)
US-10-614-524-1

Query Match 100.0%; Score 3687; DB 17; Length 3687;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGACTTCAATAGAGAAAATGAGATGAATTAATAATGCTTTATCGATTCCAGCTGTA 60
DB 1 TTGACTTCAATAGAGAAAATGAGATGAATTAATAATGCTTTATCGATTCCAGCTGTA 60
QY 61 TCGAATCATTTCCACAAAATGGATCTATCACCGAGATCGTCTGTGAGGATTTCTTTGT 120
DB 61 TCGAATCATTTCCACAAAATGGATCTATCACCGAGATCGTCTGTGAGGATTTCTTTGT 120
QY 121 ATAGCCGAGGGGATATATCAATCCACTTTGTAGCGCATCAACAGTCCAAAACGGGTATT 180
DB 121 ATAGCCGAGGGGATATATCAATCCACTTTGTAGCGCATCAACAGTCCAAAACGGGTATT 180
QY 181 AACATAGCTCGTAGAATACCTAGGTGTATTAGCGGTACCGTTTGCTGACAAAATAGCTAGT 240
DB 181 AACATAGCTCGTAGAATACCTAGGTGTATTAGCGGTACCGTTTGCTGACAAAATAGCTAGT 240
QY 241 TTTTATAGTTTTCTTTGTGTGAATTAATGCCCCCGCGCAGAGATCAGTGGGAAAATTTTC 300
DB 241 TTTTATAGTTTTCTTTGTGTGAATTAATGCCCCCGCGCAGAGATCAGTGGGAAAATTTTC 300
QY 301 CTAGAACATCTCGAACAACTTATTAATCAACAAATACAGAAAATGCTAGGAATACGGCA 360
DB 301 CTAGAACATCTCGAACAACTTATTAATCAACAAATACAGAAAATGCTAGGAATACGGCA 360
QY 361 CTGTCTCGATTACAAGTTTTAGGAGATTCCTTTTAGAGCCTATCAACAGTCACTTGAAGAT 420
DB 361 CTGTCTCGATTACAAGTTTTAGGAGATTCCTTTTAGAGCCTATCAACAGTCACTTGAAGAT 420
QY 421 TGGCTAGAAAACCGTGATGATGCAAGAACGAGAGTGTCTTTTATACCCAAATATATAGCC 480
DB 421 TGGCTAGAAAACCGTGATGATGCAAGAACGAGAGTGTCTTTTATACCCAAATATATAGCC 480
QY 481 TTAGAACTTGATTTCTTAATGCGATGCGCTTTTCGCAATTAGAACCAGAGTTCCA 540
DB 481 TTAGAACTTGATTTCTTAATGCGATGCGCTTTTCGCAATTAGAACCAGAGTTCCA 540
QY 541 TTATTAATGATATGCTCAAGCTGCAAAATTTACACCTATTATTATTAGAGAGTCCCTCT 600
DB 541 TTATTAATGATATGCTCAAGCTGCAAAATTTACACCTATTATTATTAGAGAGTCCCTCT 600
QY 601 CTTTGTGTAGTGAATTTGGGCTTACATCGCAGAAATTCACGTTTATATAGCGCCAA 660
DB 601 CTTTGTGTAGTGAATTTGGGCTTACATCGCAGAAATTCACGTTTATATAGCGCCAA 660
QY 661 GTGGAACAAACGAGAGATTAATTCGACTATTCGGTAGAATGGTATATAACAGGTCTAAAT 720
DB 661 GTGGAACAAACGAGAGATTAATTCGACTATTCGGTAGAATGGTATATAACAGGTCTAAAT 720
QY 721 AGCTTGAGAGGGACAATGCGCAAGTTGGGTGGGTATTAATCAATTCCTGATAGATCTA 780
DB 721 AGCTTGAGAGGGACAATGCGCAAGTTGGGTGGGTATTAATCAATTCCTGATAGATCTA 780
QY 781 ACGTTAGGGGTATAGATCTAGTGGCACTATTCCTCAAGCTATGACACTCGCACTTATCCA 840
DB 781 ACGTTAGGGGTATAGATCTAGTGGCACTATTCCTCAAGCTATGACACTCGCACTTATCCA 840
QY 841 ATAAATACGAGTCTCAGTTTAAACAGGGAAGTTTATACAGACCAATTTGAGGCAACAGGG 900
DB 841 ATAAATACGAGTCTCAGTTTAAACAGGGAAGTTTATACAGACCAATTTGAGGCAACAGGG 900
QY 901 GTAAATATGCAAGTATGAATTTGGTATAATAATCAATCACTTCGTTTTCGGCTATAGAG 960
DB 901 GTAAATATGCAAGTATGAATTTGGTATAATAATCAATCACTTCGTTTTCGGCTATAGAG 960
QY 961 ACTGCGGTATCCGAAGCCGCACTACTAGTTTCTAGAACTTACAACTTAAATTTTATAGC 1020
DB 961 ACTGCGGTATCCGAAGCCGCACTACTAGTTTCTAGAACTTACAACTTAAATTTTATAGC 1020
QY 1021 ACTTCATCAGATGGAGTGTCTAGGCAATGCTTACTGCGGGGCAACAATTTCAA 1080
DB 1021 ACTTCATCAGATGGAGTGTCTAGGCAATGCTTACTGCGGGGCAACAATTTCAA 1080
QY 1081 TCTCGGCCAATAGGAGCGGATTAATACCTCAACGATGGGTCTACCAATACTTCTTATT 1140

DB 1081 TCTCGGCCAATAGGAGCGGATTAATACCTCAACGATGGGTCTACCAATACTTCTTATT 1140
QY 1141 AATCCTGTGAAGATTATCAATCTCTCTCGAGACGTATATTGGACTGAATCATATGACAGGA 1200
DB 1141 AATCCTGTGAAGATTATCAATCTCTCTCGAGACGTATATTGGACTGAATCATATGACAGGA 1200
QY 1201 GTGCTTCTATGGGGAATTTTACCTTTGAAACCTATTATCATGGTGTCCCTACTGTTAGATTAA 1260
DB 1201 GTGCTTCTATGGGGAATTTTACCTTTGAAACCTATTATCATGGTGTCCCTACTGTTAGATTAA 1260
QY 1261 TTTTAGGAACCCCTCAGAAATACTTTTGAAGAGGTACTGCTAACTATATAGTCAACCTATGAG 1320
DB 1261 TTTTAGGAACCCCTCAGAAATACTTTTGAAGAGGTACTGCTAACTATATAGTCAACCTATGAG 1320
QY 1321 TCACCTGGGCTTCAATTTAAAGATTTCAGAACTGAAATTTACACGAGAAAACAACAGAACGA 1380
DB 1321 TCACCTGGGCTTCAATTTAAAGATTTCAGAACTGAAATTTACACGAGAAAACAACAGAACGA 1380
QY 1381 CCAAAATATGAATCATATAGTCAATAGTTCATCATAGGGCTCATTTCCAAATCTTAGG 1440
DB 1381 CCAAAATATGAATCATATAGTCAATAGTTCATCATAGGGCTCATTTCCAAATCTTAGG 1440
QY 1441 GTGCATGTACCACTATATCTTGGAGCGCACCGTAGTGCAGATCGTACAAATACCATTAGT 1500
DB 1441 GTGCATGTACCACTATATCTTGGAGCGCACCGTAGTGCAGATCGTACAAATACCATTAGT 1500
QY 1501 TCAGATAGCATAACAAATACCAATTCGTTGTAATCATTTCAACCTTAATTCAGGTACTCT 1560
DB 1501 TCAGATAGCATAACAAATACCAATTCGTTGTAATCATTTCAACCTTAATTCAGGTACTCT 1560
QY 1561 GTAGTCAGTGGCCAGGATTTACAGGAGGGATATTAATCCGAACCTAACGTTAATGTTAGT 1620
DB 1561 GTAGTCAGTGGCCAGGATTTACAGGAGGGATATTAATCCGAACCTAACGTTAATGTTAGT 1620
QY 1621 GTACTAAGTATGGGTCTTAAATTTTAAATAATACATTTACAGCGGTATCGCGTGAAGATT 1680
DB 1621 GTACTAAGTATGGGTCTTAAATTTTAAATAATACATTTACAGCGGTATCGCGTGAAGATT 1680
QY 1681 CGTTATGCTGCTTCTCAACAAATGGTCTGAGGGTAACTGTGCGAGGGAGTACTACTTTT 1740
DB 1681 CGTTATGCTGCTTCTCAACAAATGGTCTGAGGGTAACTGTGCGAGGGAGTACTACTTTT 1740
QY 1741 GATCAAGGATTCCTCTAGTACTATGATGCAAAATGAGTCTTTGACATCTCAATCATTTAGA 1800
DB 1741 GATCAAGGATTCCTCTAGTACTATGATGCAAAATGAGTCTTTGACATCTCAATCATTTAGA 1800
QY 1801 TTTGCGAAGATTTCTCTGTAGGTATTAGTGCATCTGGCAGTCAAACTGCTGGAATAAGTATA 1860
DB 1801 TTTGCGAAGATTTCTCTGTAGGTATTAGTGCATCTGGCAGTCAAACTGCTGGAATAAGTATA 1860
QY 1861 AGTAATAATGCGGTAGACAAACGTTTCACTTTGATAAATTTGAATTCATTTCCAAATTA 1920
DB 1861 AGTAATAATGCGGTAGACAAACGTTTCACTTTGATAAATTTGAATTCATTTCCAAATTA 1920
QY 1921 GCAACCTTCGAACGAGATACAGATTTAGAAAGGGCGCAAGAGCGGTGAATGCTCTGTTT 1980
DB 1921 GCAACCTTCGAACGAGATACAGATTTAGAAAGGGCGCAAGAGCGGTGAATGCTCTGTTT 1980
QY 1981 ACTAATACGAATCCAAAGAGATTGAAACAGATGTGACAGATTATCATATTTGATCAAGTA 2040
DB 1981 ACTAATACGAATCCAAAGAGATTGAAACAGATGTGACAGATTATCATATTTGATCAAGTA 2040
QY 2041 TCCAAATTTAGTGGGTTTATCGGATGATTTCTGTTAGATGATAAAGAGAGATTACTTT 2100
DB 2041 TCCAAATTTAGTGGGTTTATCGGATGATTTCTGTTAGATGATAAAGAGAGATTACTTT 2100
QY 2101 GAGAAAGTGAATATGCGAAAACGACTCAGTGTGAAAAGAACTTACTCCAAAGATCCAAAC 2160
DB 2101 GAGAAAGTGAATATGCGAAAACGACTCAGTGTGAAAAGAACTTACTCCAAAGATCCAAAC 2160
QY 2161 TTCAATCCATCAATTAAGCAACAGACTTCATATCTAATGAGCAATCGAATTTTCA 2220

[illegible]

Db 301 CTAGAACATGTCGACATCTTATAAGACACACAGTAACAGAAATATACTAGGATACGGCT 360
Qy 361 CTTGCTCGATTACAAAGTTTAGAGATTCTTTAGAGCTTATCAACAGTCACTTTGAAGAT 420
Db 361 CTTGCTCGATTACAAAGTTTAGAGATTCTTTAGAGCTTATCAACAGTCACTTTGAAGAT 420
Qy 421 TGGCTAGAAACCGTGATGATGCAAGAACGAGAGTCTCTTTATACCCATATATAGCC 480
Db 421 TGGCTAGAAACCGTGATGATGCAAGAACGAGAGTCTCTTTATACCCATATATAGCC 480
Qy 481 TTGAAACTTGATTTCTTAATGCGATGCGCTTTTCGCAATTAGAACCAAGAGTTCCA 540
Db 481 TTGAAACTTGATTTCTTAATGCGATGCGCTTTTCGCAATTAGAACCAAGAGTTCCA 540
Qy 541 TTATTAATGATATAGTCAAGCTGCAAAATTTACACCTATATTTATTTAGAGATGCCCTCT 600
Db 541 TTATTAATGATATAGTCAAGCTGCAAAATTTACACCTATATTTATTTAGAGATGCCCTCT 600
Qy 601 CTTTTTGGTAGTGAATTTGGGCTTACATCGCAGAAATTCACGTTATTTATGAGCGCAA 660
Db 601 CTTTTTGGTAGTGAATTTGGGCTTACATCGCAGAAATTCACGTTATTTATGAGCGCAA 660
Qy 661 GTGGAACAAACGAGAGATTTATTCGCACTATTGCGTAGAATGGTATAATACAGGTTAAAT 720
Db 661 GTGGAACAAACGAGAGATTTATTCGCACTATTGCGTAGAATGGTATAATACAGGTTAAAT 720
Qy 721 AGCTTAGAGGGAACAAATGCGCAAGTTGGTGGCTTATTAATCAATTTCCGTAGAGATCTA 780
Db 721 AAATTTAGAGGGAACAAATGCTGAAAGTTGGTGGCTTATTAATCAATTTCCGTAGAGATCTA 780
Qy 781 ACGTTAGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGACACTCGCACTTATCCA 840
Db 781 ACGTTAGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGACACTCGCACTTATCCA 840
Qy 841 ATAAATACGAGTGTCTCAGTTTAAACAGGGAAGTTTATACAGACGCAATTTGGAGCAACAGG 900
Db 841 ATGAATACCAAGTGTCTCAATTTAAACAGGGAAGTTTATACAGATCCAATTTGGAGNACAAT 900
Qy 901 GTAAAT-----ATGGCAAGTATGAATGGTATTAATTAATGAATGACCTTCGTTTCCGCT 954
Db 901 GCACCTTCAGGATTTGCAAGTACGAAATGGTTTAAATAATGAATGACCACTCGTTTCTGCC 960
Qy 955 ATAGAGACTCGGTTATCCGAAGCCCGCATCTACTGATTTCTAGAACAACTTACAAAT 1014
Db 961 ATAGAGCTCGGTTATTAGGCTTCCGCACTCTCTGATTTTCAGAACAGCTTACAAAT 1020
Qy 1015 TTTAGCACTTCATCACGATGAGTGTCTACTAGGCATATGACTTACTGGCGGGGCAACA 1074
Db 1021 TTCAGCGTATTAAGTCGATGGAGTAATCTCAATATATGAATTAATGAGTGGGATAGA 1080
Qy 1075 ATTCOAATCTCGGCAATAGGAGGCGGATTTAAATACCTCAACGATGGGCTCAACAATACT 1134
Db 1081 CTTGAATTCGGCAACAATAAGGGGCTCAATTAAGTACCTGGACACACGCGAAATACCAATACT 1140
Qy 1135 TCATTAAATCTGTAAGATTATCACTCTCTCGAGACGCTATATTGGACTGATCATAT 1194
Db 1141 TCATTAAATCTGTAAGATTATCACTCTCTCGAGACGCTTATAGAACAGATCAAT 1200
Qy 1195 GCAGGAGTGTCTTATGGGAATTTACTTGAACCTATTGATGGTGCCTTACTGTTAGA 1254
Db 1201 GCAGGATAAAT- ----ACTTCAACTACTCTCTGGAATGGAGTACCTTGGGCTAGA 1254
Qy 1255 TTTAAATTTAGGAACCTCAGATACATTTTGAAGAGGTACTGCTAATATAGTCAACCC 1314
Db 1255 TTTAAATTTAGGAATCCCTCGAATCTCTT- --AGAGGTAGCCTTCTCTATCTATAGGG 1311
Qy 1315 TATGAGTCACTCGGCTTCAATTAAGATTTCAGAACTGAATTTACCACAGAAACAACA 1374
Db 1312 TATCTGGAGTGGGACACAACTATTTGATTCAGAACTGAATTTACCACAGAAACAACA 1371
Qy 1375 GAACGACCAATATTAATGAATCATATAGTATAGGTTATCTCACATAGGCTCATTTCCAA 1434

Db 1372 GAACGACCAAAATTAATGAATCTTACAGTCATAGATTATCTAATATAAGACTAATATCAGGA 1431
Qy 1435 TCTAGGGTGCATGTATCCAGTATATTTCTTGACGCGACCGTAGTCAGATCTGTAACAATACC 1494
Db 1432 AACACTTTGAGAGCACCGATATATTTCTTGACGCGACCGTAGTCAGATCTGTAACAATACC 1491
Qy 1495 ATTAGTTTCAGATAGCATAAACACAAATACCAATTCGTAATAATCATTTCAACCTTTAATTCAGGT 1554
Db 1492 ATTAGTTTCAGATAGCATAAACACAAATACCAATTCGTAATAATCATTTCAACCTTTAATTCAGGT 1551
Qy 1555 ACCTCTGTAGTCAAGTGGCCAGGATTTTACAGGAGGGGATATAATTCGAACTAACTGTTAAT 1614
Db 1552 ACCTCTGTAGTCAAGTGGCCAGGATTTTACAGGAGGGGATATAATTCGAACTAACTGTTAAT 1611
Qy 1615 GGTAGTGTAATAAGTATGGGTCTTAATTTTAAATAATACATCATTTACAGCGGTATCGCGTG 1674
Db 1612 GGTAGTGTAATAAGTATGGGTCTTAATTTTAAATAATACATCATTTACAGCGGTATCGCGTG 1671
Qy 1675 AGAGTTTCGTTATCTCTCTCAAAACAAATGCTCTGAGGGTAACTGTTCGAGGGAGTACT 1734
Db 1672 AGAGTTTCGTTATCTCTCTCAAAACAAATGCTCTGAGGGTAACTGTTCGAGGGAGTACT 1731
Qy 1735 ACTTTTGATCAAGGATTTCCCTAGTACTATGAGTGCAAATGAGTCTTTTGACATCTCAATCA 1794
Db 1732 ACTTTTGATCAAGGATTTCCCTAGTACTATGAGTGCAAATGAGTCTTTTGACATCTCAATCA 1791
Qy 1795 TTTAGATTTGCAGAAATTTCTGTAGGTATTTAGTGCATCTGGCAGTCAAACTGCTGNAAT 1854
Db 1792 TTTAGATTTGCAGAAATTTCTGTAGGTATTTAGTGCATCTGGCAGTCAAACTGCTGNAAT 1851
Qy 1855 AGTATAGTAATAATGCAAGTACACAAAGCTTTTCACTTTTGATAAAAATTTGAATTTCAATTTCCA 1914
Db 1852 AGTATAGTAATAATGCAAGTACACAAAGCTTTTCACTTTTGATAAAAATTTGAATTTCAATTTCCA 1911
Qy 1915 ATTTACTGCAACCTTCGAAGCAGAAATAGATTTTGAAGGGCGCAAGAGCGGTGAATGCT 1974
Db 1912 ATTTACTGCAACCTTCGAAGCAGAAATAGATTTTGAAGGGCGCAAGAGCGGTGAATGCT 1971
Qy 1975 CTGTTTACTTAATAGGAATCCAAGAAATTTGAAACAGATGTGACAGATTTATCATATTGAT 2034
Db 1972 CTGTTTACTTAATAGGAATCCAAGAAATTTGAAACAGATGTGACAGATTTATCATATTGAT 2031
Qy 2035 CAAGTATCCAATTTAGTGGCGTCTTTATCGATGAATTTCTGTAGTAAAAAGAGAGAA 2094
Db 2032 GAAGTATCCAATTTAGTGGCGTCTTTATCGATGAATTTCTGTGATGAAAGAGAGAA 2091
Qy 2095 TTTACTTGAGAAAGTGAATAATGCAAAACGACTCAGTGTGATGAAAGAACTTTACTCCAAGAT 2154
Db 2092 TTTACTTGAGAAAGTGAATAATGCAAAACGACTCAGTGTGATGAAAGAACTTTACTCCAAGAT 2151
Qy 2155 CCAAACTTCACATCCATCAATAGCAACCAAGCTTCAATCTACTACTAATGAGCAATCGAAT 2214
Db 2152 CCAAACTTCACATCCATCAATAGCAACCAAGCTTCAATCTACTAATGAGCAATCGAAT 2211
Qy 2215 TTCACATCTATCCATGAAACAACTCTGAAACATGGAATGGTGGGAAAGTGAGAACATTAACAATC 2274
Db 2212 TTCACATCTATCCATGAAACAACTCTGAAACATGGAATGGTGGGAAAGTGAGAACATTAACAATC 2271
Qy 2275 CAGGAAGGAAATGACGTATTTAAAGAAATTAAGTGCACACTACCGGGGACTTTTAATAGAG 2334
Db 2272 CAGGAAGGAAATGACGTATTTAAAGAAATTAAGTGCACACTACCGGGGACTTTTAATAGAG 2331
Qy 2335 TGTATTCGAGCGTATTTATATCAAAAATAGGAGTCCGAAATTAAGCTTATACCTCCG 2394
Db 2332 TGTATTCGAGCGTATTTATATCAAAAATAGGAGGCGGAAATTAAGCTTATACCTCCG 2391
Qy 2395 TACCAATTAAGAGGGTATATTGAAGATAGTCAAGATTTTAGAGATATATTGATTTGGTTAT 2454
Db 2392 TACCAATTAAGTGGCTATTATGAAGATAGTCAAGATTTTAGAGATATATTGATTTGGTTAT 2451
Qy 2455 AATGCGAAACATGAACAACTTTGGATGTTCCAGGTACCGAGTCCGATATGGCGGCTTTCAAGTT 2514
Db 2452 AATGCGAAACATGAACAACTTTGGATGTTCCAGGTACCGAGTCCGATATGGCGGCTTTCAAGTT 2511

```
QY 2515 GAAAGCCCAATCGAAGGTCGGAGAACCGAATCGATCGGACACACATTTTGAATGGAAT 2574
DB 2512 GAAAGCCCAATCGAAGGTCGGAGAACCGAATCGATCGGACACACATTTTGAATGGAAT 2571
QY 2575 CCTGATCTAGATTGTTCTCTCGAGAGATGGAGAAAAATGTGGCATCATTCCTCATCATTTTC 2634
DB 2572 CCTGATCTAGATTGTTCTCTCGAGAGATGGAGAAAAATGTGGCATCATTCCTCATCATTTTC 2631
QY 2635 TCTTTGGATATTGATATTGGATGCACAGACTTGCATCAGAAATCTAGCGGTGTGGTGGA 2694
DB 2632 TCTTTGGATATTGATATTGGATGCATAGACTTGCATCAGAAATCTAGCGGTGTGGTGGA 2691
QY 2695 TTCAGATTAAAGACGAGGAGGTCTCCTGAGACTAGGAACTCTGGAATTTATTGAAGAG 2754
DB 2692 TTCAGATTAAAGACGAGGAGGTCTCCTGAGACTAGGAACTCTGGAATTTATTGAAGAG 2751
QY 2755 AAACCATTTATTAGAGAGACACTGCTCTGTTGAAGAGAGCAGAGAAAAAATGGAGAGAC 2814
DB 2752 AAACCATTTATTAGAGAGACACTGCTCTGTTGAAGAGAGCAGAGAAAAAATGGAGAGAC 2811
QY 2815 AAACGTGAAAAAATCTCAATTTGAAAAAAGAGTATATACAGAGGCAAAAGAGCTGTG 2874
DB 2812 AAACGTGAAAAAATCTCAATTTGAAAAAAGAGTATATACAGAGGCAAAAGAGCTGTG 2871
QY 2875 GATGCTTTATTGTAGATTCTCAATATAATAGATTACAAGGGATACAAACATTTGGCATG 2934
DB 2872 GATGCTTTATTGTAGATTCTCAATATATAGATTACAAGGGATACAAACATTTGGCATG 2931
QY 2935 ATTTCATGCGCAGATAAATCTGTTTCATCGAATTCGAGAGCTTATCTGTCAGAAATATCT 2994
DB 2932 ATTTCATGCGCAGATAAATCTGTTTCATCGAATTCGAGAGCTTATCTTTCAGAAATATCT 2991
QY 2995 GTTATCCCGGTGTAAATGCGGAAATTTTCAAGAAATTAGAAGTCGCATTTACACTGCA 3054
DB 2992 GTTATCCCGGTGTAAATGCGGAAATTTTGAAGAAATTAGAAGTCGCATTTACACTGCA 3051
QY 3055 ATCTCCCTTATACGATGCGAGAAATGTCTGTTAAAAATGGTGATTTTAAATAATGGAATGCA 3114
DB 3052 ATCTCCCTTATACGATGCGAGAAATGTCTGTTAAAAATGGTGATTTTAAATAATGGAATGCA 3111
QY 3115 TGTGGAATCTAAAAGGCGATGATAGATGATACACAGAGCCATCACCGTTCTGCTCTGTT 3174
DB 3112 TGTGGAATCTAAAAGGCGATGATAGATGATACACAGAGCCATCACCGTTCTGCTCTGTT 3171
QY 3175 ATCCAGAAATGGGAAGCAGAGTGTCAAAAGCAGTTCGCGTCTGTCGCGGCGCGTGGCTAT 3234
DB 3172 ATCCAGAAATGGGAAGCAGAGTGTCAAAAGCAGTTCGCGTCTGTCGCGGCGCGTGGCTAT 3231
QY 3235 ATCTCTCGTGTCAAGCGTACAAAGAGGATATGAGAGGGTGTGTAAACGATCCATGAA 3294
DB 3232 ATCTCTCGTGTCAAGCGTACAAAGAGGATATGAGAGGGTGTGTAAACGATCCATGAA 3291
QY 3295 ATCCGAGAAATACAGAGCAACTAAATTTAAAACTGTGAAGAGGAGGATGATATCCA 3354
DB 3292 ATCCGAGAAATACAGAGCAACTAAATTTAAAACTGTGAAGAGGAGGATGATATCCA 3351
QY 3355 ACGGATACAGGAACTGTGATGATTATGATCTGACACCAAGGTACAGAGTATGTAATTC 3414
DB 3352 ACGGATACAGGAACTGTGATGATTATGATCTGACACCAAGGTACAGAGTATGTAATTC 3411
QY 3415 CGTAATCTCGATATGAGATGATATGAAAGTTGATACACTACAGCATCTGTTAAATACAAA 3474
DB 3412 CGTAATCTCGATATGAGATGATATGAAAGTTGATACACTACAGCATCTGTTAAATACAAA 3471
QY 3475 CCGACTTATGAGAGAGAAACGTATACAGATGTACGAGAGATATCATTTGTGATATGAC 3534
DB 3472 CCGACTTATGAGAGAGAAACGTATACAGATGTACGAGAGATATCATTTGTGATATGAC 3531
QY 3535 AGAGGGTATGTGAATTTACCACTACAGCTGTTTATATGACAAAGAAATTAGAATAC 3594
DB 3532 AGAGGGTATGTGAATTTATCCACCGTACAGCTGTTTATATGACAAAGAAATTAGAATAC 3591
```

```
QY 3595 TTCCGAGAAACCGATAGGATGATGATGAGATTGGAGAAACCGAGGAAAGTTTATTGTA 3654
DB 3592 TTCCGAGAAACCGATAGGATGATGATGAGATTGGAGAAACCGAGGAAAGTTTATTGTA 3651
QY 3655 GACAGCGTGAATTTACTCTCTTATGGAGGAATAG 3687
DB 3652 GACAGCGTGAATTTACTCTCTTATGGAGGAATAG 3684

RESULT 4
US-10-809-953-9
; Sequence 9, Application US/10809953
; Publication No. US20040181825A1
; GENERAL INFORMATION:
; APPLICANT: Van Mellaert, Herman
; APPLICANT: Botterman, Johan
; APPLICANT: Van Rie, Jeroen
; APPLICANT: Joos, Henk
; TITLE OF INVENTION: RECOMBINANT PLANT EXPRESSING NON-COMPETITIVELY BINDING Bt INSECTIC
; TITLE OF INVENTION: CRYSTAL PROTEINS
; FILE REFERENCE: 021565-078
; CURRENT APPLICATION NUMBER: US/10/809,953
; PRIOR FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US/09/661,016
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: PCT/EP90/00905
; PRIOR FILING DATE: 1990-05-30
; PRIOR APPLICATION NUMBER: GB 89401499.2
; PRIOR FILING DATE: 1989-05-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 3687
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3687)
US-10-809-953-9

Query Match 85.0%; Score 3133.6; DB 18; Length 3687;
Best Local Similarity 91.1%; Pred. No. 0;
Matches 3373; Conservative 0; Mismatches 299; Indels 30; Gaps 3;

QY 1 TTCACTTCAAAATAGGAAAAATGAGAAATGAAATATAAAATGCTTTATCGATTCCAGCTGTA 60
DB 1 TTCACTTCAAAATAGGAAAAATGAGAAATGAAATATAAAATGCTTTATCGATTCCAGCTGTA 45
QY 61 TCGAATCATTTCCACACAAATGGATCTATCACAGATGCTCGTATTGAGGATCTTTGTTGT 120
DB 46 TCGAATCATTTCCGACAAATGGATCTATTTACAGATGCTCGTATTGAGGATGCTTTGTTGT 105
QY 121 ATAGCGGAGGGGAATATATCAATCCACTTTGTAGCGCATCAACAGTCCAAACGGGTATT 180
DB 106 ATAGCGGAGGGGAACAAATATGATTCCTATTTGTAGCGCATCAACAGTCCAAACGGGTATT 165
QY 181 AACATAGCTGGTGAATATCTAGGTGTTATTAGGCGTACCGTTGCTGACAAATAGTAGT 240
DB 166 AACATAGCTGGTGAATATCTAGGCGTATTGGGCGTACCGTTTCTGCGACAACTAGTAGT 225
QY 241 TTTTATAGTTTCTTGTGTTGTAATTTATGCGCCCGCGGAGAGATCAGTGGGAAATTTTC 300
DB 226 TTTTATAGTTTCTTGTGTTGTAATTTATGCGCCCGCGGAGAGATCAGTGGGAAATTTTC 285
QY 301 CTAGAACATGTCGAAACAACTTATAAAATCAACAAATACAGAAATGCTAGGAATACGGCA 360
DB 286 CTAGAACATGTCGAAACAACTTATAAAATCAACAAATACAGAAATGCTAGGAATACGGCT 345
QY 361 CTTCCTCGATTACAAGGTTTATGAGGATTCCTTTAGAGCTTATCAACAGTCACTTTGAAGAT 420
DB 346 CTTCCTCGATTACAAGGTTTATGAGGATTCCTTCAGAGCTTATCAACAGTCACTTTGAAGAT 405
QY 421 TGGCTAGAAAAACCGTGTGATGATGCAAGAACGAGAGATGTTCTTTTATATCCCAATATATAGCC 480
```


Qy 602 TTTTGTAGTGAATTTGGGCTTACATCGCAGGAAATTCACGTTATATGAGCGCCAAAG 661
 Db 602 TGTTCGGATCTGAGTTCGGATTTACTTCTCAAGAGATTCAAAGATACCTACGAGAGACAAG 661
 Qy 662 TGGAAACACGAGAGATTTTCCGACTATTCGCGTAGAATGGTATAATACAGGTTCTAATA 721
 Db 662 TTGAGAAAGACTAGAGAGTACTCTGACTACTGCGGTAGGTGTAACAACACTGGATTTGAACA 721
 Qy 722 GCTTTGAGAGGACAAATCGCCAAAGTTGGGTGCGTTTAAATCAATTCGCTAGAGATCTAA 781
 Db 722 ACCTTAGAGGAACCTAAACGCTGAGTCTTGGCTTAGATACCAACAGTTCAGAGAGATCTTA 781
 Qy 782 GCTTTAGGGGTATTAAGTCTAGTGGCACTATTCCTCAAGTATGACACTCGGCATTTATCCAA 841
 Db 782 CTCTTGGAGTTCTTGAATCTTGTTCCTTGTTCCTTGTTCCTCATCTTACGATCTAGAGTGTACCCCTA 841
 Qy 842 TAATATGAGTGTCTCAGTTAAACAGGGAAGTTTATACAGCGCAATTTGGAGCACAGGGG 901
 Db 842 TGAACACTTCTGCTCAACTTACTAGAGAGATCTACATCTGATCCAAATCGGAAGAACTAAACG 901
 Qy 902 TA-----AATATGGCAAGTATGAATTTGGTATATAATAATATGACCTTTCGTTTCCGCTA 955
 Db 902 CTCATCTGGATTCGCTTCTACTAACTGGTTCAACACACAGCTTCCATCTTCTCTGCTA 961
 Qy 956 TAGAGACTGGGTTATCCGAAGCCCGCATCTACTTGTATTTCTAGAACAACTTACAAATTT 1015
 Db 962 TCGAGGCTGAGTGTACAGACCAACACATCTTCTTGACTTCCAGAGCAACTTACTATCT 1021
 Qy 1016 TTAGCACTTATACAGATGGAGTGTCTACTAGGCATATGACTTACTTGGCGGGGACACAA 1075
 Db 1022 TCTCTGTCTTCTTAGATGGTCTTAACACTCAGTACATGAACTACTGGGTTGGACATAGAC 1081
 Qy 1076 TTCAATCTCGGCCAATAGGAGGCGGATTAATACTCTCAACGCAATGGTCTACCAATVACTT 1135
 Db 1082 TTGAGTCTAGAACATACAGAGATCTCTTCTACTTCTACTCTAGTAAACACTTAACTT 1141
 Qy 1136 CTATTAATCTGTAAAGTATCAATTTCTCTCGAGACGTATATGAGCTGAACTCAATATG 1195
 Db 1142 CTATCAACCCAGTTACTCTTCAGTTTCACTTCTAGAGATGTGTACAGAACTGAGTCTTTCG 1201
 Qy 1196 CAGAGTGTCTTATGGGGAATTTACCTTGAACCTTATCTAGTGTGCTCTACTTGTAGAT 1255
 Db 1202 CTGGAATCAACAT-----TCTTCTTACTACTCCAGTGAACGAGTTCTCTTGGGCTAGAT 1255
 Qy 1256 TTAATTTTAGGAACCTCTCAGAACTTTTGAAGAGGTACTGCTTAACTATAGTCAACCCCT 1315
 Db 1256 TCAACTGGAGAAACCAATGAACTCTCTT--AGAGGTTCTTGTGTACACCAATTGGAT 1312
 Qy 1316 ATGAGTCACTGGGCTTCAATTTAAAGATTCAGAACTGAAATACCAACAGAAACACAG 1375
 Db 1313 ACACCTGGAGTTGGTACCCAGTTGTTCGATTTCTGAGACTGAGCTTCCACAGAGACTACTG 1372
 Qy 1376 AACGACCAATATGAATCATATAGTATAGTATCTACATAGGCTTATCTACATAGGCTTATTCACAA 1435
 Db 1373 AGAGACCAAACTAGAGTCTTACTCTCATAGACTTCTTAACTTCGTTTATCTCTGGAA 1432
 Qy 1436 CTAGGCTGATGTACCAAGTATATCTTGGAGCGACCGGTAGTGCAGATCGTACAAATACCA 1495
 Db 1433 ACACCTTAGAGCTCCAGTGTACTCTTGGACTCATAGATCTGCTGATAGAACTTAAACCA 1492
 Qy 1496 TTAGTTCAGATAGATTAACAAATACCAATTTGGTAAATCATTCACCTTTAATTCAGGTA 1555
 Db 1493 TCTCTTCTGATTTCTTACTCACTCAGATTCACCTTGTGAAGTCTTCAACTTGAACCTCTGAA 1552
 Qy 1556 CCTCTGAGTACAGTGGCCAGGATTTACAGAGGGGATATAATCCGAACTAAAGTTAATG 1615
 Db 1553 CTTCTGTGTCTTGGACCAAGGATTTACTGGAGAGACATCATCAGAACTTAACTGTAACG 1612
 Qy 1616 GTAGTGTACTAAGTATGGGCTTAAATTTTAAATATATCATCATACAGCGGTATCGCGTGA 1675
 Db 1613 GATCTGTCTTCTTAGGGATTTGAACTTCAACACACTTCTCTTCAAGATACAGAGTTA 1672
 Qy 1676 GAGTTCGTTATGCTGCTTCTCAAAACAATGGTCTGAGGGTAACTGTTCGGAGGAGTACTA 1735

Db 1673 GAGTTAGATACGCTGCTTCTCAAACTATGTTCTTAGAGTTACTGTTGGAGGATCTACTA 1732
 Qy 1736 CTTTTCGATCAAGGATTTCCCTAGTACTATGATGCAATGATGCTTTGACATCTCAATCAT 1795
 Db 1733 CTTTTCGATCAAGGATTTCCCATCTACTATGCTGCTAACGAGTCTCTTACTTCTCAATCTT 1792
 Qy 1796 TTAGATTTGAGAAATTTCTGTAGGTATTAAGTGCATCTGCGAGTCAAACTGCTGGAAATAA 1855
 Db 1793 TCAGATTCGCTGAGTTCCCAAGTTGGAATCTCTGCTTCTGATCTCAAACTGCTGGAATCT 1852
 Qy 1856 GTATAGTAAATAGCAGGTAGACAAAGCTTTCATCTTTGATTAATAATTAAGTATCAATCCAA 1915
 Db 1853 CTATCTCTAAACAAGCTGGAAGACAAACTTTCACACTTCGACAAAGATTTGAGTTCATTTCCAA 1912
 Qy 1916 TTACTGCAACCTTCGAGGACAGAAATACGATTTTGAAGGGCGCAAGGGCGGTGAATGCTC 1975
 Db 1913 TCACTGCTCTCTCGAGGCGAGTCTGACTTTGGAAGAGACAGAGGGCGGTGAATGCTC 1972
 Qy 1976 TGTTTACTAATACGAATCCAAAGAAAGATTGAAAAACAGATGTGACAGATTTATCATATTGATC 2035
 Db 1973 TGTTCATCTCGTCCAAATCAGATTGGGCTCAAGACAGATGTGACTGACTATCACATCGATC 2032
 Qy 2036 AAGTATCCAAATTTAGTGGCGTGTATTTCGATGAAATTCCTCTTAGATGAAAGAGAGAAAT 2095
 Db 2033 GCGTTTCCAACTTGTGTGAGTGCCTCTCTGATGAGTTCTGTTTGGATGAGAGAGAGAGT 2092
 Qy 2096 TACTTCCAGAAAGTAAATATCGGAACGACTGATGATGAAGAACTTACTTCCAGATC 2155
 Db 2093 TGTCCGAGAAAGTCAAAACATGCTTAAGCGATTAGTATGAGCGGAACTTGTCTTCAAGATC 2152
 Qy 2156 CAAACTTTCATCATCCATCAATTAAGCAACAGACTTTCATATCTACTAATGAGCAATCGAAT 2215
 Db 2153 CCAACTTTCGCGGATCAACAGGCACTA----- 2181
 Qy 2216 TCACATCTATCCATGAACAATCTGAAACATGGATGGTGGGGAAGTGAAGACATTTACAAATCC 2275
 Db 2182 -----GATCGTGGATGGAGGGAAGTACGGACATCACCATTC 2218
 Qy 2276 AGGAAGAAATGACGTATTTAAAGAGAATTTACGTACACACTACCGGGGACTTTTAAATGAT 2335
 Db 2219 AAGAGGTGATGATGTTCAGAGAGAACTATGTTACGCTCTTGGGTACCTTTGATGAT 2278
 Qy 2336 GTTATCCGAGTATTTATATCAAAAAATAGGAGGTTCGAAATTTAAAGCTTTATCTCGCT 2395
 Db 2279 GCTATCCAACTACCTGTACCAAGATAGATGAATCGAACTCAAAGCTCACAAAGAT 2338
 Qy 2396 ACCAATTAAGAGGTATTTGAAGATGATCAAGATTTAGAGATATATTTGATTCGTTAT 2455
 Db 2339 ACCAGTTGAGAGGTATCATCGAGGACAGTCAAGACCTTGGAGATCTACCTCATCAGATACA 2398
 Qy 2456 ATCGGAAACATGAACATTTGGATGTTCCAGGTACCGAGTCCGATGCGGCTTTTCAGTTG 2515
 Db 2399 ACCGCAAAATGAGACAGTCAATGTGCTGGAGCGGTTCACCTCGGCCACTTTTACGCC 2458
 Qy 2516 AAAGCCCAATTCGGAAGGTGCGGAGAACCGAATCGATCGGACCAACATTTTGAATGGAATC 2575
 Db 2459 CAACTCCCATCGG----- 2471
 Qy 2576 CTGATCTAGATTTCTCTCGAGAGATGGAGAAATAATGTGGGCAATCAATCCCATCTTCT 2635
 Db 2472 -----CAAGTGTGCCCATCACTCACACCTTCT 2500
 Qy 2636 CTTTGGATATTTGATATTTGGATGCACAGCTTGCATCAGAAATCTAGCGGTGTGGTGGTAT 2695
 Db 2501 CTTTGGACATAGACGTGTGCTGTACCGACTGAAACGAGACCTCGGTGTGGTGGTGTATCT 2560
 Qy 2696 TCAAGATTAAGACGAGGAGGTCTGCAAGACTAGGAAATCTGGAATTTTATTTGAAGAGA 2755
 Db 2561 TCAAGATCAAGACTCAAGATGGCCATGCCAGGCTAGGCAATCTGGAGTTTCTAGAGAGA 2620
 Qy 2756 AACCATTTTAGGAGAGCACTGTCTGCTGTGAGAGAGCAGAGAAAAAATGAGAGAGACA 2815


```

Db 2621 AACCACTTGTGGAGAGCCCTCGCTAGAGTGAGAGGGCTGAGAGAGAGTGGAGGACA 2680
Qy 2816 AACGTGAAACATCAATTTGAAACAAACGAGTATATACAGAGGCAAAAGAGCTGTGG 2875
Db 2681 AGAGAGAGAGTGGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2740
Qy 2876 ATGCTTTATTTAGATCTCAATATATATAGATTACAGGGGATACAAAATTTGGCATGA 2935
Db 2741 ACGCTCTGTTTGTGAAGTCTCAGTATGATAGGCTCCAAGCTGATACCAACATAGCTATGA 2800
Qy 2936 TTCAATCGGCAGATATAATCTTTCATCGAATTCGAGAGGCTTATCTCTCAGAAATTAATCTG 2995
Db 2801 TTCAATCGTCAGACAAACGCTTCATAGCAATTCGGAGAGCTTACCTTCTCGAATTAGCG 2860
Qy 2996 TTATCCCGGTGTAATTCGGAATTTTGAAGAAATTAAGAGGTGCGATATATCACTGCAA 3055
Db 2861 TGATTCGGGTGTCAATGCTCTATCTTTGAAGAGTTAGAAGGGCGCATCTTCACTGCAAT 2920
Qy 3056 TCTCCCTATAGATCGAGAAATGCTGTTAAATGTTGATTTTAAATAGATTAGATAGCAT 3115
Db 2921 TCTCCTTGTATGATCGAGGAATGTCAATCAAGATGTTGATTTCAACAATGGGCTATCCT 2980
Qy 3116 GCTGGAATGTAAAGGSCATGTAGATCT---ACAACAGAGCCATCACCGTCTCTGCTCTTG 3172
Db 2981 GCTGGAATGTAAAGGSCATGTAGATGTAGAAGAACAGAAATCACCGTCTCTGCTCTTG 3040
Qy 3173 TTATCCAGAAATGGGAAGAGAGTGTCAACAGAGTTCGCGTCTGTCGCGGGCGTGGCT 3232
Db 3041 TTGTTCTGATGGAGAGAGAGTGTCAACAGAGTTCGTTGCTGCTGCTGCTGGCT 3100
Qy 3233 ATATCTCCGTGTACAGGTACAAAGAGGATATGAGAGGGTGTGTTAAACGATCCATG 3292
Db 3101 ACATTTCTGTTTACCGGTACAAAGAGGATACGGAAGGTTGGTGTCAACATACAG 3160
Qy 3293 AATCGAGAAATACAGAGCACTAAATTTAAAACTGTGAAGAGAGAGAGTGTATC 3352
Db 3161 AGATTGAGAAACACACCGAGCTGAAGTTACAGAACTCGCTCGAGGAGAAAGTCTACC 3220
Qy 3353 CAACGGATACAGAACTGTAAATGATTATCTGACACACCAAG-----GTACAGCAGTAT 3406
Db 3221 CAACACACCGTAACTTGCATGACTACACTGGACTCAAGAGGAGTATGAGGTTACTT 3280
Qy 3407 GTAATCCCGTAAATGTGGATATGAGGATGATATGAAGTTGATATACAGCATCTGTTA 3466
Db 3281 ACATTTCTCGAATCGAGGATACGATGGAGCTATGAGAGCAACTCTTCTGTACCCGCTG 3340
Qy 3467 ATTACAAACCGCTTATGAGAGAGAAACGATATACAGATGTACGAGAGATATCATTTGTG 3526
Db 3341 ACTATGATCAGCCTATGAGGAGAGGCTTACACCGATGAGCGTAGGGAACAATCCTTGG 3400
Qy 3527 AATATGACAGAGGTATGTGAATTTATCCACACTTACCAGCTGGTTATATGACAAAAGAT 3586
Db 3401 AATTAACAGAGCTATGGGACTACACACCGTTTACCGCGGCTATGTCAACCAAGAGT 3460
Qy 3587 TAGAATATTTCCAGAAACCGATAGATATGATGATGATGATGAGAGAAACGGAAGGAGT 3646
Db 3461 TAGAGTACTTTCCAGAAACCGCAAGGTTTGGATTGAGATTGAGAGAAACGGAAGGACAT 3520
Qy 3647 TTATTGTAGACAGCGTGAATTAATCTCTTATGGAGAA 3684
Db 3521 TCATTGTTGATAGCGTGGAGTTACTTCTGATGGAGAA 3558

```

```

RESULT 6
US-09-988-462-6
; Sequence 6, Application US/09988462
; Publication No. US20030046726A1
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; Desai, Nalini M.
; Lewis, Kelly S.
; Kramer, Vance C.
; Warren, Gregory W.

```

```

; Evola, Stephen V.
; Crossland, Lyle D.
; Wright, Martha S.
; Merlin, Ellis J.
; Launis, Karen L.
;
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; INSECTICIDAL ACTIVITY IN MAIZE
;
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Syngenta Biotechnology, Inc.
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/988,462
; FILING DATE: 20-No. US20030046726A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/547,422
; FILING DATE: 11-APR-2000
; APPLICATION NUMBER: US 08/459,504
; FILING DATE: 02-JUN-1995
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-188051
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3624 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Synthetic DNA"
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3621
; OTHER INFORMATION: /product= "Full-length, maize
; optimized cry1B"
; /note= "disclosed in Figure 6."
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
;
; US-09-988-462-6

```

```

Query Match 40.6%; Score 1495.6; DB 10; Length 3624;
Best Local Similarity 63.7%; Pred. No. 0;
Matches 2310; Conservative 0; Mismatches 1299; Indels 15; Gaps 2;

Qy 79 ATGGATCTATCACGAGATCTCGTATTGAGGATTTCTTTGTGTATAGCGAGGGAATAAT 138
Db 1 ATGGACCTGTGCTGCCGACGCCGCGCATCGAGGACAGCTGTGCATCGCCGAGGCAACAC 60
Qy 139 ATCAATCCACTTGTAGCGCATCAACAGTCCAAACGGGTATTAAACATAGCTGTGTAATA 198
Db 61 ATCGACCCCTTCGTGAGCGCAGCACCGTGCAGACGGCATCAACATCGCCGCGCATC 120
Qy 199 CTAGGTGTTATAGCGTACCGTTTGTGGACAAATAGCTAGTTTATAGTTTCTTGT 258
Db 121 CTGGGCGTGTGGGCGTGGCCCTTTCGCGGCGCAGCTGCGCCAGCTTCTACAGCTTCTCGTGT 180

```


Db 2341 GAGGACAGCCAGGACCTGGAGATCTACCTGATCGCTACACGCCAAGCAGCAGACCCCTG 2400
Qy 2476 GATGTTCCAGGTACCGAGTCCGATGCGCGCTTTTCAGTTGAAAGCCCAATCGGAAGGTGC 2535
Db 2401 GACGTGCCCGCACCGAGAGCTGTGGCCCTGAGCGTGGAGAGCCCATCGCGCGCTGC 2460
Qy 2536 GGAAACCGAATCGATGGCAGCAATTTTGAATGGAATCTGATCTAGATTTGTTCTTCG 2595
Db 2461 GCGGAGCCCAACCGCTGCGCCCTCACTTCGAGTGGAAACCCGACCTGGACTGCGAGCTGC 2520
Qy 2596 AGAGATGGAGAAATGTGGCATCTCCCATCTTTCTTTTGGATATTTGATTTGGA 2655
Db 2521 GCGACCGCGAGAAATGTGGCCACCAACAGCCACCACTTTCAGCCTGGACATCGACGTGGC 2580
Qy 2656 TGCACAGACTTGCATGAGAAATCTAGGCGTGTGGGTGATTTCAAGATTAAGACCCAGAA 2715
Db 2581 TGCACCGACTGCACGAGAACTGGGCTGTGGGTGATTTCAAGATTAAGACCCAGAG 2640
Qy 2716 GGTGATGAAAGACTAGGAAATCTGGAATTTTGAAGAGAAACCAATTTATTAGGAGAGCA 2775
Db 2641 GGCACCGCCCTGGGCAACTGGAGTTTCATCGAGGAGAAAGCCCTGCTGGGCGAGGCC 2700
Qy 2776 CTGCTCTGTGAAGAGCAGAGAAATTTGAGAGCAACCTGGAAGCAACCTGGAATTTCT 2835
Db 2701 CTGAGCCGCGTGAAGCGCGGAGAAAGTGGCGCAAGCGCGGAGAAAGCTGCAGCTG 2760
Qy 2836 GAAACAAAAAGATATATACAGAGCGCAAAAGAACTGTGGATGCTTTATTGTTAGATTCT 2895
Db 2761 GAGCCAAAGCGGTGTACACGAGGCCAAGGAGCCCTGGAGCCCTGTTCTGGAGCAGC 2820
Qy 2896 CAATATATATAGATTACAGCGGATACAAACATTTGGCATGATTCATGCGGAGATTAAT 2955
Db 2821 CAGTACGACCGCTGCAGGCGCAGCAACCAATCGGCATGATCCACGCGCGCAAGCTG 2880
Qy 2956 GTTTCATGAAATTCAGAGGCTTATCTGTGCAAAATATCTGTATATCCCGGTGTAATGCG 3015
Db 2881 GTGACCGCATCCCGAGGCGCTACTCTGAGCGAGCTGCGCGGTATCCCGCGGTGAACGCC 2940
Qy 3016 GAAATTTTGAAGAAATAGAGGTGCGATTTACTGCAATCTCCCTATACGATGCGGAGA 3075
Db 2941 GAGATCTTCGAGAGCTGGAGGCGCAATCATACCGGCATCAGCTGTAGCAGCCCGC 3000
Qy 3076 AATGTCGTTAAAAATGTGATTTTAAATAGATTAGCATGCTGGAATGTAAGAGGCGAT 3135
Db 3001 AACGTGTGAAGAACGCGACTTCAACACGCGCTGACCTGCTGGAACGTGAAGGCGCAC 3060
Qy 3136 GTAGATGTACAAAGAGCCATCAGCTTCTGCTGTTATCCAGAAATGGGAAGAGCAAA 3195
Db 3061 GTGACGTGCAGCAGAGCCACACCGCAGCGACCTGGTGTATCCCGAGTGGGAGCGCGAG 3120
Qy 3196 GTGTCAACAGCGTTCCGCTGTGTCGCGGCGTGGCTATATCTCCGTCACAGCGGTAC 3255
Db 3121 GTGACGAGCGCGTGGCGGTGTCGCGGCTGACATCTTCGCGGTGACCGCCCTAC 3180
Qy 3256 AAAGAGGGATATGAGAGGGTGTGTAAACGATCATGAAATCGAGAAACAATACAGACGAA 3315
Db 3181 AAGGAGGCTACGCGAGGCGTGTGACCATCCACGAGATGAGAAACAACACCGACGAG 3240
Qy 3316 CTAAATTTTAAATCTGGAAGAGAGAGTGTATCCACCGGATCAGGAACGTGTAAAT 3375
Db 3241 CTGAAGTTCAAGAACCGCGAGGAGAGGAGGTGTACCCACCGCACCGGCACTGCAAC 3300
Qy 3376 GATTATATCTCACACCAAGGTACAGC-----AGTATGTAATTCCTGTAATGCT 3423
Db 3301 GACTACACCGCCCAAGGCGCACCGCGCTGCGCGAGCGCTGCAACAGCGCGCAAGCC 3360
Qy 3424 GGATATGAGGATGATGAAAGTTGATCTACAGCATCTGTAAATTAACAACCGACTTAT 3483
Db 3361 GGCTACGAGGACGCTACGAGGTGCAACACCGCGAGCGTGAATCAAGCCCACTAC 3420
Qy 3484 GAAGAGAAACGTATACAGATGTATCGAAGAGATTAATCATTTGTGTAATATGACAGAGGTAT 3543

Db 3421 GAGGAGAGACCTTACACCGAGTGGCGCGGACACCACTGCGAGTAGCAGCGGCTAC 3480
Qy 3544 GTGAATTTATCCACCACTACCAGCTGGTTATATGACAAAAGAAATAGAAATCTTCCCAGAA 3603
Db 3481 GTGAATTTATCCCGCGTGGCGCGCTACGTGACCAAGGAGCTGGAGTACTTCCCAGAG 3540
Qy 3604 ACCGATTAAGTATGATGATGAGATTGGAGAAACCGAAGGAAAGTTTATTTAGACAGCGTG 3663
Db 3541 ACCGACACCGTGTGATCGAGATCGCGGAGACCGAGGGCAAGTTTCATCGTGGACAGCGTG 3600
Qy 3664 GAATTTACTCTCTTATGGAGGAATAG 3687
Db 3601 GAGCTGCTGCTGATGGAGGATAG 3624

RESULT 7
US-09-826-660-5
; Sequence 5, Application US/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; FILE REFERENCE: WA-714XCD1
; CURRENT APPLICATION NUMBER: US/09/826,660
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 3522
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-09-826-660-5

Query Match 38.28; Score 1408.4; DB 9; Length 3522;
Best Local Similarity 65.74; Pred. NO. 0;
Matches 2243; Conservative 0; Mismatches 1061; Indels 108; Gaps 9;

Qy 285 TCAGTGGGAAATTTCTCAGAACATGCGAACACTTATAAATCAACAATAACAGAAAA 344
Db 207 TGATTGGAGCTTATTTCTTTACAGATTGAACATTTGAGCAAGAAATAGAAACATT 266
Qy 345 TGCTAGGAATACGGCACTTCTCGATTACAAGGTTTAGGAGATTCTTTTAGAGCTTATCA 404
Db 267 GGAAGGAAACCGGCAATTACTACATTACGAGGTTAGCAGATAGCTATGAAATTTATAT 326
Qy 405 ACAGTCTATGAAGATTGGCTAGAAAACCGTGATGATGCAAGACGAGAGTGTCTTTA 464
Db 327 TGAAGCACTAAGAGAGTGGGAAGCAATCCTAATAATSCAATTAAGGGAAGATGTGCG 386
Qy 465 TACCAATATATAGCCTTAGAACCTTGATTCTTTAATGCGATGCGCTTTTCGCAATTAG 524
Db 387 TATTCGATTTGCTAATACAGACGAGCTTTAATAACAGCAATAAATTTTACACTTAC 446
Qy 525 AAACCAAGAAAGTTCCATTTAATGTTATATGCTCAAGCTGCAAAATTTACACCTTATT 584
Db 447 AAGTTTTGAAATCCCTCTTTTATCGGCTATGTTCAAGCGCGGAATTTTACATTATCACT 506
Qy 585 ATTGAGAGATGCTCTCTTTTGGTAGTGAATTTGGCTTACATCGCAGGAAATTCACG 644
Db 507 ATTAAGAGACGCTGTATCTGTTGGGAGGTTGGGAGCTGGATATAGCTACTGTGTAATA 566
Qy 645 TTATTATGAGCGCAAGTGGGAACAAACGAGAGATTATTCGAGCTATTTCGCTAGATGTA 704
Db 567 TCATTATATAGATTAAATAATCTTTTCTAGATATACGAAACATTGTTTGGACACATA 626

Qy 705 TAATACAGGCTTAATAGCTTTCAGAGGACAAATGCGCAAGTTGGGTGCGCTTAATACTA 764
 Db 627 CAATCAGGATTAAGAACTTAAGAGGTACTAATCTCGCAATGGCGCAAGATTCATCA 686
 Qy 765 ATTCGGTAGAGATCTAAGCTTAGGGGTATTAGATCTAGTGCGCACTATTCCTCAAGCTATGA 824
 Db 687 GTTTAGGAGAGATTTAAACACTTACTGTATTAGATATGCTTCTCTTTTCCGAAGTACGA 746
 Qy 825 CACTCGCACTTATCCATTAATACAGGTCTCAGCTTAACAGGGAAGTTTATACAGAGCG 884
 Db 747 TGTAGAACATATCCAAATTCNAAGCTCATCCCAATTAACAGGGAATTTATACAAGTTC 806
 Qy 885 AATTGGAGCAACAGGGGTAAATATGGCAAGTATGAATTTGGTATTAATAATATGACACCTTC 944
 Db 807 AGTAATTGAGGATTCCTCAGTTCTGC-----TAATATACCTAA 845
 Qy 945 GTTTTCGGCTATAGAGACTGGGTTATCCGAAGCCGGAATCTACTGTATTTCTAGAAC 1004
 Db 846 TGGTTTTAATAGGGCGGAATTTGGAGTTAGACCGCCCATCTTATGACCTTTATGAA--- 902
 Qy 1005 ACTTACAAATTTTAGCACTTCATCAGCATGGAGTCTACTAGGCATATGACTTACTGGCG 1064
 Db 903 -----TTCTTTGTTGTAACTGCAGAGACTGTAGAGTCAAACTGTGTGGGGAGG 953
 Qy 1065 GGGGCACACAATTCAAATCTCGCCAAATAGGAGCGGATTAATACTCAACGCATGGGTC 1124
 Db 954 ACCTTAGTTAGTTTACGAATAACGGCTGGTTAAACCGTATAAAATTTCCCTAGTTACGGGGT 1013
 Qy 1125 TACCAATACTTCTAATCTGTAAGATTAATCAATCTTCTCTCGAGAGCTAATTTGGAC 1184
 Db 1014 CTTCAATCTGGTGGCCCAATTTGGATTTGCAGATGAGGATCCACGTCCTTTTATTCGGAC 1073
 Qy 1185 TGAATCATATGACAGAGTCTTCTATCGGGAATTTTACCTTGAACCTATTATGCTGTC 1244
 Db 1074 ATTAACAGATCTCTTTTGTGTCAGAGGAT-----TTGGGAATCCTCATTAAGTACT 1127
 Qy 1245 TACTGTTAGATTTAAATTTTAGAACCTCTCAGAATPACTTTTGAAGAGGTACTGCTAACTA 1304
 Db 1128 GGGCTTTAGGGAGTAGCAATTTCAACAACTGGTACGAAACACACCCGGAACATTTAGAAA 1187
 Qy 1305 TAGTCAACCTATAGTACCTGGGCTTCAATTAAGATTTCAAGAACTGAATTAACACC 1364
 Db 1188 TAGTGGGACCATAGATTTCTCTAGATGAATCCCACTCAGGATTAATAGTGGGCAAC--TT 1246
 Qy 1365 AGAAACACAGAGACCAATTAATGAATCATATAGTCATAGTATCTCACATAGGGCT 1424
 Db 1247 GGAATGATTAAGTCATGTTAATCATGTTAATTTGACGATGCGCAGGTGAGATTT 1306
 Qy 1425 CATTTCAATCTAGGGTGCATGTACAGTATATTTTGGACGACCGGTAGTGCGAGTCG 1484
 Db 1307 CAGGAAGTGAATCATGGAG--AGCTCCAATGTTTCTTTGGACGACCGGTAGTGCACCCC 1364
 Qy 1485 TACAAATACCAATTAAGTTCAGATAGCATACACAAATACCAATGGTAAATCAATCAACCT 1544
 Db 1365 TACAAATACCAATTAAGTTCAGAGAGGATTTACTCAATACCAATGGTAAAGCACAATCACT 1424
 Qy 1545 TAATTCAGGTACCTCTGTAGTCAGTGCCCGAGGATTTTACAGGAGGATATAATCCGAAC 1604
 Db 1425 TCAGTCAGTACTACTGTGTAGAGAGGCGGGTTTACGGAGGAGATTAATCTTCAAG 1484
 Qy 1605 TAACGTTAATGGTATGATTAAGTATGGGTCTTAATTTTAAATTAATACATCATTTACAGCG 1664
 Db 1485 AACAAAGTGGAGGACCAATTTGCTTATCTAATTTGTTAAATAATAATGGGCAATTAACCCCAAAG 1544
 Qy 1665 GTATCGGTGAGAGTTCGTTATGCTGCTTCTCAACAAATGGTCTGAGGGTAACTGTCGG 1724
 Db 1545 GTATCGTGAAGAAATACGCTATGCTCTACTACAAATCTAAGAAATTTACGTAACGGTTC 1604
 Qy 1725 AGGAGTACTACTTTTGTATCAAGGATTTCCCTAGTACTAGTGCCTAATGAGTCTTTGAC 1784
 Db 1605 AGGTGAACGGATTTTCTGCTCAATTTTACAAACAAATGGATACCGGTGACCCATTAAC 1664
 Qy 1785 ATCTCAATCATTTAGATTTGAGAAATTTCTGTTAGGTATTAGTGCATCTGGCAGTCAAC 1844

Db 1665 ATTCCAATCTTTAGTTACGCAACTAATTAATACAGCTTTTACATTCCTCAATGAGCCAGAG 1724
 Qy 1845 TGCT---GGAATTAAGTATAAGTATAATGAGGTAGTACAAAGCTTTCACCTTTGATAAAT 1901
 Db 1725 TAGTTTTCACAGTAGGTGCTGATATCTTTAGTTTTCAGGGAATGAAGTTTATATAGACAGATT 1784
 Qy 1902 TGAATTCATTTCCAACTTACTGCAACCTTTCGAAGCAGATACGATTTTGAAGAGGGCGCAAGA 1961
 Db 1785 TGAATTCATTTCCAGTTTACTGCAACATTTTGAAGCAGATATGATTTTGAAGAGCACAATA 1844
 Qy 1962 GGGCGTGAATCTCTGTTTACTAATACGAATCCAAGAGATTTGAAAACAGATGTGACAGA 2021
 Db 1845 GGGCGTGAATGCGCTGTTTACTTCTATAAACCAAAATAGGGATATAAAACAGATGTGACGGA 1904
 Qy 2022 TTATCATATTGATCAAGTATCCAAATTTAGTGGCGTGTATTTCGGATGAATTTGCTTTAGA 2081
 Db 1905 TTATCATATTGATCAAGTATCCAAATTTAGTGGATTTGTTTATCAGATGAATTTTGTCTGGA 1964
 Qy 2082 TGAAGAGAGAGAAATTTACTTCGAGAAAGTGAATATGCGAAACGACTCAGTGCATGAAGAAA 2141
 Db 1965 TGAAGAGCAGAAATTTGTCGAGAAAGTCAAAACATGCGAAGGACTCAGTGCATGAGCGGAA 2024
 Qy 2142 CTTTACTCCAAGATCCAACCTTCACTCAATCAATGAAGCAACCGAGCTTCATATCTACTAA 2201
 Db 2025 TTTTACTTCAAGATCCAACCTTCAAGGCACTCAATAGGCACTAGAC----- 2070
 Qy 2202 TGAGCAATCGAATTTACATCTATCCATGAACTCTGAACATGGATGGTGGGGAAGTGA 2261
 Db 2071 -----CGTGGTTGGAGAGGAAGTAC 2090
 Qy 2262 GAACATTTACAAATCCAGGAAGAAATGACGTATTTTAAAGAGAAATTCAGTCACTACCGGG 2321
 Db 2091 GGAATTTACCATCCAAGAGGAGATGACGTATTTCAAGAAATTTATGTCACATACCAGG 2150
 Qy 2322 GACTTTTAAATGAGTGTATCCGACGTATTTATATCAAAAAATAGGAGAGTCGGAATTTAAA 2381
 Db 2151 TACTTTTGTAGTGTGTATCCAACTGTTTATATCAAAAAATAGATGAGTCGAAATTTAAA 2210
 Qy 2382 AGCTTATATCTCGCTCAATTAAGAGGTATATTGAAGATGTCAGATTTAGAGATATA 2441
 Db 2211 ACCCTATCTCTGTTTCAATTAAGAGGTATATCGAGGATAGTCAAGACTTTAGAAATCTA 2270
 Qy 2442 TTTGATTCGTTATAATGCGAAACATCAACATTTGGATTTTCCAGGTACCGAGTCCGATG 2501
 Db 2271 TTTGATCCGCTATAATGCAAAACACGAAACAGATAATGCTAGGTACGGTCTTTATG 2330
 Qy 2502 GCGCTTTTCAAGTTGAAGCCCAATCGGAAGGTGCGGAGAACCGAATCGATGCGCACACA 2561
 Db 2331 GCGCTTTTCAAGTCCAAATCGAAGAGTGGAGAACCGAATCGATGCGCGCCACA 2390
 Qy 2562 TTTTGAATGGAATCCTGATCTAGATTTGTTCTCGAGAGTGGAGAAATATGCGCATCA 2621
 Db 2391 CTTTGAATGGAATCCTGATCTAGATTTGTTCTCGAGAGCGGGGAAATATGTCACATCA 2450
 Qy 2622 TTCCCATCACTTTCTCTTTGGATATTGATATTGGATGACAGACTTGCATGAGAAATCTAGG 2681
 Db 2451 TTGCGCATCTTTCTCTTTGGACATTCATGTTGATGTTACAGACTTAAATGAGGACTTAGA 2510
 Qy 2682 CGTGTGGTGGTATTCAAGATTGAAGCGCAGGAGGTTCATGCAAGACTAGGGAATCTGGA 2741
 Db 2511 TGTATGGTGGTATTCAAGATTGAAGCGCAGGATGGCCATGCAAGACTAGGAAATCTAGA 2570
 Qy 2742 ATTTATTGAAGAAACCATTTATTAGGAGAGCACTGCTCTGTTGTTGAAGAGAGCAGAGAA 2801
 Db 2571 GTTTCTCGAAGAGAAACCATTTAGTCGGGAGCACTAGCTCTGTTGTTGAAGAGAGAGAA 2630
 Qy 2802 AAAATGAGAGACAAACGTCGAAATTAATCAATTTGAAAAACAAACGAGTATATACAGAGC 2861
 Db 2631 AAAATGAGAGATAAACGTCGAAATTTGGAATTTGGAATTTGGAATTTGTTTATTAAGAGGC 2690
 Qy 2862 AAAAGAGCTGTGGATGCTTTTATTGTTAGATTCTCAATATAATAGATTACAAGCGGATAC 2921

Db 2691 AAAAGAACTCTAGATGCTTTATTTGTAACTCTCAATATATGATCAATTAACAAGCGGATAC 2750
 Qy 2922 AAACATTTGGCAGATTCATCGGCGAGATAAATCTTTCATCGAATTCGAGAGCTTATCT 2981
 Db 2751 GAATATTTGCCATGATTCATCGGCGAGATAAATCGTTTCATAGAAATTCGGGAAGCGTATCT 2810
 Qy 2982 GTCAAGATTAATCTGTTATCCCGGCTGTAATCGCGGAATTTTGAAGAAATTAAGAGTCG 3041
 Db 2811 TCCAGAGTTATCTGTGATTCGCGGTGTAATGTAGACATTTTCGAAGAAATTAAGAGGCG 2870
 Qy 3042 CATATCACTCAATCTCCCTATACGATCGCAGAAATGTCTTAAATATGCTGATTTAA 3101
 Db 2871 TATTTTCACTGCAATCTCTTATATGATCGCAGAAATGTCTTAAATATGCTGATTTAA 2930
 Qy 3102 TAATGGATTAAGCATGCTGGAATTAAGAGGCGATGTAGATGT---ACAACAGACCATCA 3158
 Db 2931 TAATGGCTTATCATGCTGGAACGTGAAAGGCGATGTAGATGTAGAAAGAACAAACCA 2990
 Qy 3159 CCGTCTCTGCTGTTATCCAGAAATGGGAGCAGAGTGTCAACAGCATTCGCGTCTG 3218
 Db 2991 CCGTTCGGTCCCTGTTGTTCCGGAATGGGAAACGAGAGTGTCAACAGAAATTCGTTCTG 3050
 Qy 3219 TCCGGGCGTGGCTATATCTCTGTCACAGCGTACAAAGAGGATATGAGAGGTTG 3278
 Db 3051 TCCGGGCTGGCTATATCTCTGTCACAGCGTACAAAGAGGATATGAGAGGTTG 3110
 Qy 3279 TGTAAACGATCAATGAATTCGAGAAACAATACACAGCAACTAAAATTTAAAACCTGTGAAGA 3338
 Db 3111 CGTAACCATTCATGAGATCGAGAAACAATACACAGCAACTGAAGTTTAGCAACTGCGTAGA 3170
 Qy 3339 AGAGGAAGTGTATCCACGGATACAGAAACGTGTAAATGATTAATCTGCAACACCAAGGTAC 3398
 Db 3171 AGAGGAAGTGTATCCAAACCAACACCGGTAAACGTGTAAATGATTAATCTGCAAAATCAAGAAGA 3230
 Qy 3399 A-----GCAGTATGTAATCCCGTAACTGCTGGATATGAGATGCATATGAAGTTGATAC 3452
 Db 3231 ATACGGGGTGGTACACTTCCCGTAACTGCTGGATATGAGCAAACTTATGGAAGCAATTC 3290
 Qy 3453 TACAGCATCTGTTAATTAACAACCGACTTATGAAGAAAGAAACGATATACAGATGTACGAAG 3512
 Db 3291 TTCTGTACAGCTGATATGCTGCTAGTCTATGAAGAAATTCGATACAGATGACGCAAG 3350
 Qy 3513 AGATAATCTGTAATGACAGAGGATGTGAATATCCACCACTACAGCTGTTA 3572
 Db 3351 AGACAAATCTTGTGAATCTAACAGAGATATGGGGATTAACACCACTACAGCTGCTA 3410
 Qy 3573 TATGACAAAGAAATTAAGAACTTCCAGAAACCGATAAGGTATGAGATGAGATGAGGA 3632
 Db 3411 TGTGACAAAGAAATTAAGATTAATCCAGAAACCGATAAGGTATGAGATGAGATGAGGA 3470
 Qy 3633 AACGGAAGGAAAGTTTATTTAGACAGCGTGAATTTACTCTTATGAGGAA 3684
 Db 3471 AACGGAAGGAAATTCATCGTGACAGCGTGAATTTACTCTTATGAGGAA 3522

RESULT 8
 US-09-837-961-7
 ; Sequence 7, Application US/09837961
 ; Publication No. US20040058860A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Payne, Jewel
 ; APPLICANT: Sick, August
 ; TITLE OF INVENTION: No. US20040058860A1el Bacillus thuringiensis Isolate Active Again
 ; FILE OF INVENTION: and Genes Encoding No. US20040058860A1el Lepidopteran-Active Tox
 ; CURRENT APPLICATION NUMBER: US/09/837,961
 ; CURRENT FILING DATE: 2001-04-19
 ; PRIOR APPLICATION NUMBER: US 09/521,344
 ; PRIOR FILING DATE: 2000-03-09
 ; PRIOR APPLICATION NUMBER: US 08/933,891
 ; PRIOR FILING DATE: 1997-09-19
 ; PRIOR APPLICATION NUMBER: US 08/356,034
 ; PRIOR FILING DATE: 1994-12-14

; PRIOR APPLICATION NUMBER: US 08/210,110
 ; PRIOR FILING DATE: 1994-03-17
 ; PRIOR APPLICATION NUMBER: US 07/865,168
 ; PRIOR FILING DATE: 1992-04-09
 ; PRIOR APPLICATION NUMBER: US 07/451,261
 ; PRIOR FILING DATE: 1989-12-14
 ; PRIOR APPLICATION NUMBER: US 371,955
 ; PRIOR FILING DATE: 1989-06-27
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 7
 ; LENGTH: 3522
 ; TYPE: DNA
 ; ORGANISM: Bacillus thuringiensis
 ; US-09-837-961-7
 Query Match 38.2% Score 1408.4; DB 11; Length 3522;
 Best Local Similarity 65.7%; Pred. No. 0;
 Matches 2243; Conservative 0; Mismatches 1061; Indels 108; Gaps 9;
 Qy 285 TCAGTGGGAAATTTTCTTAGAACATGTCGAACCACTTTATAATCAACAAATAACAGAAAA 344
 Db 207 TGATTGGAGCTTATTTCTTTTACAGATTGAACAATTCATTGAGCAAGAATAGAAACATT 266
 Qy 345 TGCTAGGAATACGGCACTTCCTCGATTACAGAGTTTAGGAGATTCCTTTAGAGCCTATCA 404
 Db 267 GGAAGGAACCGGCAATTTACTACATTTACGAGGTTAGCAGATAGCTATGAAATTTATAT 326
 Qy 405 ACAGTCACTTTGAAGATTGGCTAGAAACCGTATGATGCAAGACGAGAGTGTCTTTA 464
 Db 327 TGAAGCACTAAGAGAGTGGGAAGCAATCTTAATATGCACAATTAAGGGAAGATGTGCG 386
 Qy 465 TACCAATATATAGCCCTTAGAACTTTGATTTTCTTAATCGCATGCGCTTTTCGCAATTAG 524
 Db 387 TATTCGATTTGCTAATACAGACGAGCTTTAATACAGCAATAAATAATTTTACACTTAC 446
 Qy 525 AAACCAAGAGTTCCATTTAATATGATATGCTCAAGCTGCAAAATTTACACTTATTT 584
 Db 447 AAGTTTTGAAATCCCTCTTTTATCGGCTATGTTCAAGCGCGAAATTTACATTTATCACT 506
 Qy 585 ATTGAGAGATGCTCTCTTTTGGTAGTGAATTTGGGCTTACATCGCAGGAAATTCACG 644
 Db 507 ATTAAGAGACGCTGTATCGTTTGGGAGGTTGGGACTGGATATAGCTACTGTGTAATAA 566
 Qy 645 TTATTTATGACGCGCAAGTGGAAACAAACGAGAGATTTATTCGCACTTATTCGCTAGAAATGGA 704
 Db 567 TCATTATAATAGATTAAATAATCTTATTATAGATATACGAAACATTTGTTGGACATA 626
 Qy 705 TAATACAGGCTTAATAGCTTTGAGAGGGAACAATGCGCAAGTTGGGTGCGTTAATAATCA 764
 Db 627 CAATCAAGGATTAAGAAACTTAAGAGGTAATACTACTCGAATGGGCAAGATTCATCA 686
 Qy 765 ATTCCGTAGAGATCTAAGTTAGGGTATTAGATCTAGTGGCACTATTCGCCAGCTATGA 824
 Db 687 GTTTAGAGAGATTTTAACACTTACTGTATTAGATATCGTTGCTCTTTTCCGAACTAGCA 746
 Qy 825 CACTCGCACTTATCCCAATAATACAGTGTCTAGTTAAACAGGGAAGTTTATACAGACGC 884
 Db 747 TGTATTAGACATATCCCAATTCAAACGTCATCCCAATTAACAGGGAATTTATACAGTTC 806
 Qy 885 AATTGGAGCAACAGGGGTAAATATGCAAGTATGAATTTGGTATTAATAATATGACCTTC 944
 Db 807 AGTAATTTAGGATTCCTCAGTTCTGC-----TAATATACCTAA 845
 Qy 945 GTTTTCCGTATAGAGACTCGGTTATCCGAAGCCGCACTACTTACTTCTTAGAACA 1004
 Db 846 TGGTTTTAATAGGCGGAATTTGGAGTTAGACCGCCCATCTTTATGACTTTTATGAA--- 902
 Qy 1005 ACTTACAAATTTTAGCACTTCATCAGATGGAGTGTCTACTAGGCATATGACTTACTGGCG 1064
 Db 903 -----TTCCTTTGTTGTAATCGCAGAGACTGTTAGAGTCAAACTGTGGGAGG 953
 Qy 1065 GGGGCACAAATTCATCTCGGCCAAATAGAGGCGGATTAATACTCAACGCATGGGTC 1124

Db 954 ACCTTAGTTAGTTCACGAAATACGGCTGGTAAACCGTATAAATTTCCCTAGTTACGGGGT 1013
 Qy 1125 TACCAATACCTTCTATTAATCTGTAAGTATTAATCAATCTCTCGAGACGTATATTGGAC 1184
 Db 1014 CTTCAATCTGGTGGCCCAATTTGGATTCAGATGAGGATCCACGCTCTTTTATACGGAC 1073
 Qy 1185 TGAATCATATACAGAGTGTCTTCTATGGGAAATTTACCTTGAACCTATTCAATGTGTCCC 1244
 Db 1074 ATTATCAGATCCTGTTTGTTCGAGGAGAT-----TTGGGAATCCTCATTAATGACT 1127
 Qy 1245 TACTGTTAGATTTAATTTTAGGAACCTCAGAATFACCTTTTGAAGAGGTACTGCTAACTA 1304
 Db 1128 GGGCTTTAGGGGAGTAGCATTTCAACAAACCTGGTACGAACACACACCGCAACATTTAGAAA 1187
 Qy 1305 TAGTCACCCCTATGAGTCACCTGGCTTCAATTAAGAAGATTCAGAACTGAATTAACACC 1364
 Db 1188 TAGTGGGACCAATAGATTCTCTAGATGAATCCCACTCAGGATTAATAGTGGGGCACCC-TT 1246
 Qy 1365 AGAAACAACAGAACGACCAATTAATGAATCATATAGTCATAGGTTATCTCACATPAGGCT 1424
 Db 1247 GGAATGATTATAGTCATGTATTAATCAATGTTACATTTGTACGATGGCCAGGTGAGATT 1306
 Qy 1425 CATTTCAAACTTAGGGTGCATGTACCAGTATATTTCTTGGACGCCCTGATGCGAGATCG 1484
 Db 1307 CAGGAAGTGATTATGTGAG--AGCTCCAAATGTTTCTTGGACGCCCTGATGCAACCCC 1364
 Qy 1485 TACAAATACCAATTAGTTAGTACATACATACCAATACCAATGTTGTAATAATCAATCAACT 1544
 Db 1365 TACAAATACCAATTAGTCCGGAGAGGATTTACTCAAAATACCAATGTTGTAATAATCAATCAACT 1424
 Qy 1545 TAAATCAGGTACCTCTGTAGTCAGTGGCCAGGATTTACAGGAGGGGATATAATCCGAAC 1604
 Db 1425 TCAGTCAGGTACTACTGTTGTAAGAGGCCGGGTTTACGGGAGGAGATTTCTTCAAG 1484
 Qy 1605 TAACTGTTAATGTTAGTACTAATGATGATGGTCTTAAATTTAATAATACATTTACAGCG 1664
 Db 1485 AACAAAGTGGAGCAATTTGCTTATCTACTATTTGTTTAAATAATAATGGGCAATTAACCCCAAG 1544
 Qy 1665 GTATCGGTGAGGTTGTTTATGCTGCTTCTCAACAAATGGTCTGAGGTTACTGTCGG 1724
 Db 1545 GTATCGTCAAGAAATACGCTATGCTCTACTACAAATCTAAGAAATTTACGTAACGGTTGC 1604
 Qy 1725 AGGAGTACTACTTTTGCATCAAGGATTTCCCTAGTACTATGATGCAATGATCTTTGAC 1784
 Db 1605 AGGTGAACGGATTTTGTCTGCTCAATTTAACAACAATGGATACCGGTGACCAATTAAC 1664
 Qy 1785 ATCTCAATCATTTAGATTGTCAGAAATTTCTGTAGGTATTAGTGCATCTGGCAGTCAAC 1844
 Db 1665 ATTCCAATCTTTTAGTTACGCAACTATTAAATACAGCTTTTACATTTCCCAATGAGCCAGAG 1724
 Qy 1845 TGCT---GGATAGTATAGTATAATGAGGTAGACAAACGTTTTCATTTTGNATAAAT 1901
 Db 1725 TAGTTTACAGTAGGTGCTGATCTTTTAGTTACAGGAATGAAGTTTATATAGACAGATT 1784
 Qy 1902 TGAATTCATTTCCAAATTAAGTCAACCTTTCAAGACAGAAATACATTTAGAAAGGGCGCAAGA 1961
 Db 1785 TGAATTCATTTCCAGTTACTGCAACATTTGAGCAGAAATATGATTTAGAAAGACACAAA 1844
 Qy 1962 GGGGTTGAATGCTCTGTTTACTAATACGAATTCGAAGAGATTTGAAAACAGATGTGACAGA 2021
 Db 1845 GGGGTTGAATGCTGTTTACTTCTATAAACCAATAGGAGTAAACACAGATGTGACGGA 1904
 Qy 2022 TTATCATATTGATCAAGTATCCAAATTTAGTGGCGGTTTATCGGATCAATTCGCTTAGA 2081
 Db 1905 TTATCATATTGATCAAGTATCCAAATTTAGTGGATTTTATCAGATGAATTTTGTCTGGA 1964
 Qy 2082 TGAAGAGAGAAATTTACTTGAAGAGTCAAAATATGCGAAACGACTCAGTGTATGAAAGAAA 2141
 Db 1965 TGAAGAGGAGAAATTTGTCGAGAGAGTCAAAATGCGAGCGACTCAGTGTATGAGCGGAA 2024
 Qy 2142 CTTACTCCAGATCCAACTTCAATCCATCAATTAAGCAACGAGCTTTCATATCTATAA 2201

2025 TTTACTTCAAGATCCAAACTTTCAAGGCAATCAATAGGCAACTAGAC----- 2070
 Qy 2202 TGAGCAATCGAATTTACATCTATCCATGAACAAATCTGAACATCGATGTTGGGAAGTGA 2261
 Db 2071 -----CGTGGTTGGAGAGGAAGTAC 2090
 Qy 2262 GAACATTTACAAATCCAGGAAGAAATGACGTATTTTAAAGAGAAATTTACCTCACACTACCGGG 2321
 Db 2091 GGATATTACCAATCCAAAGAGAGATGACGTATTTCAAGAGAAATTTATGTCACACTACCAGG 2150
 Qy 2322 GACTTTTAATGAGTGTATCCGACGTATTTATATATCAAAAAATAGGAGATCGGAATTTAA 2381
 Db 2151 TACCTTTGATGAGTGTATCCAAAGCTATTTATATCAAAAAATAGATGAGTCGAAATTTAA 2210
 Qy 2382 AGCTTATCTCGCTACCAATTTAGAGGGTATTTAGAGATAGTCAAGATTTAGAGATATA 2441
 Db 2211 ACCCTATCTCGTTATCAATTTAAGAGGGTATATCGAGGATAGTCAAGACTTTAGAAATCTA 2270
 Qy 2442 TTTGATTCGTTTAAATCCGAAACATGAACATTTGGATGTTTCCAGGTACCCGAGTCCGTTATG 2501
 Db 2271 TTTGATCCGCTATATGCAAAAACAGAAACAGTAAATGTCTAGGTACGGTCTTTTATG 2330
 Qy 2502 GCCCTTTTCAGTTGAAAGCCCAATCCGAAAGGTGCGGAGAACCGAATCGATGCGCACCA 2561
 Db 2331 GCCGCTTTTCAGTCCAAAGTCCAAATCAGAAAGTGTGGAGAACCGAATCGATGCGGCCACA 2390
 Qy 2562 TTTTGAATGAAATCCTGATCTAGATTTGTTCTCCAGAGATGGAGAAATAATGTCGCATCA 2621
 Db 2391 CTTTGAATGAAATCCTGATCTAGATTTGTTCTCCAGAGAGCGGGGAAATAATGTCACATCA 2450
 Qy 2622 TTCCCATCATTTCTCTTTTGGATTTGATATTGGATGACAGACTTGCATCAGAAATCTAGG 2681
 Db 2451 TTTGCATCATTTCTCTCTTGGACATTTGATTTGGATGTACAGACTTAAATGAGGACTTAGA 2510
 Qy 2682 CGTGTGGTGGTATTTCAAGATTAAGACGCGAGGAGTCTATGCAAGACTAGGGAATCTGGA 2741
 Db 2511 TGTATGGTGTATTTCAAGATTTAAGACGCGAAGATGGCCATGCAAGACTTAGGAAATCTAGA 2570
 Qy 2742 ATTTATTGAAGAAACCAATTTATAGGAGAACACTGTCTCGTGTGAAGAGACGAGAGAA 2801
 Db 2571 GTTTCTCGAAGAAACCAATTTAGTCCGGGAGCACTAGCTCGTGTGAAAGACGAGAGAA 2630
 Qy 2802 AAAATGGAGAGACAAACGTTGAAATACTCAATTTGAAACAAAAACGAGTATATACAGAGC 2861
 Db 2631 AAAATGGAGAGATAACGTTGAAATAATTTGAAATTTGAAACAAAAATATTGTTTATAAGAGGC 2690
 Qy 2862 AAAAGAGCTGTGATGCTTTTATTTAGTATTTCTCAATATAATAGATTAACAGCGGATAC 2921
 Db 2691 AAAAGAACTGTATGATGCTTTTATTTGTAACCTCTCAATATGATCAATTTACAGCGGATAC 2750
 Qy 2922 AAACATTTGGCATCATTCATCGCGCAGATAAATCTTTGTTTCATCGAATTCGAGAGGCTTATCT 2981
 Db 2751 GAATTTGCCATGATTTATCGCGCAGATAAATCGTGTTCATAGAAATTCGGAGAGGCTATCT 2810
 Qy 2982 GTCAGAAATTTATCTGTTTATCCCGGTTGTAATCGGAAATTTTGAAGAAATTTAGAGGTGCG 3041
 Db 2811 TCCAGAGTTTATCTGATTTCCGGTGTAAATGTAGACATTTTCGAAGAAATTTAAAGGGCGC 2870
 Qy 3042 CATTTATCAGTGAATCTCCCTATACATGCGAGAAATGTCTGTTAAAAATGCTGATTTAA 3101
 Db 2871 TATTTTCACTGCAATCTCTCTATATGATGCGAGAAATGTCTATTTAAAAACCGTATTTCAA 2930
 Qy 3102 TAATGATTTAGCATGCTGGAATCTTAAAGGCGCATGTAGATGT---ACAACAGAGCGCAATCA 3158
 Db 2931 TAATGGCTTATCATGCTGGAACTGTAAGGCGCATGTAGATGTAGAGAAACAAACACCA 2990
 Qy 3159 CCGTTCCTGCTTTTATCCAGAAATGGGAAGCAGAAAGTGTCAACAGCTTCCGCTGTG 3218
 Db 2991 CCGTTCGGTCTTGTGTTTCCGGAATGGGAAGCAGAAAGTGTCAACAGAACTTCTGTGTG 3050
 Qy 3219 TCCGGGCGGTGGCTATATCTCTCGTGTACAGCGTACAAAGAGGATATCGAGAGGGTTG 3278
 Db 3051 TCCGGGTCGTGGCTATATCTCTGTCAGCGTACAAAGGGGATATGGAGAAAGTTG 3110

3279	Qy	TGTTAACGATCCATGAATTCGAGAAACAATACAGACGAACCTAAAAATTTAAAAACTGTGAAGA	3338
3111	Db	CGTTAACCATTTTCATCAGATTCGAGAAACAATACAGACGAACCTGAAGTTTATAGCAACTCGGTAGA	3170
3339	Qy	AGAGGAAGTGTATCCAAACGGATACAGAAACGTGTAATGATTATATCTGCACACCAAGGTAC	3398
3171	Db	AGAGGAAGTCTATCCAAACAAACACGGTAACCGTGTAAATGATTATATCTGCAATCAAGAAGA	3230
3399	Qy	A-----GCAGTATGTTAAATCCCGTAATGCTTGGATATGAGGATGCATATGAAAGTTGTATC	3452
3231	Db	ATACGGGGGTGCGTACACTTCCCGTAATCGTGGATATGACGAACCTTATGGAACCAATTC	3290
3453	Qy	TACAGCATCTGTTTAAATTACAAACCGAATTATGAAAGAAAGAAACGTAATACAGATGTCGAAG	3512
3291	Db	TTCTGTACCAAGCTGATTTATGCGTCAGTCTATGAAAGAAAAATCGTATATACAGATGACCAAG	3350
3513	Qy	AGATAATCATTTGTGAATATGACAGAGGGTATGTGAATATCCACCACCTACCGCTCGTTA	3572
3351	Db	AGACAAATCCTTGTGAAATCTTAACAGAGGATATGGGGATTTACACACCACTACCAAGCTGGCTA	3410
3573	Qy	TATGACAAAAAGAAATTAGAATACTTCCACAGAAACCGATAAGGTATGGATTTCGAGATTGGAGA	3632
3411	Db	TGTGACAAAAGAAATTAGAGTACTTCCACAGAAAACCGATAAGGTATGGATTTCGATCCGAGA	3470
3633	Qy	AACGGAAGGAAAGTTTATTGTAGACACGGTGGAAATTACTCCTTATGAGGAA	3684
3471	Db	AACGGAAGGAAACATTTCACTCGTGGACACGCTGGAATTACTCCTTATGAGGAA	3522

RESULT. T 9

```

US-10-825-751-7
; Sequence 7, Application US/10825751
; Publication No. US20040194165A1
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel
; APPLICANT: Sick, August J.
; TITLE OF INVENTION: Novel Bacillus thuringiensis Isolate Active Against Lepidopteran
; TITLE OF INVENTION: Pests, and Genes Encoding Novel Lepidopteran-Active Toxins
; FILE REFERENCE: MA-43CDF2D4
; CURRENT APPLICATION NUMBER: US/10/825,751
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 09/837,961
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/521,344
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 08/933,891
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: US 08/356,034
; PRIOR FILING DATE: 1994-12-14
; PRIOR APPLICATION NUMBER: US 08/210,110
; PRIOR FILING DATE: 1994-03-17
; PRIOR APPLICATION NUMBER: US 07/865,168
; PRIOR FILING DATE: 1992-04-09
; PRIOR APPLICATION NUMBER: US 07/451,261
; PRIOR FILING DATE: 1989-12-14
; PRIOR APPLICATION NUMBER: US 371,955
; PRIOR FILING DATE: 1989-06-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 3522
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-10-825-751-7

Query Match 38.2%; Score 1408.4; DB 18; Length 3522;
Best Local Similarity 65.7%; Pred. No. 0;
Matches 2243; Conservative 0; Mismatches 1061; Indels 108; Gaps 9;

Qy 285 TCAGTGGGAAATTTTCCTAGAACATGTCGAAACAACCTTATAATCAACAATAAACAGAAA 344
Db 207 TGATTGAGCTATTCTCTTTTACAGATTGAAACAATTGATTTCGAGCAAGAAATAGAAACATT 266

```


1425 CAITTCACAACTAGGTGTCATGTACAGATATATCTTTGGACGACCGTAGTGCAGATCG 1484
 1307 CAGGAAGTGAATCATGAG--AGCTCCAATGTTTCTTTGGACGACCGTAGTGCACCCC 1364
 1485 TACAATACCAATTAGTTCAGATAGCAATAACAATAACCAATTTGGTAAATCAATTCACACT 1544
 1365 TACAATACCAATTTGATCCGAGAGGATTAATCTCAATACCAATTTGGTAAAGCACATACACT 1424
 1545 TAATTCAGGTACCTCTGTAGTCAGTGCAGGATTTTACAGGAGGATATATCCGAAC 1604
 1425 TCAGTCAGGTACTACTGTGTAGAGGGCCCGGTTCAGGGAGGATATCTTCGACG 1484
 1605 TAACGTTAAATGGTAGTACTTAAGTATGGGTCTTAATTTTAAATAATACATCAATTACAGCG 1664
 1485 AACAGTGGAGGACCAATTCCTTATATACTAATTTTAAATAATAAATGGGCAATACCCCAAG 1544
 1665 GTATCGGTGAGAGTTCGTTATGCTGCTTCTCAACAATGGTCTGAGGTTAATCTGTCGG 1724
 1545 GTATCGTGCAGAAATACGCTATGCTCTACTACAAATCTAAGAAATTTACGTAACGGTTGC 1604
 1725 AGGAGTACTACTTTTTCATCAAGGATTCCTAGTACTATGAGTGCAAAATGAGTCTTTGAC 1784
 1605 AGGTGAACGGATTTTTCGCTCAATTTAACAACAATGATACCGGTACCCCAATTAAC 1664
 1785 ATCTCAATCAATTTAGATTTTCAGAAATTTCTGTAGGTATTAGTGCATCTGCGCATCAAC 1844
 1665 ATCCCAATCTTTAGTTACGCACTAATTAATACAGCTTTTACATTCCTCAATGAGCAGAG 1724
 1845 TGCT---GGAAATAGTAAATAGTAAATGAGGTAGCAAAAGTTTCACCTTTGATTAAT 1901
 1725 TAGTTTCACAGTAGTGTCTGATCTTTTAGTTACAGGAATGAAGTTTATATATAGACAGATT 1784
 1902 TGAATTCATTTCCAAATTAATCTGAAAGTAAATGAGTAAATTTTGAAGGGGCGAAG 1961
 1785 TGAATTCATTTCCAGTTACTGCAACATTTGAAGCAGAAATGATTTTGAAGAGGACACAAA 1844
 1962 GCGGTGAATGCTCTGTATTACTAATACGAATTCGAAGAAATTTGAACAGATGTGACAGA 2021
 1845 GCGGTGAATGCTCTGTATTACTTAAACCAATAGGATTAACACAGATGTGACGGA 1904
 2022 TTATCATATTGATCAAGTATCCAAATTTAGTGGCGGTGTTATCGGATGAATTCGCTTAGA 2081
 1905 TTATCATATTGATCAAGTATCCAAATTTAGTGGATTTTATCAGATGAATTTGTCTGGA 1964
 2082 TGAAGACAGAGAAATTTCTGGAAGTGAATATGCGAAACGACTCAGTGTATGAAGAAA 2141
 1965 TGAAGACGAGAAATTTGCGAGAAATGCAACATGCGAGGACTCAGTGTATGAGCGGAA 2024
 2142 CTTACTCCAAGATCCAACTTCATCCATCAATTAAGCAACAGACTTTCATATCTACTAA 2201
 2025 TTTACTTCAAGATCCAACTTCAAGGCATCAATAGGCACTAGAC----- 2070
 2202 TGACCAATCGAATTTACATCTATCCATGAACAACTCTGAACATGGATGGTGGGGAAGTGA 2261
 2071 -----CGTGGTTGGAGGGAAGTAC 2090
 2262 GAACATTTACAATCCAGGAAGAAATGACGTATTTTAAAGAGAAATTTACGTCACACTTACCGGG 2321
 2091 GGATTTACCAATCCAAAGAGGAGATGACGTATTTCAAAGAAATTTATGTCACACTACAGG 2150
 2322 GACTTTTAAATGAGTGTATCCGAGTATTTATATCAAAAAATAGGAGAGTCGGAATTTAAA 2381
 2151 TACCTTTGATGAGTGTATCCAACTTATATCAAAAAATAGATGAGTCGAAATTTAAA 2210
 2382 AGCTTATCTCGCTACCAATTTAAGAGGATATTTGAAGATAGTCAAGATTTAGAGATATA 2441
 2211 ACCCTATCTCGTTTCAATTTAAGAGGATATTCAGGATAGTCAAGACTTAGAAATCTA 2270
 2442 TTTGATTCGTTTAAATCGAAACATGAACATTTGATTTCCAGGTACCGAGTCCGATG 2501
 2271 TTTGATCCGCTATTAATGCAAAACACGAAACGTAATTTGCTAGTAGTACGGTCTTTATG 2330
 2502 GCGCTTTTCAGTTGAAAGCCCAATTCGAAGGTGCGGAGAACCGGAATCGATGCGCACCA 2561

2331 GCCGCTTCAGTCCAAAGTCCAATCAGAAAGTGTGGAGAACCGAATCGATGCGGCCACA 2390
 2562 TTTTGAATGAATCCCTGATCTAGATTTGTTCTCGAGAGATGGAGAAAATGTGCGCATCA 2621
 2391 CTTTGAATGAATCCCTGATCTAGATTTGTTCTCGAGAGACGGGAAAATGTGCGCATCA 2450
 2622 TTCCCATCAATTTCTCTTTGGATATTGATATTGGATGACAGACTTTCATGAGAAATCTAGG 2681
 2451 TTGCGATCAATTTCTCTTTGGACATTTGATTTGGATGTACAGACTTAATTCAGGACTTAGA 2510
 2682 CGTGTGGTGGTATTCAGATTTAAGACGCAAGAGGTCTATGCAAGACTAGGGAATCTGGA 2741
 2511 TGTATGGGTGATTTCAAGATTAAAGCGCAAGATGGCCATGCAAGACTAGGAATCTAGA 2570
 2742 ATTTATTGAAGACAAACCATTTATTAGGAGAACACTCTCTCGTGTGAGAGACGAGAA 2801
 2571 GTTTCTCGAAGAAACCATTTAGTCGGGGAAGCACTAGCTCGTGTGAAAAGAGCAGAA 2630
 2802 AAAATGGAGACAAACGCTGAAAAAATACTAATTTGGAAACAAACAGAGTATATACAGAGC 2861
 2631 AAAATGGAGAGTAACGTTGAAAAATTTGGAAATTTGGAAACAAATATTGTTTATAAGAGC 2690
 2862 AAAAGAGCTGTGGATCTTTTATTGTTAGATTTCTCAATATAATAGATTACAAGCGGATAC 2921
 2691 AAAAGAAATCTGTAGATGCTTTATTGTTAAACTCTCAATATGATCAATTTACAAGCGGATAC 2750
 2922 AAACATTTGGCATGATTCATCGCGCAGATAAATCTGTTTCATCGAATTCGAGAGCTTATCT 2981
 2751 GAATATTTGCGCATGATTCATCGCGCAGATAAATGTTTCATAGAAATTCGGGAAGCGTATCT 2810
 2982 GTCAGAAATATCTGTTATCCCGGTGTAAATCGGAAATTTTGAAGAAATTAGAAGGTGCG 3041
 2811 TCAGAGTTATCTGTGATTCGCGGTGTAATGTAGACATTTTCGAAGAAATTAAGAGGCG 2870
 3042 CATTTACATGCAATCTCCCTATACGATGCGAAGAAATGTCGTTTAAATCGTGAATTTTAA 3101
 2871 TATTTTCACTGCAATCTCTCTATATGATGCGAAGAAATGTCATTTAAACCGGTGATTTCAA 2930
 3102 TAATGATTTAGCATGCTGGAAATGTAAGGGCATGTAGATGT---ACAACAGAGCCATCA 3158
 2931 TAATGGCTTATCATGCTGGAAACGTAAGGGCATGTAGATGTAGAGAACAAACACCA 2990
 3159 CCGTTCCTGCTCTTTGTTATCCAGAAATGGAAGCAGAGTGTCAAGACAGTTCGCGTCTG 3218
 2991 CCGTTCGGTCTCTTTGTTTCCGGAATGGGAAGCAGAGTGTCAAGAAATTCGTTGCTG 3050
 3219 TCCGGGCGTGGCTATATCTCCGTGTCAAGCGTACAAAGAGGATATCGAGAGGTTG 3278
 3051 TCCGGGTGCTGGCTATATCTCTGTCACAGCGTACAAAGGGGATATCGGAAGGTTG 3110
 3279 TGTAAACGATCCATGAAATCGAGAACAAATACAGACGAACTAAAATTTTAAACACTGTGAAGA 3338
 3111 CGTAACCAATTCATGAGATCGAGAACAAATACAGACGAACTGAGTTTATGCAACTGCGTAGA 3170
 3339 AGAGGAAGTGTATCCCAACGGATACAGAACGTCGTAATGATTATATCTGCACACCAAGGTAC 3398
 3171 AGAGGAAGTGTATCCCAACCAACACCGTAACTGTAATGATTATATCTGCAAAATCAAGAAGA 3230
 3399 A-----GCAGTATGTAATTTCCCGTAAATGCTGATGAGGATGCAATGAAAGTTGATAC 3452
 3231 ATACGGGGTGCCTACACTTTCCCGTAAATCGTGGATATGACGAACTTTATGGAAGCAATTC 3290
 3453 TACAGCATCTGTTTAAATTTTACAAACCGCTTATGAAGAAAGAAACGCTATACAGATGTACCAAG 3512
 3291 TTCTGTACCAAGCTGATTTATGCGGTGAGTCTATGAAGAAATAATCGTATACAGATGACGAG 3350
 3513 AGATAATCATTTGTGAATATGACAGAGGATGTGAATTTATCCCACTACAGCTGGTTA 3572
 3351 AGACAATCTCTTGTGAATCTAAACAGAGGATATGGGATTTACACCACTACAGCTGGCTA 3410
 3573 TATGACAAAGAAATTAGAATATCTTCCAGAAACCGATAGGTATGATTTGAGATTGAGAG 3632

Db 3411 TGTGACAAAGAAATTAGAGTACTTCCAGAAACCGATAAGATGATGGATTGAGATCGGAGA 3470

Qy 3633 AACGGAAGGAAGTTATTGAGACGCGTGGAAATTAAGTCTTATGAGGAA 3684

Db 3471 AACGGAAGGAACATTCTCGTGGAGCAGCGTGAATTAAGTCTTATGAGGAA 3522

RESULT 10

US-09-873-873-25

; Sequence 25, Application US/09873873

; Patent No. US20020064865A1

; GENERAL INFORMATION:

; APPLICANT: Malvar, Thomas

; APPLICANT: Gilmer, Amy Jelen

; TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad-Spectrum S-Endotoxins

; FILE REFERENCE: MEMO:210--2

; CURRENT APPLICATION NUMBER: US/09/873,873

; CURRENT FILING DATE: 2001-08-20

; PRIOR APPLICATION NUMBER: US 09/253,341

; PRIOR FILING DATE: 1999-02-19

; PRIOR APPLICATION NUMBER: US 08/922,505

; PRIOR FILING DATE: 1997-09-03

; PRIOR APPLICATION NUMBER: US 08/754,490

; PRIOR FILING DATE: 1996-11-20

; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 25

; LENGTH: 3534

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Hybrid Delta-Endotoxin

; NAME/KEY: CDS

; LOCATION: (1)...(3531)

US-09-873-873-25

Query Match 38.0%; Score 1402; DB 9; Length 3534;

Best Local Similarity 65.7%; Pred. No. 0;

Matches 2243; Conservative 0; Mismatches 1070; Indels 99; Gaps 10;

Qy 285 TCAGTGGGAAATTTCTAGAACATGTCGAAACATTTAATAATCAACAAATAACAGAAA 344

Db 213 TCAATGGAGCATTTCTTGACAAATTGAACGTTAATTAACAAAGAAATAGAAGATT 272

Qy 345 TGCTAGGAATACGGCACTTGCTCGATTACAGGTTTAGGAGATTCTTTTAGAGCCTATCA 404

Db 273 CGCTAGGAACCAAGCCATTTCTAGATTAGAAGGACTAAGCAATCTTTATCAAAATTTAGC 332

Qy 405 ACAGTCACTGGAAGATTGGCTAGAAAACCGGTGATGATGCAAGACGAGAGAGTGTCTTTA 464

Db 333 AGAATCTTTTAGAGAGTGGGAAGCAGATCCTACTAATCCAGCAATTAAGAGAGAGATGCG 392

Qy 465 TACCAATATATAGCCTTAGAATCTGATTTCTTAATGCGATGCGCTTTTCGCAATTAG 524

Db 393 TATTCAATTCANTGACATGAACAGTGCCCTTAACACCGCTATTCCTCTTTTGGAGTTCA 452

Qy 525 AAACCAAGAAAGTTCATTTAATGATGATGCTCAAGCTGCAAAATTTACACCTATTATT 584

Db 453 AATATTACAGTTCCTCTTTATCAGTATATGTTCAAGCTGCAAAATTTACATTTATCAGT 512

Qy 585 ATTGAGAGATGCTCTCTTTTGGTGTAGTGAATTTGGGCTTACATCGCAGGAAATTCACG 644

Db 513 TTTGAGAGATGTTTCAGTGTTTTGACAAAGGTGGGATTTGATGCCGCACTATCAATAG 572

Qy 645 TTATTATGAGCGCAAGTGGNACAAACGAGAGATTTATCCGACTATTTCGCTAGAAATCGTA 704

Db 573 TCGTTAATAAGATTAACTAGGCTTTATTGGCAACTATACAGATCATGCTGTACGCTGGTA 632

Qy 705 TAATACAGGTCTAAATAGCTTGAGAGGCAAAATGCGCAAGTTGGGTGCGTTATAATCA 764

Db 633 CAATACGGGATTAGAGGTGTATGGGACCGGATTTCTAGAGATTGGATAGATATAATCA 692

Qy 765 ATTCGCTAGAGATCAACGTTAGGGGTATTAGATTCTAGTGGCACTATTCCCAAGCTATGA 824

Db 693 ATTTAGAAAGAAATTAACACTAAGTATTAGATATCGTTCTTCTATTTCGAACTATGA 752

Qy 825 CACTCGCACTTATCCCAATAAATACGAGTGTCTAGTTAAACAGGGAAGTTTATACAGAGC 884

Db 753 TAGTAGAACGTAATCCAAATTCGAACAGTTTCCCAATTAACAAGAGAAATTTATACAAACC 812

Qy 885 A--ATTGGAGCAACAGGGGTAATATATGCGAAGTATGAATTTGGTATATAATAATATGCACT 942

Db 813 AGTATTAGAAAAATTTTGTATGTTATTTTTCAGGGCTCGGCTCAGGCAATGAAGAAGTAT 872

Qy 943 TCGTTTTTCGCTATAGAGACTGCGGTTATTCGAAGCCCGCATCTACTTGTATTTTCTAGAA 1002

Db 873 TAGAGTCCCAATTTGATGATATCTTAACAGTATTAACCAATCTATACGGATGCTCATAG 932

Qy 1003 CAACCTTACAATTTTTCAGCTTTCATCAGATGGAGTGTCTACTAGGCATATGACTTACTGG 1062

Db 933 GGGTTATTATTATTTGGTCAGGGCATCA-----AATAATGCTCTCTCTGTAGGTT 983

Qy 1063 GGGGGGCAACAATTTCAATCTCGGCCAATAGGAGGCGGATTAATATCTCAACGATGGG 1122

Db 984 TTCGGGGCCAGAATTTCACTTTTCGCTATATGGAACCTATGGA-----ATGCA 1032

Qy 1123 TCTACCAATACTTCTTATTATCTGTAAAGATTATCAATTTCTCTCGAGACGTATATTGG 1182

Db 1033 GCTCCACAACAGTATTGTGTCTCAACTAGTCAGGGCGGTATAGAACATTTATCGTCC 1092

Qy 1183 ACTGAATCATATGCAAGAGTCTTCTATGGGAAATTTTACCTTGAACCTATTTCATGGTGT 1242

Db 1093 ACTTTATATAGAACCTTTTAAATATAGGGATAAATAATCAACAATCTCTGTTCTTGAC 1152

Qy 1243 CCTACTGTTAGATTTAATTTTAGAACCTCCTCAGAAATCTTTTGAAGAGGTACTGCTAAC 1302

Db 1153 GGGAC-----AGAAATTTGCTTATGGAACCTCTCAAAATTTGCCATCCGCTGTATACAGAA 1208

Qy 1303 TATAGTCAACCTTATGATCACTGGGCTTCAATTAAGAGTTTCAAGAACTG-AAATACC 1361

Db 1209 AAGCGGAACCGGTAGATTTCGCTGGATGAAATACCGCCACAGAAATCAACGTCGCCACTAG 1268

Qy 1362 ACCAGAAACCAACAGAACGACAAATATGAATCATATATAGTATCATAGTTATCTCATAGG 1421

Db 1269 GCAAGGATTAGTATCGATGATTAAGCCATGTTCAATGTTTCGT-----TCAGGCTTAG 1322

Qy 1422 GCTCATTTCAATCTAGGTTGCAATGATGATGATGATGATGATGATGATGATGATGATGATG 1481

Db 1323 TAATAGTAGTGTAGTATAATTAAGAGCTCCAAATGTTTCTTTGGACGCAACCGTAGTCAAC 1382

Qy 1482 TCGTACAAATACCAATTTAGTTTCAATGATGATGATGATGATGATGATGATGATGATGATG 1541

Db 1383 CCCTACAAATACCAATTTAGTCCGAGAGGATTTACTCAAAATACCATTGGTAAAGACATAC 1442

Qy 1542 CCTTAATTCAGGTACCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1601

Db 1443 ACTTCAGTCACTATCTGTTAGAGGCGCGGTTTACGGGAGAGATATCTTCG 1502

Qy 1602 AACTAACGTTTAAATGTTAGTGTATGATGATGATGATGATGATGATGATGATGATGATG 1661

Db 1503 ACAGAACAGTGGAGGACCAATTTGCTTATGTTTAAATATAATTAATTAATTAATTAATTA 1562

Qy 1662 GCGGTATCGGTGAGAGTTCGTTATGCTGTTTCTCAACAAATGCTCTGAGGGTAACTGT 1721

Db 1563 AAGGTATTCGTGCAAGAAATACGCTATGCTCTACTACAAATCTAAGAAATTTACGTAACGG 1622

Qy 1722 CGGAGGAGTACTTCTTTCATCAAGGATTTCCCTAGTACTATGATGATGATGATGATGATG 1781

Db 1623 TGCAAGTGAACGATTTTTCGCTGATTTTACAAACAAATGATGATGATGATGATGATG 1682

Qy 1782 GACATCTCAATCAATTTAGATTTGAGAAATTTCTGTAGGTATTAGTGTGATGATGATG 1841

Db 1683 AACATTCCAATCTTTTAGTTACGCAACTAATTAATACAGCTTTTACATTTCCCAATGAGCA 1742

Qy 1842 AACTGCT---GGAATAAGTATAGTAAATATGCGAGGTAGACAAACGTTTCTCATTGTATA 1898

Db 1743 GAGTAGTTTACAGTAGGTCGTGATCTTTTAGTTTACAGGAATGAAGTTTATATAGACAG 1802
 Qy 1899 AATTGAATTCATTCCTCAATTAATCTGCAACTTTCGAGCAGATACAGTTTGAAGGGCGCA 1958
 Db 1803 ATTITGAATTTGATTTCCAGTTACTGCAACATTTGAAGCAGATATGATTTGAAGAGCACA 1862
 Qy 1959 AGAGCGGCTGAATGCTCTGTTTACTAATACGAATCCAAAGAGATGGAAGATGGAACAGATGTAC 2018
 Db 1863 AAAGCGGCTGAATGCTGTTTACTTCTAATACCAATAGGNTAAACAGATGTAC 1922
 Qy 2019 AGATTATCATTTGATCAAGATTCATCAATTTAGTGGCGTGTATTCGATGAATTCGCTT 2078
 Db 1923 GGATTATCATATTGATCAAGATTCATCAATTTAGTGGATTTTATCAGATGAATTTGTCT 1982
 Qy 2079 AGATGAAGAGAGAAATTTACTTGAAGACTGCAATATGCGAAGCACTCAGTATGTAAG 2138
 Db 1983 GGATGAAGAGAGAAATTTGTCGAGAAAGTCAAAATGCGAAGCACTCAGTATGAGCG 2042
 Qy 2139 AAACCTTACTCCAAGATCCAAACTTTCATCATCAATTAAGCAACCAAGCTTCATATCTAC 2198
 Db 2043 GAATTTACTTCAAGATCCAACTTCAAGGATCAATAGGCAACTAGAC----- 2091
 Qy 2199 TAATGAGCAATCGAATTTTCATCTATCTATCCATGAACAACTTGAACATGATGGTGGGAAG 2258
 Db 2092 -----CGTGGTTGAGAGGAAG 2108
 Qy 2259 TGAGCAATTTACATCCAGGAGGAATGACGTATTTAAGAGAAATTTACGTCACTACCTACC 2318
 Db 2109 TAGCGATTTACCATCCAAAGAGAGATGACGTATTTCAAGAAATTTATGTCACTACCTACC 2168
 Qy 2319 GGGGACCTTTTAATGAGTGTATCCGAGCTATTTATATCAAAAAATAGGAGAGTCGGAAT 2378
 Db 2169 AGGTACCTTTTATGAGTGTATCCAACTATTTGTATCAAAAAATCGATGAATCAAAAT 2228
 Qy 2379 AAAAGCTTTATCGCTACCAATTAAGAGGGTATTTGAAGAGATGTCAGAAATTTAGAT 2438
 Db 2229 AAAAGCTTTTACCGCTTATCAATTAAGAGGGTATTCGAAGAGATGTCAGAAATTTAGAAAT 2288
 Qy 2439 ATATTGATTCGTTTATTAATCGAAACATGAACATTTGATGTTCCAGGTACCGAGTCCGT 2498
 Db 2289 CTATTTAATTCGCTACAAATCGAAACATGAACAGTAAATGTGCCAGGTACGGGTTCCTT 2348
 Qy 2499 ATGCCCGCTTTTACGTTGAAAGCCCAATCGGAAGTGGGAGAACCGGAATCGATGCGCACC 2558
 Db 2349 ATGCCCGCTTTTACGCCCAAGTCCAATCGGAAGTGGGAGAGCCGAATCGATGCGCGCC 2408
 Qy 2559 ACATTTGAATGGAATCCTGATCTAGATTTGTTCTGCGAGAGATGGAGAAATTTGTCGCGCA 2618
 Db 2409 ACACCTTGAATGGAATCCTGACTTAGATTTGTTCTGTTAGGGATGGAGAAAGTGTGCCCA 2468
 Qy 2619 TCATTCCTCATCTTCTTTTGGATATTGATATTGGATGACACAGCTTGCATCAGAACTCT 2678
 Db 2469 TCATTCCTCATCTTCTTTTGGATATTGATATTGGATGACACAGCTTAAATGAGGACCT 2528
 Qy 2679 AGCGGTGCGGTGGTATTTCAAGATTTAAGACGCGAGAGGTTCATGCAAGACTAGGGGAATCT 2738
 Db 2529 AGGTGATGCGGTGATCTTTAAGATTAAGACGCAAGATGGCAGCAAGACTAGGGGAATCT 2588
 Qy 2739 GGAATTTATGAAGAGAAACCATTTATGAGAGAGCACTGCTCTCGTGTGAAGAGAGCAGA 2798
 Db 2589 AGAGTTTCTCGAAGAGAAACCATTTATGAGAGAGCGCTAGCTGCTGTGGAAGAGCGGA 2648
 Qy 2799 GAAAAATGAGAGACAAACGCGAAGCTGCAATTTGGAACCAAAACGAGTATATACAGA 2858
 Db 2649 GAAAAATGAGAGACAAACGCGAAGCTGCAATTTGGAATGGAACCAAAATTCGTTTATTAAGA 2708
 Qy 2859 GGCAAAAGAGAGCTGTGGATGCTTTATTTGATGATTTCTCAATATAATAGATTACAAGCGGA 2918
 Db 2709 GGCAAAAGAGATCTGATGATGCTTTATTTGAACTCTCAATATATGATCAATTAACAAGCGGA 2768
 Qy 2919 TACAACATTTGGCATGATTTATCGGCGAGATAAATCTGTTTCATCGAATTCGAGAGGCTTA 2978
 Db 2769 TACGAATTTGCCATGATTTATCGGCGAGATAAATCGTGTTCATAGCATTCGAGAAAGCTTA 2828

Qy 2979 TCTGTGACGAATTTATCTGTTATCCGGGTGTAAATCGGAAATTTTGAAGAAATTTAGAAAGG 3038
 Db 2829 TCTGCTGAGCTGTCTGTGATTCGGGTGTCAATCGGCTATTTTGAAGAAATTTAGAAAGG 2888
 Qy 3039 TCGCATTTATCAGTCGAATCTCCCTATATACGATGCGAGAAATGTCTGTTAAAAATGTTGATTT 3098
 Db 2889 GCGTATTTTACATGCAATCTCCCTATATGATGCGAGAAATGTCTATAAAAATGTTGATTT 2948
 Qy 3099 TAATATGATTTAGCATGCTGGAATGTAAAGGGCATGTAGATGT---ACAACAGAGCCCA 3155
 Db 2949 TAATAATGGCTTATCTGCTGGAACTGAAAGGGCATGTAGATGTAGAGAAACAAACAA 3008
 Qy 3156 TCACCGCTTCTGCTCTGTTTATCCAGAAATGGGAAGCAGAGTGTCAACAGCAGTTCGCGT 3215
 Db 3009 CCAACGTTTCGTCCTTGTGTTCCGGAATGGGAAGCAGAGTGTCAAGAAATTTGTTGT 3068
 Qy 3216 CTGTCGGGGCGGTGCTATATCTCCGTGTCAAGCGGTACAAAGAGGGATATGAGAGGG 3275
 Db 3069 CTGTCGGGGCGGTGCTATATCTCTGTCACAGCGTACAGAGGGATATGAGAAAG 3128
 Qy 3276 TTGTTGTAACGATCCATGAATCGAGAAACATACAGAGCACTAAAAATTTAAAACTGTGA 3335
 Db 3129 TTGCGTAAACCATTTCAATGAGATCGAGAAACATACAGAGCACTGAAGTTTAGCAACTGCGT 3188
 Qy 3336 AGAAGAGGAAGTGTATCCCAACGGATACAGAACTGTGAATGATTATCTGCACACCAAGG 3395
 Db 3189 AGAAGAGGAATCTATCCAAATTAACACGGTAACTGTGAATGATTATCTGTAATCAAGA 3248
 Qy 3396 TACAGCAGTATGTAATTTCCGCTAATCTGATATAGGATGTCATATGAAAGTTGATCTAC 3455
 Db 3249 AGAATACGGAGGTGCGT-----ACATCTCTGTAATCGAGGATATAACGAAGCTCTTC 3302
 Qy 3456 AGCATCTGTTAATTAACAAACCGACTTATGAGAGAAACGTTATACAGATGTCAGAGAGA 3515
 Db 3303 CGTACCAGCTGATTTATGCGCTAGTCTATGAAGAAAAATCGTATACAGATGGAGAGAGA 3362
 Qy 3516 TAATCATTTGAAATATGACAGAGGGTATGTGAATTTATCCACCTACCACTCGTTGTTATAT 3575
 Db 3363 GAATCTTTGTAATTTAAACAGGGGTATAGGNTATACGCCACTACCGTTGTTGTTATGT 3422
 Qy 3576 GACAAAGAAATTAGAATATCTCCAGAAACCGGATAAGGTATGGAATGAGATTGGAAGAAC 3635
 Db 3423 GACAAAGAAATTAGAATATCTCCAGAAACCGGATAAGGTATGGAATGAGATTGGAAGAAC 3482
 Qy 3636 GGAAGGAAAGTTTATTTAGACAGCGTGAATTTACTCTTATGAGAGGAATAG 3687
 Db 3483 GGAAGGAAATTTATCTGTGACAGCGTGAATTTACTCTTATGAGAGGAATAG 3534

RESULT 11

US-09-916-956A-25
 ; Sequence 25, Application US/09916956A
 ; Publication No. US20030017571A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Malvar, Thomas
 ; APPLICANT: Gilmer, Amy Jelen
 ; TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad-Spectrum S-Endotoxins
 ; FILE REFERENCE: MECO:2111--1
 ; CURRENT APPLICATION NUMBER: US/09/916,956A
 ; CURRENT FILING DATE: 2001-07-27
 ; PRIOR APPLICATION NUMBER: US 09/253,331
 ; PRIOR FILING DATE: 1999-02-19
 ; PRIOR APPLICATION NUMBER: US 08/922,505
 ; PRIOR FILING DATE: 1997-09-03
 ; PRIOR APPLICATION NUMBER: US 08/754,490
 ; PRIOR FILING DATE: 1996-11-20
 ; NUMBER OF SEQ ID NOS: 35
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 25
 ; LENGTH: 3534
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence

```

;
; FEATURE:
; OTHER INFORMATION: Hybrid Delta-Endotoxin
; NAME/KEY: CDS
; LOCATION: (1)..(3531)
US-09-916-956A-25

Query Match      38.0%; Score 1402; DB 10; Length 3534;
Best Local Similarity 65.7%; Pred. No. 0;
Matches 2243; Conservative 0; Mismatches 1070; Indels 99; Gaps 10;

Qy      285 TCAGTGGGAAATTTTCTTAGAACATGTGGAACAATTAATAATCAACAATAAACAAGAAA 344
Db      213 TCAATGGAGCGCAATTCCTGTGCAAAATGAAACAGTTAATTAACCAAGAATAGAAAGATT 272
Qy      345 TGCTAGGAATACGGCACTTGCTCGATTACAAGGTTTATAGGAGATTCCTTTAGAGCGTATCA 404
Db      273 CGCTAGGAACCAAGCCATTTCTAGATTAGAAGGACTAAGCAATCTTTATCAAAATTAGCG 332
Qy      405 ACAGTCACTTGAAGATTGGCTAGAAAACCGTGATGATGAAGAAGACGAGAAGTGTTCTTTA 464
Db      333 AGAATCTTTTAGAGAGTGGGAAGCAGATCCTTACTAATCCAGCATTAAGAGAAGAGATGCG 392
Qy      465 TACCCAAATATAGCCTTAGAATCTGATTTCTTAATGCGATGCGCTTTTCGCAATTAG 524
Db      393 TATTCAATTCAAATGACATGAACAGTGCCCTTACAACCGCTATTCCTCTTTTTCGAGTTCA 452
Qy      525 AAACCAAGAAGTTCATATTATTAATGCTATATGCTCAAGCTGCAAAATTTACACTATTATT 584
Db      453 AAATTATCAAGTTCCTCTTTTATCAGTATATGTTCAAGCTGCAAAATTTACATTTATCAGT 512
Qy      585 ATTGAGAGATGCTCTCTTTTGGTGTAGTAATTTTGGGCTTACATCGCAGGAAATTTCAACG 644
Db      513 TTTGAGAGATGTTTTCAGTGTTTTGCAAAAGGTGGGGATTTGATGCGCGCACTATCAATAG 572
Qy      645 TTATTATGCGGCCAAGTGGGAACAAACGAGAGATATTCCGACTATTTCGCTAGATGCGTA 704
Db      573 TCGTTATTAATGAATTTAACTAGGCTTTATTGGCACTTATACAGATCATGCTGTCACGCTGTA 632
Qy      705 TAATACAGGTTCTAAATAGCTTTGAGAGGGAACAATGCGCAAGTTGGGTGGCTTATAATATCA 764
Db      633 CAATACGGGATTAGAGCGTGTATGGGACCGGATTTCTAGAGATTGGATTAAGATATATATCA 692
Qy      765 ATTCGCTAGAGATCTAACGTTTGGGGTATTAGATCTTAGTGGAATTTCCCAAGCTATGA 824
Db      693 ATTTAGAAGAGAAATTAACACTAACTGATTAGATATGATGTTCTCTATTTCGGAACACTATGA 752
Qy      825 CACTCGCACTTATCCATAAATACGAGTGCTCAGTTTAAACAGGGAAGTTTATACAGAGCG 884
Db      753 TAGTAGAACGTTATCCAAATTCGAACAGTTTCCCAATTTAAACAGAGAAAATTTATACAAACCC 812
Qy      885 A--ATTGGAGCAACAGGGGTAAATATGCAAGTATGAATTTGGTATAATAATATGCACT 942
Db      813 AGTATTAGAAAATTTTGATGGTAGTTTTCGAGGCTTCGGCTCAGGGCATAGAAAGATAT 872
Qy      943 TCGTTTTTCGCTATAGAGACTGCGGTTTATCCGAAGCCGCACTACTTGTATTTTCTAGAA 1002
Db      873 TAGGAGTCCACATTTTGATGGATATACTTAAACAGTATAACCATCTATACGGATGCTCATAG 932
Qy      1003 CAACCTTACAATTTTATGACCTTTCATCATCGATGAGAGTGCTACTAGGCATATGACCTTACTGG 1062
Db      933 GGGTTATTATTATTGGTTCAGGGCATCA-----AATAATGGCTTCTCTCTGTGAGGGTT 983
Qy      1063 CGGGGGCACACAATTTCAATCTCGCCCAATAGGAGGCGGATTAATATCCTCAACGCAATGGG 1122
Db      984 TTGGGGGCGCAAGATTCACCTTTTCGCTATATGGAACTATGGGAA-----ATGCA 1032
Qy      1123 TCTACCAATACTTCTATTAAATCCTGTGAAGATTATCATTTCTCTCGAGAGCTATATTGG 1182
Db      1033 GCTCCACAACAACGATTATTGTGCTCAACTAGTTCAGGCGGTGATAGAACATTAATCGTCC 1092
Qy      1183 ACTGAATCATATGACGAGGTGCTTCTATATGGGGAATTTTACCTTTGAACCTTATTCATGGTGT 1242
Db      1093 ACTTTATATAGAAGACCTTTTAAATATAGGAGATAAATAATCAACAACTATCTGTCTTTGAC 1152

```

QY 2319 GGGACCTTTTAATGAGTGTATCCGAGTATTTATCAAAAAATAGGAGTCCGAAAT 2378
 Db AGGTACCTTTTATGAGTGTATCCGAGTATTTATCAAAAAATAGGAGTCCGAAAT 2378
 QY 2379 AAAAGCTTTATCTGCTACCAATTAAGAGGATATTTGAAGATAGTCAAGATTTAGAGAT 2438
 Db AAAAGCTTTATCCGCTTATCAATTAAGAGGATATTTGAAGATAGTCAAGATTTAGAGAT 2438
 QY 2439 ATATTTGATTTGATTAATGAGGAAATGAAATGATTTCCAGTACCGAGTCCGT 2498
 Db CTATTTATTTGCTTCAATGAGGAAATGAAATGATTTCCAGTACCGAGTCCGT 2498
 QY 2499 ATGCCCGCTTTTCACTTGAAGCCCAATCGGAAGTGCAGAAACCGAATCGATCGCAGC 2558
 Db ATGCCCGCTTTTCACTTGAAGCCCAATCGGAAGTGCAGAAACCGAATCGATCGCAGC 2558
 QY 2559 ACATTTTGAATGGAATCCTGATCTAGATTTGTTCTGCGAGATGGAAGAAATGTCGCGA 2618
 Db ACATTTTGAATGGAATCCTGATCTAGATTTGTTCTGCGAGATGGAAGAAATGTCGCGA 2618
 QY 2619 TCATTTCCATCATTTCTTTTGGATATTTGATTTGGAATGCACAGATTTGCATGAGATCT 2678
 Db TCATTTCCATCATTTCTTTTGGATATTTGATTTGGAATGCACAGATTTGCATGAGATCT 2678
 QY 2679 AGCGTGTGGTGTATTTCAAGATTTAAGACGCGAGGAAGTTCATCAAGACTTAGGGAATCT 2738
 Db AGCGTGTGGTGTATTTCAAGATTTAAGACGCGAGGAAGTTCATCAAGACTTAGGGAATCT 2738
 QY 2739 GGAATTTTGAAGAGAAACCATTTATGAGAGAGCATCTGCTGCTGAGAGAGAGAGA 2798
 Db GGAATTTTGAAGAGAAACCATTTATGAGAGAGCATCTGCTGCTGAGAGAGAGAGA 2798
 QY 2799 GAAAAAATGAGAGACAAACGTGAAAAATCAATTTGAAAAACCAACAGATATATACAGA 2858
 Db GAAAAAATGAGAGACAAACGTGAAAAATCAATTTGAAAAACCAACAGATATATACAGA 2858
 QY 2859 GCGAAAAAGAGCTGTGGATGCTTTATTTGAGATTTCTCAATATATATAGATTTACAAGCGGA 2918
 Db GCGAAAAAGAGCTGTGGATGCTTTATTTGAGATTTCTCAATATATATAGATTTACAAGCGGA 2918
 QY 2919 TACAAACATTTGGCATGATTTATGCGGAGATATAAATCTGTTTCATCGAATTCGAGAGGCTTA 2978
 Db TACAAACATTTGGCATGATTTATGCGGAGATATAAATCTGTTTCATCGAATTCGAGAGGCTTA 2978
 QY 2979 TCTGTCAAGATTTATCTGTTATCCCGGTGTAATGCGGAAATTTTCAAGATTTAGAGG 3038
 Db TCTGTCAAGATTTATCTGTTATCCCGGTGTAATGCGGAAATTTTCAAGATTTAGAGG 3038
 QY 3039 TCGCATTTATCACTGCAATCTCCCTATACGATGCGAGAAATGTCGTTAAAAATGCTGATTT 3098
 Db TCGCATTTATCACTGCAATCTCCCTATACGATGCGAGAAATGTCGTTAAAAATGCTGATTT 3098
 QY 3099 TATATATGATTTAGCATGCTGGATGTAAGAGGCGATGATGT---ACAAACAGAGCCA 3155
 Db TATATATGATTTAGCATGCTGGATGTAAGAGGCGATGATGT---ACAAACAGAGCCA 3155
 QY 3156 TCACCGTTCTGCTGTTATCCAGAAATGCGAAGAGAGAGTGTCAAGAGCTTCCGCT 3215
 Db TCACCGTTCTGCTGTTATCCAGAAATGCGAAGAGAGAGTGTCAAGAGCTTCCGCT 3215
 QY 3216 CTGTCGCGGCGTGGCTATATCTTCCGTGTACAGCGTACAAAGAGGATATGAGAGGG 3275
 Db CTGTCGCGGCGTGGCTATATCTTCCGTGTACAGCGTACAAAGAGGATATGAGAGGG 3275
 QY 3276 TTGTTTAAACCATTCATGAGATTCGAGAAATACAGAGCAATTAATTAAGCTGTA 3335
 Db TTGTTTAAACCATTCATGAGATTCGAGAAATACAGAGCAATTAATTAAGCTGTA 3335
 QY 3336 AGAAGAGGAAGTGTATCCAGCGGATACAGAAACGTGTAATGATTTACTGCAACCAAGG 3395
 Db AGAAGAGGAAGTGTATCCAGCGGATACAGAAACGTGTAATGATTTACTGTAATCAAGA 3395
 QY 3396 TACAGCATGATGTAATTTCCCGTAATGCTGGATATGAGGATGCAATGAAAGTTGATCTAC 3455

Db 3249 AGAATACGAGGTGCGT-----ACATTTCTCTGTAATCGAGGATATAACGAAGTCTCTTC 3302
 QY 3456 AGCATCTGTTTAATTAACAAACCGACTTATGAAGAGAAACGATATACAGATGTACGAAGAGA 3515
 Db 3303 CGTACCAGCTGATTTGCGTCTATGAAGAAAAATCGTATACAGATGGAAGAGAGA 3362
 QY 3516 TAATCATTTGGAATATACAGAGGCTATGTAATTTATCCACCACTACCGACTGCTTATAT 3575
 Db 3363 GAATCTTGTGAATTTAAACAGAGGATATAGGATTTACACGCCACTACCGATGTTATGT 3422
 QY 3576 GACAAAAGAAATTAAGATTAATTTCCAGAAACCGATATAGGATTTGAGATTTGAGAAAC 3635
 Db 3423 GACAAAAGAAATTAAGATTAATTTCCAGAAACCGATATAGGATTTGAGATTTGAGAAAC 3482
 QY 3636 GGAAGGGAAGTATTTGTAAGACAGCGTGGAAATTTACTCTTTATCGGGAATAG 3687
 Db 3483 GGAAGGGAACATTTATCGTGGACAGCGTGGAAATTTACTCTTTATCGGGAATAG 3534

RESULT 12
 US-09-997-914-25
 ; Sequence 25, Application US/09997914
 ; Publication No. US20030119158A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gilmer, Amy Jelen
 ; TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad Spectrum d-Endotoxins
 ; FILE REFERENCE: 11792.0215.DVUS01 MECO:215--1
 ; CURRENT APPLICATION NUMBER: US/09/997,914
 ; CURRENT FILING DATE: 2001-11-30
 ; PRIOR APPLICATION NUMBER: US 09/261,040
 ; PRIOR FILING DATE: 1999-03-02
 ; PRIOR APPLICATION NUMBER: US 08/754,490
 ; PRIOR FILING DATE: 1996-11-20
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 25
 ; LENGTH: 3534
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Hybrid Delta-Endotoxin
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(3531)
 ; US-09-997-914-25

Query Match 38.0%; Score 1402; DB 10; Length 3534;
 Best Local Similarity 65.7%; Pred. No. 0;
 Matches 2243; Conservative 0; Mismatches 1070; Indels 99; Gaps 10;

QY 285 TCAGTGGGAATTTTCTAGAACATGTCGAACAACTTATAAATCAACAAATAACAGAAA 344
 Db 213 TCAATGGAGCGAATTTCTGTACAAATGAACTTAATTAACCAAGAATAGAGATTT 272
 QY 345 TGCTAGGAATACCGCACTTGTCTCGATTACAAGGTTTAGGAGATTTCTTTAGAGCTTATCA 404
 Db 273 CGCTAGAACCAAGCCATTTCTAGATTAGAGGACTAAGCAATCTTTATCAAAATTTACGC 332
 QY 405 ACAGTCACTTGAAGATTTGGCTAGAAAACCGTGTATGATGCAAGAACGAGAGAGTGTCTTTA 464
 Db 333 AGAATCTTTTAGAGAGTGGGAAGCAGATCCTACTAATCCAGCATTAAGAGAGAGATGCG 392
 QY 465 TACCAATATATAGCTTAGAATCTGATTTTCTTAATGCGATCCGCTTTTCGCAATTTAG 524
 Db 393 TATTCAATTAATGACATGAACAGTCCCTTACACCGCTATTTCTCTTTTTCGAGTTCA 452
 QY 525 AAACCAAGAGTTTCCATTTATTAATGTTATATGCTCAAGCTGCAAAATTTACACCTATTATT 584
 Db 453 AAATTTCAAGTTCTCTTTTATCAGTATATGTTCAAGCTGCAAAATTTACATTTATCAGT 512
 QY 585 ATTGAGAGATGCTCTCTTTTTCGTTAGTGAATTTGGCTTACATCGCAGAAATTTCAACG 644

Db 513 TTTGAGAGATGTTTCAGTGTTTGGACAAAGGTGGGATTTGATCGCGGACTATCAATAG 572
Qy 645 TTATTATGAGCCGCAAGTGGACAAACGAGAGATTAATTCGACATTAATTCGCTAGATGGTA 704
Db 573 TCGTTAATGATTAATACTAGGCTTAATGGCAACTATACAGATCATGCTGACGCTGGTA 632
Qy 705 TAATACAGGTCTAATAGCTTGAGAGGGACAAATGCCCAAGTTGGGTGGCTTAATCA 764
Db 633 CAATACGGGATTAGAGCGGTGATGGGACCGGATCTAGAGATTGGATAAGATATAATCA 692
Qy 765 ATTCGCTAGAGATCTAACGTTTAGGGTATTAGATCTAGTGCCACTATTCCCAAGCTATGA 824
Db 693 ATTTAGAAGAGAAATTAACACTACTGTATTAGATATCGTTCTCTATTTCGCACTATGA 752
Qy 825 CACTCGCATTAATCCAATAAATACGAGTCTCAAGTAAACAGGGAAGTTTATACAGACGC 884
Db 753 TAGTAGAACGTTATCCAAATTCGAAACAGTTTCCCAATTAACAGAGAAATTTATACAAACCC 812
Qy 885 A--ATTGGAGCAACAGGGTAAATATGCGCAAGTATGAATGGTATATAATATGCACT 942
Db 813 AGTATTAGAAAATTTGATGGTAGTTTTCGAGGCTCGGCTCAGGGCATAGAAAGATAT 872
Qy 943 TCGTTTTCCGCTATAGAGACTGCGGTTATCCGAAGCCGCACTACTGTTGATTTTCTAGAA 1002
Db 873 TAGGAGTCCACATTTGATGGATATCTTAACAGTATAACCACTATACGATGCTCATAG 932
Qy 1003 CAACCTTACAAATTTTACACTTCATCAAGTGGAGTGTCTACTAGGCATATGACTTACTGG 1062
Db 933 GGGTTATTATTATTTGGTCAGGGCATCA-----AATAATGCTTCTCCTGTAGGGTT 983
Qy 1063 CGGGGGCACACAATCAATCTCGGCCAATAGGAGCGGATTAATATCTCAACGCAATGGG 1122
Db 984 TTCGGGGCCAGAATTCATTTTCGCTATATGGAACATATGGGA-----ATGCA 1032
Qy 1123 TCTACCAATATCTTATTAATCTGTGAAGATTATCAATCTCTCTCGAGAGGTATATGG 1182
Db 1033 GCTCCACACACATGTTTGTCTCACTAGGTGAGGGGTGTATAGAACATTAATCTGCTC 1092
Qy 1183 ACTGAATCATATGACGAGGTGCTTCTATGGGAATTTACCTTGAACCTATTTCAATGTTGTC 1242
Db 1093 ACTTTATAGAACACCTTTTAATATAGGGATAAATAATCAACAACATCTCTGTTCTTGAC 1152
Qy 1243 CTTACTGTTAGATTAATTTTAGAACCTCAGAAATCTTTTGAAGAGGTACTGTCTAAC 1302
Db 1153 GGGAC-----AGAATTTGCTTATGGAACCTCTCAAAATTTGCCATCCGCTGTATACAGAA 1208
Qy 1303 TATAGTCAACCTATGATGACCTGGGCTCAATTTAAAGATTCCAGAACTG-AAATTACC 1361
Db 1209 AAGCGGAACGGTAGATTCGCTGGATGAATATACCGCCACAGAAATCAACGTCGCCACTAG 1268
Qy 1362 ACCAGAAACACAGAACGACCAATTAATGAAATCATATAGTATAGTATATCTCAATAGG 1421
Db 1269 GCAAGGATTTAGTCAATCGATTAAAGCAATGTTCAATGTTTCGT-----TCAGGCTTTAG 1322
Qy 1422 GCTCATTTCAATCTAGGTGCAATGATACAGATATATCTTTGGACCGACCGTAGTGAGA 1481
Db 1323 TAATAGTAGTGTAAAGTAAATAGAGCTCCAATGTTTTCTTGGACGACCGTAGTGCAAC 1382
Qy 1482 TCGTACAAATACCAATTAGTTCAGATAGCATACCAATTAACCAATACCAATGCTTAAATCA 1541
Db 1383 CCCTACAAATACAAATGATCGGAGAGATTAATCAATACCAATACCAATGTTGTAAGACATAC 1442
Qy 1542 CTTTAAATTCAGGTACTCTGTAGTTCAGTGGGCCAGGATTTACAGAGGGGATATAATCCG 1601
Db 1443 ACTTCAGTCAGTACTACTGTTGAAGGGCCCGGTTTACGGGAGAGATATCTTCTCG 1502
Qy 1602 AACTAACGTTAATCGGTAGTGTACTAAGTATGGGTCTTAAATTTTAATATACATCAATACA 1661
Db 1503 ACGAAACAGTGGAGGACCAATTTGCTTATCTATTTGTTTAAATATAATTAATGGCAATTA 1562
Qy 1662 CGGTTATCGGTAGAGTTGTTATGCTGTTCTCAAAACATGCTCTCAGGGGTAACTGT 1721
Db 1563 AAGGTATCGTCAAGAATACGCTATGCTCTACTACAAATCTAAGAAATTTACGTAACGGT 1622

Qy 1722 CGGAGGAGTACTACTTTTGTATCAAGGATTCCTCTAGTACTATAGTGCAAATAGATCTTT 1781
Db 1623 TGCAGGTGAACGGGATTTTGTCTGTTCAATTTAAACAAACAAATGATACCGGTGACCCATT 1682
Qy 1782 GACATCTCAATCAATTTAGATTTTCAGAAATTTCTGTAGGTATTTAGTGCATCTCGCAGTCA 1841
Db 1683 AACATCCAAATCTTTTAGTTACGCAACTATTAATACAGCTTTTATACATTTCCCAATGAGCCA 1742
Qy 1842 AACTGCT---GGAATAAGTATAAGTATAATATGCAAGGTAGACAAACGTTTTCATTTGTATAA 1898
Db 1743 GAGTAGTTTTCACAGTAGTGTCTGATACTTTTAGTTTCAAGGAAATGAAGTTTATATAGACAG 1802
Qy 1899 AATTGAATTCATTTCCAAATTAATCTGCAACCTTCGAAAGCAAGATACGATTTAGAAAGGGGCA 1958
Db 1803 AATTGAATTTAGTTTCCAGTTACTGCAACATTTTGAAGCAGAAATATGATTTAGAAAGAGCACA 1862
Qy 1959 AGAGGCGTCAATGCTCTGTTTACTAATACGAATCCAAAGAGATTGAAACAGATGTGAC 2018
Db 1863 AAGGCGGTGAATGCGCTGTTTCTTCTATAACCAATAGGGATATAAACAGATGTGAC 1922
Qy 2019 AGATTATCATATTGATCAAGTATTCCAATTTAGTGGCGTGTTTATTCGGATGAATTTCTGCT 2078
Db 1923 GGATTATCATATTGATCAAGTATCCAAATTTAGTGGATTGTTTATCAGATGAATTTTGTCT 1982
Qy 2079 AGATGAAAAGAGAGAAATTAATCTGGAAGGTGAATATTCGGAACGACTCAGTGTATGAAG 2138
Db 1983 GGATGAAAAGCGAGAAATTTGTCGAGAAAGTCAAAACATGCGAAGCGACTCAGTGTATGAGCG 2042
Qy 2139 AAATCTTACTCCAGATCCAACTTTCATCCATCAATAAAGCAACGACATTCATATCTAC 2198
Db 2043 GAATTTACTTCAAGATCCAACTTCAAGGATCAATAGGCAACTAGAC----- 2091
Qy 2199 TAATGAGCAATCGAAATTTACATCTATCCATGAACAATCTGAACATGAGTGGTGGGAG 2258
Db 2092 -----CGTGGTTGGAGAGAG 2108
Qy 2259 TGAGAACATTTCAATCCAGGAAGAAATGACGTATTTTAAAGAGAAATTCGTCACACTACC 2318
Db 2109 TAGCGATATTACCATCCAAAGAGAGATGACGTATTTCAAAGAAATTTATGTACACTACC 2168
Qy 2319 GGGGACTTTTAATGAGTGTATCCGAGTATTTATATCAAAATATAGGAGATCGGAAT 2378
Db 2169 AGGTACCTTTGATGAGTGTCTCAACATATTTGTATCAAAATATCGATGAATCAAAAT 2228
Qy 2379 AAAAGCTTATCTACGCTACCAATTTAAGAGGTATATTGAAGATAGTCAAGATTTTAGAGAT 2438
Db 2229 AAAAGCCTTTACCGTTTATCAATTTAAGAGGTATATCGAAGATAGTCAAGACTTTAGAAAT 2288
Qy 2439 ATATTTGATTCGTTATTAATCGGAACATGAAACATTTGGATTTCCAGGTACCGAGTCCGT 2498
Db 2289 CTATTTAATTCGCTACCAATGCAAAACATGAAACAGATAAATGTGCCAGGTACGGTTCCT 2348
Qy 2499 ATGGCGCTTTTCAGTTGAAGCCCAATCGGAAGTGGGAGAACCGAATCGATCGCGCAC 2558
Db 2349 ATGGCGCTTTTCAGCCCAAGTCCAATCGGAAGTGGGAGAGCCGAATCGATCGCGCC 2408
Qy 2559 ACATTTTGAATGGAATCTGATCTAGATTTCTCTCGAGAGATGGAGAAAATGTGGGCA 2618
Db 2409 ACACCTTGAATGGAATCTGATTTAGATTTGTTGTTAGGATGGAGAAAGTGTGGCCA 2468
Qy 2619 TCATTTCCCATCTTTCTTTTGGATATTTGATATTTGGATGCAAGACTTGCATGAGAAATCT 2678
Db 2469 TCATTTCCCATCTTTCTTTTGGATATTTGATGATGATGATGATGATGATGATGATGATGAT 2528
Qy 2679 AGGCTGTGGTGGTATTCAAGATTAAGACGAGAAAGTTCATGCAAGACTTAGGGAATCT 2738
Db 2529 AGGTGTATGGGTGATCTTTAAGATTAGACGCAAGATGGGCAACGCAAGACTTAGGGAATCT 2588
Qy 2739 GGAATTTATTTGAAGAGAAACCATTTATTTAGGAGAGCACTGTCTGCTGTGAAGAGAGAGA 2798
Db 2589 AGAGTTTCTCGAAGAGAAACCATTTAGTAGGAGAGCGCTAGTCTGTGTGAAGAGAGCGGA 2648

```

Qy 2799 GAAAAATGGAGACAAACCTGTAAGAACTCAATTTGAAACAAACAAACGAGTATATACAGA 2858
Db 2649 GAAAAATGGAGACAAACCTGTAAGAACTCAATTTGAAACAAACAAACGAGTATATACAGA 2708
Qy 2859 GGCAGAGAGAGCTGGAGTCTTTATTTGAGATCTCAATATATATAGATACAGCGGA 2918
Db 2709 GGCAGAGAGAGCTGGAGTCTTTATTTGAGATCTCAATATATATAGATACAGCGGA 2768
Qy 2919 TACAAACATTTGGCATGATTCATCGGCGAGATATACTTTGTTTCATCGAATTCGAGAGGCTTA 2978
Db 2769 TACAGATATTCGCAATGATTCATCGGCGAGATATACTTTGTTTCATCGAATTCGAGAGGCTTA 2828
Qy 2979 TCTGTGAGAAATATCTGTATTCGCGGTGTAATTCGCGAAATTTTGAAGAAATTTAGAAGG 3038
Db 2829 TCTGCTGAGCTGTGTGATTCGCGGTGTAATTCGCGAAATTTTGAAGAAATTTAGAAGG 2888
Qy 3039 TCGCATATACCTGCAATCTCCCTATAGGATCGAGAAATGTCGTTTAAATTTGATTT 3098
Db 2889 GCGTATTTTCACTGCAATCTCCCTATAGGATCGAGAAATGTCATTTAAATTTGATTT 2948
Qy 3099 TAATAATGGATTAGCATGCTGGAATGTAAAGAGGCGATGATGCT---ACAACAGAGCCA 3155
Db 2949 TAATAATGGCTTATCTGCTGGAACGTAAGAGGCGATGATGATGAGAGCAACAAACAA 3008
Qy 3156 TCACCGTTCTGCTGTTGTTATCCAGAAATGGGAAGCAGAGTGTCAACAGCAGTTCCGCT 3215
Db 3009 CCAACGTTCCGCTGCTGTTGTTGTCGGAATGGGAAGCAGAGTGTCAACAGAAAGTTCCGT 3068
Qy 3216 CTGTCCGGGGGCTGCTATATCTCCCTGCTGTCAGAGCTACAAAGAGGATTTGAGAGGG 3275
Db 3069 CTGTCCGGGGGCTGCTATATCTCCCTGCTGTCAGAGCTACAAAGAGGAGGATTTGAGAGGG 3128
Qy 3276 TTGTGTAACGATCCATGAAATTCGAGAAACAAATACAGAGCAACTTAAATTTTAAACACTGTA 3335
Db 3129 TTGCTGAACCAATTCATGAGATCGAGAACATACAGAGCAACTGAGTTTACCACTGCT 3188
Qy 3336 AGAAGAGAGAGTGTATCCACGGGATACAGAACTGTAAATGATTTACTGACACCAAGG 3395
Db 3189 AGAAGAGAGAGTGTATCCAAATAACACGGTAACGTTGTAATGATTTACTGTAATCAAGA 3248
Qy 3396 TACAGCAGTATGTAATTTCCCGTATGCTGGATGAGATGATGATGATGATGATGATGATGAT 3455
Db 3249 AGAATACGGAGGTCGCT-----ACATCTCTGTAATTCGAGGATATTAACAGAGCTCTTC 3302
Qy 3456 AGCATCTGTTTAAATCAAAACCGACTTATGAAGAGAAACGATATACAGATGTACGAAGAGA 3515
Db 3303 CGTACAGAGCTGATTTGCGTCAGTCTATGAGAGAAATCGTATACAGATGAGAGAGAGA 3362
Qy 3516 TAATCATTTGTAATACAGAGAGGATGTAATTTATCCACCTACCACTGCTGTTATAT 3575
Db 3363 GAATCCTTTGTAATTAACAGAGGATATAGGATTTACAGCCTACCACTGCTGTTATAT 3422
Qy 3576 GACAAAGAAATAGAAATCTTCCAGAAACCGGATAGGATGATGATGATGATGATGATGATGAT 3635
Db 3423 GACAAAGAAATAGAAATCTTCCAGAAACCGGATAGGATGATGATGATGATGATGATGATGAT 3482
Qy 3636 GGAAGGGAAGTTTATTTGAGACAGCTGGAATTTACTCCTTATGAGGAAATAG 3687
Db 3483 GGAAGGGAACATTTATCTGTGACAGCTGGAATTTACTCCTTATGAGGAAATAG 3534

```

```

RESULT 13
US-10-365-645-25
; Sequence 25, Application US/10365645
; Publication No. US20030182682A1
; GENERAL INFORMATION: Thomas
; APPLICANT: Malvar, Amy Jelen
; TITLE OF INVENTION: Antibodies Immunologically Reactive with Broad-Spectrum
; TITLE OF INVENTION: Delta-Endotoxins (Amended)
; FILE REFERENCE: 11792, 0210.DVUS02 (MECO:210--3)
; CURRENT APPLICATION NUMBER: US/10/365,645
; CURRENT FILING DATE: 2003-02-12

```

```

; PRIOR APPLICATION NUMBER: US 09/873,873
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 09/253,341
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: US 08/922,505
; PRIOR FILING DATE: 1997-09-03
; PRIOR APPLICATION NUMBER: US 08/754,490
; PRIOR FILING DATE: 1996-11-20
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Hybrid Delta-Endotoxin
; NAME/KEY: CDS
; LOCATION: (1)..(3531)
; US-10-365-645-25

Query Match      38.0%; Score 1402; DB 16; Length 3534;
Best Local Similarity 65.7%; Pred. No. 0;
Matches 2243; Conservative 0; Mismatches 1070; Indels 99; Gaps 10;

Qy 285 TCAGTGGGAAATTTTCTAGAACATGTCGAACAACTTATAAATCAACAAATAACAGAAAA 344
Db 213 TCAATGGAGCGCATTTCTGTACAAATGGAACAGTTAAATTAACCAAGATAGAGAAAT 272
Qy 345 TGCTAGGAATPACGGCACTTCTCGATTACAAGTTTAGGAGATTCCTTTAGAGCCTATCA 404
Db 273 CGCTAGGAACCAAGCCATTTCTAGATTAGAAAGCACTTAAGCAATCTTTATCAAAATTTACGC 332
Qy 405 ACAGTCACTTTGAAGATTGGCTAGAAACCGTGATGATGCAAGAACGAGAGTGTCTTTA 464
Db 333 AGAATCTTTTAGAGAGTGGGAGCAGATCCCTACTAATCCAGCATTAAGAGAGATGCG 392
Qy 465 TACCAATATATAGCCTTTAGAACTTGATTTTCTTAATGCCATGCCGCTTTTCGCAATTAG 524
Db 393 TATTCAATTAATGACATGAACAGTGCCTTACACCGCTATTTCTCTTTTGCAGTTCA 452
Qy 525 AAACCAAGAGAGTTCCATTTATTAATGTTATGCTCAAGCTGCAAAATTTACACCTATTAT 584
Db 453 AAATTTATCAAGTTCTCTTTTATCAGTATATGTTTCAAGCTGCAAAATTTACATTTATCAGT 512
Qy 585 ATTGAGAGATGCTCTCTTTTTCGTAGTGAATTTGGCTTTACATCGCAGGAAATTTCAACG 644
Db 513 TTTGAGAGATGTTTTCAGTGTTTTGAACAAAGTGGGATTTGATGCCGCGACTATCAATAG 572
Qy 645 TTATTATGAGCGCAAGTGGAAACAAACGAGAGATTTATTCGACTATTTCGCTAGAAATGGTA 704
Db 573 TCGTTATATGATTTAATAGGCTTATTCGCAACTATACAGATCATGCTGTACGCTGTA 632
Qy 705 TAATACAGGCTCTAAATAGCTTTGAGAGGACAAATGCCGCAAGTTGGGTGGCTTTATATCA 764
Db 633 CAATACGGGATTAGAGCGTGTATGGGACCGGATTTCTAGAGATTTGGAATAGATATATCA 692
Qy 765 ATTCCGTAGAGATCTAACGTTAGGGTATTAGATCTAGTGGCACTATTCGCCAGCTATGA 824
Db 693 ATTTAGAGAGAAATTAACACTAACTGTATTAGATATCGTTTCTCTATTTCCGAACTAIGA 752
Qy 825 CACTCGCACTTATCCCAATAAATACAGATGCTCAGTTTAAACAAAGGGAAGTTTATACAGCGC 884
Db 753 TAGTAGAACGTAATCCAAATTCGAACAGTTTCCCAATTAACAAAGAGAAATTTATACAAACCC 812
Qy 885 A--ATTGAGAGCAACAGGGTAAATATATGCAAGTATGAATTTGGTATTAATTAATGACCT 942
Db 813 AGTATTTAGAAAATTTTGTGTGTATTTTCGAGCTCGGCTCAGGGCATAGAAAGAGTAT 872
Qy 943 TCGTTTTCCGCTATAGAGACTGCGGTTTATCCGAAGCCCGCATCTACTTGTGATTTCTTAGAA 1002
Db 873 TAGAGTCCACATTTGATGATATATACTTAACAGTAAACCTCTATACGAGTCTCATAG 932

```

QY 1003 CAACCTTACAAATTTTACGACTTTCATCAGATGGAGTCTACTAGGCATATGACTTACTGG 1062
Db 933 GGGTTATTATTATTTGGTCAGGGCATCA-----AATAATGGCTTCTCTGTAGGGTT 983
QY 1063 CGGGGGCACACAAATTCAAATCTCGGCCCAATAGAGCGGATTAATAATACCTCAACGCATGGG 1122
Db 984 TTCCGGGCCAGAAATTCATCTTTCGCTATATGGAACCTATGGGA-----ATGCA 1032
QY 1123 TCTACCAATACTTCTATTAATCTCTGTAGATATATCAATCTCTCGAGACGTATATGG 1182
Db 1033 GCTCCACAACAACCAATTTGTGTCTCAACTAGGTCAAGGCGGTATAGAAACATATATCGTCC 1092
QY 1183 ACTGAATCATATGAGGAGTCTCTATGGGAATTTACCTTGAACCTATTCATGGTGTG 1242
Db 1093 ACTTTATAGAAGACCTTTTAATATAGGGAATAATAATCAACAACTATCTGTTCCTTGAC 1152
QY 1243 CCTACTGTAGATTTAATTTTAGAAACCTCAGAAATACTTTTGAAGAGAGTACTGCTAAC 1302
Db 1153 GGGAC-----AGAAATTCCTTATGGAACCTCTCAAAATTTGCCATCCCTGTATACAGAA 1208
QY 1303 TATAGTCAACCCCTATAGTCACTGGGCTTCAATTAAGAATTCAGAAACCTG-AAATPACC 1361
Db 1209 AAGCGGAACGCTAGATTCGCTGGATGAATAACCGCCACAGAAATAACAACGTGCCACCTAG 1268
QY 1362 ACCAGAAACACAGAACCAAAATTTGAATCATATAGTATAGTATCTCATATAGG 1421
Db 1269 GCAAGGATTTAGTCAATGATTAAGCCATGTTTCAATGTTTCGT-----TCAGGCTTTAG 1322
QY 1422 GCTCATTTCAAACTAGGCTGATGTACAGATATATTTTGGACGCACCGTAGTGAGA 1481
Db 1323 TAATAGTAGTATATATAGAGCTCCAAATGTTTCTTGGACGCACCGTAGTGCAAC 1382
QY 1482 TCGTACAAATACCAATAGTTCAGATAGCATAAACAATAACCAATGGTAAATCAATCAA 1541
Db 1383 CCCTACAAATACAAATGATCCGAGAGGATTTACTCAAAATACCAATGGTAAAGCACATAC 1442
QY 1542 CCTTAATTCAGGTACTCTGTAGTCACTGCGCCAGGATTTTACAGGAGGATATATCCG 1601
Db 1443 ACTTCAGTCAAGTACTACTGTGTAAGAGGCGCGGTTTACGGGAGGAGATATCTTCG 1502
QY 1602 AACTAACGTTAAATGCTAGTACTAAGTATGGTCTTAATTTTAAATATACATCATTAACA 1661
Db 1503 ACGNACAAGTGGAGGACCAATGCTTATATCTATTTGTTTAAATAAATGGGCAATTAACCCA 1562
QY 1662 CGGCTATCGGTGAGAGTTCGTTATGCTGCTTCTCAACAATGGTCTCGAGGGAATCTGT 1721
Db 1563 AAGGTATCGTCAAGAAATACGCTATGCTCTACTACAAATCTAAGAAATTTACGTAACGGT 1622
QY 1722 CGHAGGAGTACTACTTTTGAATCAAGATTCCTCTAGTACTATAGTGCAAAATGAGTCTTT 1781
Db 1623 TGCAGGTGAACGGATTTTGTGCTCAATTTTAAACAAACATGATACCGGTGACCCCATTT 1682
QY 1782 GACATCTCAATCATTTAGATTTGAGAAATTTCTGTAGGTATTTAGTGCATCTGCGAGTCA 1841
Db 1683 AACATTCCAATCTTTTGTAGTACGCACTATTAATACAGCTTTTACATTCCTCAATGAGCCA 1742
QY 1842 AACTGCT---GGAATAAGTAAATGATGAGGTAGACAAACGTTTTCACITTTGATAA 1898
Db 1743 GAGTAGTTTACAGTAGTCTGATACCTTTTGTAGTTTCAGGGAATGGAAGTTATATAGACAG 1802
QY 1899 AATTGAATTCATTCCAATTTACTGAACTTCGTAAGAGCAATACCAATTTAGAAAGGGCGCA 1958
Db 1803 ATTTGAATTTGATTCAGTTACTGCAACATTTTGAAGCAGAAATATGATTTTGAAGAGCACA 1862
QY 1959 AGAGCGGTGAATCTGTTTACTTAATACGAATCCGAAGAGTTGAAACAGATGTGAC 2018
Db 1863 AAAGCGGTGAATCGCTGTTTACTTCTATTAACCAATAGGGATATAAACAGATGTGAC 1922
QY 2019 AGATTATCATATGATCAAGTATCCAAATTTAGTGGCGTGTGTTTATCGGATGAATTTCTGCTT 2078
Db 1923 GGATTATCATATGATCAAGTATCCAAATTTAGTGGATGTTTATCAGATGATTTTGTCT 1982
QY 2079 AGATGAAAGAGAGAAATTTACTTTGAGAAAGTGAAATATGCGAAACGACTCAGTGTATGAAG 2138

Db 1983 GGATGAAAGCGAGAAATTTGTCGAGAAAGTCAAAACATTCGAGCGACTCAGTGTATGAGCG 2042
QY 2139 AAATCTTACTCAAGATCCAAACTTTCAATCCATCAATTAAGCAACCCAGACTTCATATCTAC 2198
Db 2043 GAATTTACTTCAAGATCCAAACTTTCAAGGCAATCAATAGGCAACTAGAC----- 2091
QY 2199 TAATGAGCAATCGAATTTTCAATCTATTCATGAACAATCTGAAACATGATGGTGGGAG 2258
Db 2092 -----CGTGGTTGGAGAGGAAG 2108
QY 2259 TGAGAACATTTACATCCAGGAAGGAATGACGTATTTTAAAGAGAAATTTACGTACACTACC 2318
Db 2109 TAGCGATTTTACCATCCAAAGAGAGAGATGACGTATTTCAAGAAATTTATGTACACTACC 2168
QY 2319 GGGGACCTTTTAATGAGTGTATCCGACGTATTTATATCAAAAAATAGGAGAGTCCGAATTT 2378
Db 2169 AGGTACCTTTTGTAGTGTCTATCAACATATTTGTATCAAAAAATCGATGAATCAAAATTT 2228
QY 2379 AAAAGCTTATCTCGCTACCAATTAAGAGGGTATATTTAAAGATAGTCAAGATTTAGAGAT 2438
Db 2229 AAAAGCCTTTTACCGCTTATCAATTTAAGAGGGTATATCGAAAGATAGTCAAGACTTTAGAA 2288
QY 2439 ATATTTGATTCGTTATATCGGAAACATGAAACATTCGATGTTTCCAGGTACCGAGTCCGT 2498
Db 2289 CTATTTAATTCGCTACAAATCGAAACATGAACAGTAAATTTGTCAGGTACGGTTCCTT 2348
QY 2499 ATGCGCGCTTTTCAAGTGTGAAAGCCCAATCGGAAGGTGCGGAGAACCGAATCGATCGCACC 2558
Db 2349 ATGCGCGCTTTTACGCCCAAGTCCAATCGGAAGGTGCGGAGAGCGGAATCGATCGCGGCC 2408
QY 2559 ACATTTTGAATGGAATCTGATCTAGATTTGTTCTCGAGAGATGGAGAAATATGTGGCA 2618
Db 2409 ACACCTTTGAATGGAATCTGATTTAGATTTGTTCTGTAGGGATGGAGAAAGTGTGCCCA 2468
QY 2619 TCATCCCATCATTTCTCTTTGGATATTTGATGTCACACACTTTGATGATGAGATCT 2678
Db 2469 TCATTCGATCATTTCTCTTTAGACATTTGATGTAGGATGTACAGACTTTAATAGGACCT 2528
QY 2679 AGGCGTGTGGTGTATTTCAAGATTTAAGACGCGAGGAAGTTCATGCAAGACTTAGGGAATCT 2738
Db 2529 AGGTGTATGGTGTATTTAAGATTTAAGACGCAAGATGGGACGCAAGACTTAGGGAATCT 2588
QY 2739 GGAATTTTAAAGAGAAACCAATTTAAGAGAGCACTGTCTGTGTGAAGAGAGAGCA 2798
Db 2589 AGAGTTTCTCGAAGAGAAACCAATTTAGTAGAGAGCGCTAGCTGTGTGAAAAGAGCGGA 2648
QY 2799 GAAAATGAGAGACAAACGTCGAAACCTTACAAATTTGGAACAAACGAGTATATACAGA 2858
Db 2649 GAAAAATGAGAGACAAACGTCGAAATTTGGAATGGGAACAAATATCGTTTATAAGA 2708
QY 2859 GGCAAAAGAGCTGTGGATGCTTTATTTGTAGATTTCTCAATATAATAGATTTACAAGCGGA 2918
Db 2709 GGCAAAAGATCTGTAGTCTTTATTTGTAACTCTCAATATGATCAATTTACAAGCGGA 2768
QY 2919 TACAAACATTTGCAATTCATCGGAGATAAACTTTGTTTCATCGAATTCGAGAGGCTTA 2978
Db 2769 TACCAATTTTGCATGATTCATCGGAGATAAACGTTTTCATAGCATTCGAGAAGCTTA 2828
QY 2979 TCTGTCAAGATTTATCTGTTATCCGGGTGTAAATGCGGAATTTTTCGAAGAAATTAGAAGG 3038
Db 2829 TCTGCTGAGCTGTGTGTGATTCGGGTGTCAATTCGGGCTATTTTGAAGAAATTAGAAGG 2888
QY 3039 TCGCATTTATCACTGCAATCTCCCTATACGATGGAGAAATGTGCTTAAAAATGCTGATTT 3098
Db 2889 GCGTATTTTCACTGCAATCTCCCTATATGATGGAGAAATGTCTATTAATGCTGATTT 2948
QY 3099 TAATAATGGAATAGCATGCTGGAATGTAAAGGGCATGTAGATGT---ACAAAGAGGCCA 3155
Db 2949 TAATAATGGCTTATCTGCTGGAACGTAAGGGCATGTAGATGTAGAGAAACAAACAA 3008
QY 3156 TCACCGTTCTGCTCTGTTTATCCAGNATGGGAGCAGAGTGTCAACAGCAGTCCGCT 3215

3009	CCAACTGTTCCGTCCTCTGTTGTCGGAATGGGAAGCAAGTGTCTCAAGAAGTTCCTGT	3068
3216	CTGTCCGGGGCGTGGCTATATCTCTCCGTGTACAGCGGTACAAAGAGGGATATGAGAGGG	3275
3069	CTGTCCGGGTCGTGGCTATATCTCTTCTGTGTACAGCGGTACAAGGAGGGATATCGAGAAGG	3128
3276	TTGTGTAAACGATCCATCGAATTCGAGAACATATACAGACGAACATAAAATTTTAAAAACTGTGA	3335
3129	TTGCGTAAACCATTCATGAGATTCGAGAACATATACAGACGAACTGAAGTTTATGCAACTCCGT	3188
3336	AGAAGGGAAGTGTATCCAAACGGATACAGAAACGTGTAAATGATTATATCTGCACACCAAGG	3395
3189	AGAAGGGAATCTATCCAAATAACACGGTAAACGTGTAAATGATTATATCTGTAATCAAGA	3248
3396	TACAGCAGTATGTAAATTCGCCGTAAATGCTGGATATGAGGATGCATATGAAGTTGATCTAC	3455
3249	AGAAATCCGAGGTCGCT-----ACACTTCTCGTAATCGAGGATATAACGAAGCTCCTTC	3302
3456	AGCATCTGTTAAATACAAACCGACTATGAAGAAGAAACGTATACAGATGTACGAAGAGA	3515
3303	CGTACCAGCTGATATATGCGTCAGTCTATGAAGAAATCGTATACAGATGGACGAAGAGA	3362
3516	TATATCTTGTGAATATGACAGAGGGTATGGAATTTACACACACTACCGCTGGTTATAT	3575
3363	GAATCTCTTGTGAAATTTAACAGAGGGTATAGGGATTTACACGCCACTACCACTGGTTATGT	3422
3576	GACAAAGAATTTAGAATACATTCCACAGAAACCGATAAGGTATGGATTTCAGATTTCGAGAAAC	3635
3423	GACAAAGAATTTAGAATACATCCAGAAACCGATAAGGTATGGATTTCAGATTTCGAGAAAC	3482
3636	GGAAGGGAAGTTTATTTGTAGACAGCGTGGAAATTAATCTCTTATGGAGGAATAG	3687
3483	GGAAGGAACAATTTATCGTGTGACAGCGTGGAAATTAATCTCTTATGGAGGAATAG	3534

RESULT 14

```

US-10-672-163-25
; Sequence 25, Application US/10672163
; Publication No. US20040093637A1
; GENERAL INFORMATION:
; APPLICANT: Malvar, Thomas
; APPLICANT: Gilmer, Amy Jelen
; TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad Spectrum
; TITLE OF INVENTION: Delta-Endotoxins
; FILE REFERENCE: 11792.0215.DVUS02 MECO:2115--2
; CURRENT APPLICATION NUMBER: US/10/672,163
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US 09/997,914
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 09/261,040
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: US 08/754,490
; PRIOR FILING DATE: 1996-11-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hybrid Delta-Endotoxin
; NAME/KEY: CDS
; LOCATION: (1)..(3531)
US-10-672-163-25

```

QY	345	TCGTAGGAATAACGGCACTTGCCTCGATTACAAAGTTTATAGGAGATTCCCTTTAGAGCGCTATCA	404
Db	273	CGCTAGGAAACCAAGCCATTTCTGATTAGAGGACTAAGCAATCTTTATCAAATTTTACGC	332
QY	405	ACAGTCACTTGAAGATTGGCTAGAAAACCGTGAATGCAAGACGAGMAGTGTCTTTA	464
Db	333	AGAAATCTTTTAGAGAGTGGGAGCGAGATCCCTAATCCAGCATTAAGAGAGAGATGCG	392
QY	465	TACCCAATATATAGCCTTAGAACCTTGATTTTCTTAATCGCATGCCGCTTTTCGCAATTAG	524
Db	393	TATTCAATTCAAATGACATGAACAGTCGCCCTTACAACCGCTATTCTCTCTTTTGCAGTTCA	452
QY	525	AAACCAAGAGTTCCATTATTAATGGTATATGCTCAAGCTGCATAATTTACACCTATTAAT	584
Db	453	AAATTAACAAGTTCCCTCTTTTATCAGTATATGTTTCAAGCTGCATAATTTACATTTATCAGT	512
QY	585	ATTGAGAGATGCCCTCTCTTTTGGTAGTGAATTTGGGCTTACATCGCAGGAAATTCACACG	644
Db	513	TTTGAGAGATGTTTCAGTGTTTGGACAAGGTGGGATTTGATGCCGGACTATCAATAG	572
QY	645	TTATATTGAGCGCCAAAGTGGAACAAACGAGAGATTATTCGCACTATTTGGCGTAGAATGGTA	704
Db	573	TCGTTTAATATGATTAACTAGGCTTAATGGCAACTATACAGATCATGCTGTGACGCTGGTA	632
QY	705	TAATACAGGTCATAATAGCTTTGAGAGGACAATAATGCCCAAGTTGGGTGGCTTATATATCA	764
Db	633	CAATAACGGGATTAGAGCGTGTATGGGACCGGATTTAGAGATTGGATAGATATAATATCA	692
QY	765	ATTCGTPAGAGATCTAAACGTTAGGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGA	824
Db	693	ATTTAGAAGAGAAATTAACACTAACTGTTATTAGATATCGTTTCTCTATTTCCGAACATGA	752
QY	825	CACTCGCACATTATCCCAATAAATACGAGTGTCTCAGTTAAACAGGGAAGTTTATACAGACGC	884
Db	753	TAGTAGAACGTATCCCAATTCGAAACAGTTTCCCAATTAACAGAGAAATTTATACAAACCC	812
QY	885	A--ATTGGAGCAACAGGGGTAAATATGGCAAGTATGAATTTGGTATAATAATATGCACCT	942
Db	813	AGTATTAGAAAAATTTTGATGGTAGTTTTCAGGCTCGGCTCAGGCGATAGAGAAGTAT	872
QY	943	TCGTTTTCGCGTATAGAGATCGCGGTATACCGAAGCCCGCATCTACTTGTGATTTTCTAGAA	1002
Db	873	TAGGAGTCCACATTTGATGATATACTTAAACAGTATAAACCATCTATACGGATGCTCATAG	932
QY	1003	CAACTTACAAATTTTAGCACTTCATACGATGGAGTGTCTACTAGGCATATGACTTACTCG	1062
Db	933	GGGTTATTATTATTTGGTCAGGGCATCA-----AATAATGGCTTCTCTGTAGGGTT	983
QY	1063	CGGGGGCACAAATTCATTCGCGCAATAGGAGCGGATTAATACCTCAACGCATGGG	1122
Db	984	TTCCGGGCCAGAAATTCACCTTTCCGCTATATGAACTATGGGAA-----ATGCA	1032
QY	1123	TCCTACCAATACCTTATTAAATCTGTAAAGATTATCATTTCTCTCGAGACGTATATGG	1182
Db	1033	GTCTCCACAAACGATATGTTGTCTCAACTAGGTACAGGCGGTGATAGAAATTATCGTCC	1092
QY	1183	ACTGAATCATATGCAGAGTGTCTTCTATGGGGAATTTACCTTCGAACCTATTCATGTGTCT	1242
Db	1093	ACTTTATATAGAACCTTTTAAATATAGGATTAATAATCAACAACTATCTGTTCTTGAC	1152
QY	1243	CCTACTGTTAGATTTAAATTTTAGGAACCTTCAGAAATACCTTTTGAAGAGAGTACTGCTAAC	1302
Db	1153	GGGAC----AGAAATTTGCTTATGGAACTCTCTCAAAATTTGGCCATCCGCTGTATACAGAAA	1208
QY	1303	TATAGTCAACCCCTATGAGTCACCTCGGCTTCAATTTAAAGATTTCAGAAAACTG--AATTACC	1361
Db	1209	AACGGNAACGTTAGATTTCGTGATGAATATACCGCCACAGAAATAACACGTGCCACCTAG	1268
QY	1362	ACCAGAAACACAGAACGACAAATTTAGAAATCATATAGTCATAGGTTATCTCACATAGG	1421
Db	1269	GCAAGGATTTAGTCATCGATTAGACCATGTTTCAAATGTTTCGT-----TCAGGCTTTAG	1322

Qy	1422	GCTCATTTTCAAACTCTAGGGTGCAATGTACACAGTATATATCTTTGGACGCACCGTATGTGAGA	1481
Db	1323	TAAATAGTAGTGTAAAGTAAATAAAGAGCTCCAAATGTTTTTCTTTGGACGCACCGTATGTGCAAC	1382
Qy	1482	TCGTACAAAATACCAATTAGTTTCAGATAGCAATAACAACAATAACCAATTGCTGTAATAATCAITTCAA	1541
Db	1383	CCCTTCAAAATACAAATTGATCCGGAGAGGATTTCTCAAAATACCAATTGCTGTAATAAAGCACAATAC	1442
Qy	1542	CCTTAAATTACAGGTACCTCTGTAGTCAGTGGCCCAAGGATTTTACAGGAGGGGATATAAATCCG	1601
Db	1443	ACTTCAGTCAGGTACTACTGTGTTAAGAGGGCCGGGTTCACGGGAGAGATATCTCTTCG	1502
Qy	1602	AACATAACGTTAATGGTGTAGTACTAAGTATGGGCTTTAAATTTTAAATAATACATCAITTCACA	1661
Db	1503	ACGAACAAGTGGAGGCACATTTGCTTTATACCTATTTGTTTAAATAATAATGGGCAATTCACCCCA	1562
Qy	1662	GCGGTATCGGCTGAGAGTTGCTTATGCTGCTCTCAAAACAATGCTCTGAGGGTGAACGTG	1721
Db	1563	AAGGTATCGTGCAAGATACGCTATGCTCTACTACAANTCTAAGAATTTACGTAAACGGT	1622
Qy	1722	CGGAGGGAGTACTATTTTGTATCAAGGATTCCTCTAGTACTATGAGTGCAGAAATGAGTCTTTT	1781
Db	1623	TGCAGGTGAACGGATTTTTCGTGCTCAATTTAAACAAACAATGGATACCGTGACCCCATT	1682
Qy	1782	GACATCTCAATCATTTTATAGATTTTGAGAAATTTCTGTGTAGGTATTTAGTGCACTCTGGCAGTCA	1841
Db	1683	AACATTCCAATCTTTTATAGTTACGCAACTATTTAATACAGCTTTTACATTCCTCAATAGACCCA	1742
Qy	1842	AACGTCT---GGATAGTATAGTATAATATGCAGGTAGACAAACGTTTTCACATTTTGATAA	1898
Db	1743	GAGTAGTTTTCACAGTAGGTGCTGATCTTTTAGTTTACGGGAATGAAGTTTATATAGACAG	1802
Qy	1899	AAATTGAATTCATTCCTCAATTAATCTGCAACCTTCGAAGCAGAAATACGATTTAGAAAGGGCGCA	1958
Db	1803	ATTTGTAATTGATTCAGGTACTGCAACATTTTGAAGCAGATATGATTTAGAAAGACACA	1862
Qy	1959	AGAGCGGTGAATGCTCTGTTTACTAATAACGAATCCAAAGAAAGTTGAAAACAGATGTGAC	2018
Db	1863	AAAGCGGTGAATCGCTGTTTACTTCTTATAAACCAATAGGGGATAAAAAACAGATGTGAC	1922
Qy	2019	AGATTATCATATTGATCAAGTATCCCAATTTAGTTGGCGGTGTTATTCGATCGAATTCGTCTT	2078
Db	1923	GGATTATCATATTGATCAAGTATCCCAATTTAGTTGGATGTTTATTCAGATGAATTTTGTCT	1982
Qy	2079	AGATGAAAAGAGAGAAATTAATTGAGAAGTGAATATGCGAAACGACTCAGTGATGAAG	2138
Db	1983	GGATGAAAAGGAGAAATTTGTCGGAAGAGTCAACATGCGAGGCACTCAGTGATGAGCG	2042
Qy	2139	AAACTTACTCCAAGATCCAAACTTTCATCCATCAATCAATGAACACCGAGCTTCATATCTAC	2198
Db	2043	GAATTTACTTCAAGATCCAAACTTCAAGGCACTCAATAGGCAACTAGAC-----2091	
Qy	2199	TAATGAGCAATCGAATTTTCAATCTATTCATGAACAATCTGAACATGGATGCTGGGGAG	2258
Db	2092	-----CGTGGTTTGGAGAGGAAG2108	
Qy	2259	TGAGAACATTTACAAATCCAGGAAGAAATGAGTATTTTAAAGAGAAATTTACGTCCACACTACC	2318
Db	2109	TACGGATTTACCAATCCAAAGAGAGATGACGTATTTCAAAGAAATTTATGTCACTATACC	2168
Qy	2319	GGGACCTTTTAAATGAGTGTTATCCGAGTATTTTATATCAAAAAATAGGAGAGTCGGAATTT	2378
Db	2169	AGGTACCTTTGATGAGTGCTATCCAAACATATTTTGTATCAAAAAATCGATGAATCAAAATTT	2228
Qy	2379	AAAAGCTTATATCTGCTACCAATTTAAGAGGGTATATTTGAAGATAGTCAAGATTTAGAGAT	2438
Db	2229	AAAAGCCCTTTACCCGTTTATCAATTTAAGAGGGTATATTCGAAGATAGTCAAGACTTAGAAAT	2288
Qy	2439	ATATTTTGATTCGTTTAAATCGGAACAATGAACAATTCGATGTTTCCAGTACCGAGTCCGT	2498
Db	2289	CTATTTTAAATTCGCTACAAATCGAAACAATGAACAAGTAAATTTGTCAGGTACGGGTTCCTT	2348
Qy	2499	ATGCGCCGCTTTTCAGTTGAAAGCCCAATTCGGAAGGTGGGAGAACCGGAATCGATCGCGCAC	2558

Db 3423 GACAAAGAAATTAGATACTTCCAGAAACCGATAAGATGATGATGAGATTGAGATTGAGAAAC 3482

Qy 3636 GGAAGGGAAGTTTATTGTAGACAGCGTGGAACTTCTTATGAGGAGATAG 3687

Db 3483 GGAAGGAACATTTATCGTGGACAGCGTGGAAATTACTCTTATGAGGAATAG 3534

RESULT 15

US-10-739-482-25

Sequence 25, Application US/10739482

Publication No. US20040132975A1

GENERAL INFORMATION:

APPLICANT: Malvar, Thomas

APPLICANT: Mohan, Sivasubramanian, Sakuntala

APPLICANT: Sivapramanian, Sakuntala

TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad Spectrum

FILE REFERENCE: MECO:220--1

CURRENT FILING DATE: 2003-12-18

PRIOR APPLICATION NUMBER: US/10739,482

PRIOR FILING DATE: 2000-08-11

PRIOR APPLICATION NUMBER: US 09/636,746

PRIOR FILING DATE: 2000-08-11

PRIOR APPLICATION NUMBER: US 6,242,241

PRIOR FILING DATE: 1999-02-19

PRIOR APPLICATION NUMBER: US 6,110,464

PRIOR FILING DATE: 1997-09-03

PRIOR APPLICATION NUMBER: US 6,017,534

PRIOR FILING DATE: 1996-11-20

NUMBER OF SEQ ID NOS: 35

SOFTWARE: Patent in version 3.2

SEQ ID NO 25

LENGTH: 3534

TYPE: DNA

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: Hybrid Delta-Endotoxin

NAME/KEY: CDS

LOCATION: (1)...(3531)

US-10-739-482-25

Query Match 38.0%; Score 1402; DB 18; Length 3534;

Best Local Similarity 65.7%; Pred. No. 0;

Matches 2243; Conservative 0; Mismatches 1070; Indels 99; Gaps 10;

Qy 285 TCAGTGGGAATTTCTCTAGACATGTCGACAACTTATAAATCAACAAATACAGAAA 344

Db 213 TCAATGGGACGCAATTTCTGTACAAATGGAACAGTAAATTAACCAAGAAATAGAAAT 272

Qy 345 TGCTAGGAATACGGCACTTCTCGATTACAAAGGTTTAGGAGATTCTCTTAGAGCGCTATCA 404

Db 273 CGCTAGGAACCAAGCCATTTCTAGATTAGAGGACTAAGCAATCTTATCAAAATTAAGC 332

Qy 405 ACAGTCACTTGAAGATTGGCTAGAAAACCGTGATGATGCAAGAACGAGAAAGTGTCTTTA 464

Db 333 AGAATCTTTTAGAGAGTGGGAAGCAGATCTCTACTAATCCAGCATTAAGAAAGAGATGCG 392

Qy 465 TACCAATATAGCCTTAGAATCTGATTTCTTAATGCGATGCGCTTTTCGCAATTAG 524

Db 393 TATTCAATCAATGACATGAACAGTGCCTTTACAAACGCTATTCTCTTTTGCGAGTTCA 452

Qy 525 AAACCAAGAAAGTTCATTTAATGATGATATGCTCAAGCTGCAAAATTTACACCTATTATT 584

Db 453 AAATTATCAAGTCTCTTTTATCAGTATATGTTCAAGCTGCAAAATTTACATTTATCAGT 512

Qy 585 ATTGAGAGATGCTCTCTTTTGGTAGTGAATTTGGGCTTACATCGCAGGAATTCACG 644

Db 513 TTTGAGAGATGTTTTCAGTGTGTTGACAAAGTGGGATTTGATGCGCGCACTATCAATAG 572

Qy 645 TTATTATGAGCGCAAGTGGAAACAAACGAGAGATTATTCCGACTATTTCGCTAGAAATGGA 704

Db 573 TCGTTATATGATTTAACTAGGCTTATTGGCAACTATACAGATCATGCTGTCGCTGTTA 632

Qy 705 TAATACAGGCTTAAATAGCTTTGAGAGGGAACAAATGCGCAAGTTGGGTGGTGTATATATCA 764

Db 633 CAATACGGGATTAGACGCTGTATGGGACCGGATTTCTAGAGATTGGATAGATATATATCA 692

Qy 765 ATTCGCTAGAGATCTAAACGTTAGGGGTATTAGATCTAGTGGCACTATTTCCAAAGCTATGA 824

Db 693 ATTTAGAGAGAAATTAACACTAATCTGATTAGATATCGTTTCTCTATTTCCGAACTATGA 752

Qy 825 CACTCGCACTTATCCAAATAATACGAGTGTCTAGTTAAACAGGGAAGTTTATACAGAGC 884

Db 753 TAGTAGAACGTTATCCAAATTCGAAACAGTTTCCCAATTAACAAGAGAAATTTATACAAACC 812

Qy 885 A--ATTGGAGCAACAGCGGTAAATATATGCAAGTATGAAATGGTATATAATAATAATGACCT 942

Db 813 AGTATTAGAAAATTTTGATGGTAGTTTTCGAGGCTCGGCTCAGGCAATAGAAAGATAT 872

Qy 943 TCGTTTTCGCTATAGAGACTGCGGTATATCCGAAGCCCGCATCTACTTGTGTTTCTAGAA 1002

Db 873 TAGGAGTCCACATTTTGATGGATATCTTAACAGTATAAACCATCTATACGGATGCTCATAG 932

Qy 1003 CAATTTACAATTTTAGCACTTTCATCAGATGAGTGTCTACTAGGCATATGACTTACTGG 1062

Db 933 GGGTTATTATTGTTGTCAGGGCATCA-----ATAATGGCTTCTCTGTAGGGTT 983

Qy 1063 CGGGGCGACACAATCAATCTCGGCAATAGGAGGCGGATTAATACTCAACGCGATGGG 1122

Db 984 TTCGGGCGCAGAAATTCATTTTCGCTATATGAACTATGGGAA-----ATGCA 1032

Qy 1123 TCTACCAATCTCTTATTAATCTCTGAAGATTAATCTTCTCTCGAGACGATATATGG 1182

Db 1033 GCTCCACAACACGATTTGTTGCTCAACTAGGTGAGGGCGGTATAGAACATTTATCGTCC 1092

Qy 1183 ACTGAATCATATACGAGGAGTCTTCTATGGGAATTTACCTGCAACCTATTCATGGTGC 1242

Db 1093 ACTTTATATAGAAAGCCTTTTAATATAGGATTAATAATCAACACTATCTGTCTTGAC 1152

Qy 1243 CCTACTGTTAGATTTAAATTTTAGAAACCTCTCAGAACTATTTTGAAGAGAGTACTGTAAC 1302

Db 1153 GGGAC---AGAAATTTGTTATGGAACCTCTCAAAATTTGCCATCCGCTGTATACAGAA 1208

Qy 1303 TATAGTCAACCCCTATGAGTCACTGGGCTTCAATTTAAAGATTCAGAAACTG-AAATACC 1361

Db 1209 AAGCGGAACGGTAGATTTCGTGATGAAATACCGCACAGAAATAACAGCTGCCACTAG 1268

Qy 1362 ACCAGAAACAAACAGAACGACCAAAATTTGAATCATATAGTATAGTCTTCTCACATAGG 1421

Db 1269 GCAAGGATTAGTCACTGATTAAGCCATGTTTCATGTTTCTGTTCTGTTCTGTTAG 1322

Qy 1422 GCTCAATTTCAATCTAGGTTGATGTACAGTATATTTTGGACGACCGTATGTCAGA 1481

Db 1323 TAATAGTAGTGAAGTATAATAAGAGCTCCAATGTTTCTTGGACGACCGTAGTGCAAC 1382

Qy 1482 TCGTACAAATACATTTAGTTTCAGATAGATATAACAATAACATTTGGTAAATTCATCAA 1541

Db 1383 CCCTACAAATACAAATTTGATCCCGAGAGAGATTACTCAATACCAATTTGTTAAACACATAC 1442

Qy 1542 CCTTAAATTCAGGTACCTCTGTAGTCAAGTCCGAGGATTTTACAGGAGGAGATATAATCCG 1601

Db 1443 ACTTCAGTCAGGTACTGTTGTTAGAGGCGCGGGTTTACGGGAGGAGATATCTTCG 1502

Qy 1602 AACTAAGTTAATGGTGTACTTAAGTATGGTCTTAATTTTAAATAATACATCAATACA 1661

Db 1503 ACGAAACAGTGGAGGACCATTTGCTTATACTATTGTTTAATATAAAATGGGCAATTAACCCA 1562

Qy 1662 GCGGTATCGGTGAGAGTTCGTTATGCTGTTCTCAACAAATGGTCTCGAGGAGTACTGT 1721

Db 1563 AAGGTATCGTGCAGAAATACGTTATGCTCTACTACAAATCTAAGAAATTTACGTAACGGT 1622

Qy 1722 CGGAGGAGTACTACTTTTGGATCAAGGATTTCCCTAGTACTATGAGTGCAAAATGAGTCTTT 1781

Db 1623 TGCAGGTGAACGATTTTTCGCTGCTCAATTTAACAACAAATGAGTACCGGTGACCCAT 1682

Qy 1782 GACATCTCAATCATTTAGATTTGCAAGAAATTTCTCTGATGATTTAGTGATCTGGCAGTCA 1841

This Page Blank (uspto)

```

Db      557 TMEIGENLTSRTFRYTDFSNPFSPFRANPDIIGISEQPLFGAG-SISG-----ELYIDKIE 611
Qy      636 FIPITATFEAEYDLERAQAVNALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDSEFCLDE 695
Db      612 IILADATFEAEYDLERAQAVNALFTSSNQIGLKTVDYHIDQVSNLVCLSDSEFCLDE 671
Qy      696 KRELLEKVKYAKRLSDERNLLQDPNFTSINKQDPFISTNEQSNFTSIHQSEHGWMGSEN 755
Db      672 KRELSEKVKHAKRLSDERNLLQDPNFRGINRPD-----RGRGSTD 713
Qy      756 ITIQGNDVPEKENYVTLPGTFNECYPTLYLQKISESELKAYTRYOLRGYIEDSDLEIYL 815
Db      714 ITIQGDDVPEKENYVTLPGTFVDECYPTLYLQKIDESKLYKAYTRYELRGYIEDSDLEIYL 773
Qy      816 IRYNAKHETLDVPGTESVPLSVESPIGRGCEPNRCAPHFEMNPDLDCSCRDGCKCAHHS 875
Db      774 IRYNAKHETLDVPGTESVPLSVESPIGRGCEPNRCAPHFEMNPDLDCSCRDGCKCAHHS 833
Qy      876 HHFSLDIDIGCTDLHENLGVVVFVKIKTQEGHARLGNLEFIEBKPLLGEALSRYKRAEKK 935
Db      834 HHFTLDIDVGCCTDLNEDLGVWVIFKIKTQGHARLGNLEFIEBKPLLGEALSRYKRAEKK 893
Qy      936 WRDKREKLOLETKRVYTEAKEAVDALFVDSQYNRLQADTNIEMIHAADKLAVHRIREAYLS 995
Db      894 WRDKREKLOLETKRVYTEAKEAVDALFVDSQYNRLQADTNIEMIHAADKLAVHRIREAYLP 953
Qy      996 ELSVIPGVNAEIPFEELEGRITITSLYDARNVVKNGDFNNGLACWNVKGHVY-QQSHHR 1054
Db      954 ELSVIPGVNAEIPFEELEGRITITSLYDARNVVKNGDFNNGLACWNVKGHVYQSHHR 1013
Qy      1055 SVLVIPEWEAEVSQAVRVCGRGYILRVTAIYKEGYGEGCVTIHEIENNTDELKFKNCEE 1114
Db      1014 SVLVIPEWEAEVSQAVRVCGRGYILRVTAIYKEGYGEGCVTIHEIENNTDELKFKNCEE 1073
Qy      1115 EVYPTDTGTCDNYTA-----HQTAVCMNRNAGYEDAYEVDTTASVNYKPTYEEYTDVR 1170
Db      1074 EVYFNNTVTCCNYTGTQEEYEGT--YTSRNGQYDEAYGNNPSPADYASVYEEKSYTDGR 1131
Qy      1171 RDNHCEYDRGVNYPPLPAGVMTKELYPFETDKWIEIGETGKFTVDSVELLMEE 1228
Db      1132 RENPCSNRGYDTPPLPAGVMTKELYPFETDKWIEIGETGKFTVDSVELLMEE 1189

```

Search completed: April 21, 2005, 04:43:58
Job time : 1519 secs

```
Db 100 EGLGNFNIVYAEFKWEEDNNPATRTRVDRFRILDGLLERDIPSRISGFVPLLSV 159
Qy 185 YAAANLHLLLRDASLFGSEFGLTSOEIQRYRVEQETRDYSDYCVWYNTGLNSLRG 244
Db 160 YAAANLHLLLRDASLFGSEFGLTSOEIQRYRVEQETRDYSDYCVWYNTGLNSLRG 219
Qy 245 TNAASWRYNQFRDLTLGLVDLVALPSPYDTRYPINTSAQLTREYVYDAIGATGNMA 304
Db 220 STYQDWITYNLRDLTLGLVDLVALPSPYDTRYPINTSAQLTREYVYDAIGATGNMA 275
Qy 305 SMWYNNAPSFAIETAVIRSHLLDFLEQLTIFSTSSRSWATRHMTYWRGHTIQSRPI 364
Db 276 PQLOSVAQLPTFNWMESSAIRNPHLDLNNLTFTD---WFSVGRNFYWGGRHVTSLSI 332
Qy 365 GGLNTSTHGSTNTSINPRLSPFSDRVYWTESYAGVLL---WGIVLEPHIGVPTVRFN 420
Db 333 GGGNITSPYGREANQPPRSTFNGPVFRTLNSPTLRLLQQPWPAPPNLRGVEGEFS 392
Qy 421 FRNPQNTFE---RGTYNSQPYESPGQLKDSFETLPPTTERPNYESSHRLSHLIGLIS 477
Db 393 --TPTNSFTYRGRTV-----DSLTELPPEDNSVPPREGYSHRLCHATFVQ 436
Qy 478 QSRVHV---PVYSWTHRSADRTNTISSDSITQIPLVKSFNLSGTSVWSGPGFTGDI 533
Db 437 RSGTPTFTTGVVFSWTHRSATLNTIDPERINQIPLVKFRVMGGTSVITGPGFTGDI 496
Qy 534 RTNVGSLVSMGLNFNTSILQRYRVRVYAAO-----TWLVRVTGGSTTFDQGFPS 586
Db 497 RRTTFGDFVSLQVNSPITQRYRLFRYASSRDARVIVITGAASTGVGGQSVNMPLOK 556
Qy 587 TMSANESLTSQSFRFAEFP-----VGISASGSQTAGISISNNAAGRTQTFHDKIE 635
Db 557 TMEIGENLTSKTRFYDPSFPSPRANPDIIIGISEQLFCAG-SISGS-----ELYIDKIE 611
Qy 636 FIPITAFEAAYDLERAQAVNALFTWNPRLKTDVTDHIDQVSNLVACLDSDEFCLDE 695
Db 612 IILADATFEASDLERAQAVNALFTWNPRLKTDVTDHIDQVSNLVACLDSDEFCLDE 671
Qy 696 KRELLEKVKAKRLSDERNLQDPNFTSINKQDPFISTNEQSNFTSIHQSEHGWSN 755
Db 672 KRELSEKVKAKRLSDERNLQDPNFTSINKQDPFISTNEQSNFTSIHQSEHGWSN 713
Qy 756 ITIQGNDVFKENYVTLPGTFNCEPYLYQKIGESLKYATRYQLRGYIEDSQDLIYL 815
Db 714 ITIQGNDVFKENYVTLPGTFNCEPYLYQKIGESLKYATRYQLRGYIEDSQDLIYL 773
Qy 816 IRYNAKHETLDVCTESVPLSVESPIGRCEPNRCAPHEFWNPDLDCSCRDGEKCAHS 875
Db 774 IRYNAKHETLDVCTESVPLSVESPIGRCEPNRCAPHEFWNPDLDCSCRDGEKCAHS 833
Qy 876 HHSFLDIDIGCTDLHENLGVVWFKIQEGHARLGNLEFIEBKPLLGEALSVRKAEKK 935
Db 834 HHTFLDIDVCTDLNEDLGVVWFKIQEGHARLGNLEFIEBKPLLGEALSVRKAEKK 893
Qy 936 WRDKREKLQETKRVYVTEAKEDVALFVDSQYNRLQADTNIGMHAADKLVRHREAYLS 995
Db 894 WRDKREKLQETKRVYVTEAKEDVALFVDSQYNRLQADTNIGMHAADKLVRHREAYLS 953
Qy 996 ELSVIPGVNAIPEELEGRITLISLYDARNVKNKGDFNGLACWNVKGHDVY-QQSHR 1054
Db 954 ELSVIPGVNAIPEELEGRITLISLYDARNVKNKGDFNGLACWNVKGHDVY-QQSHR 1013
Qy 1055 SVLVIPWEAEVSAQVRCVGRGVIIRVATYKGYGEGCVTIHEIENTDELKPKNCEE 1114
Db 1014 SVLVIPWEAEVSAQVRCVGRGVIIRVATYKGYGEGCVTIHEIENTDELKPKNCEE 1073
Qy 1115 EVYPTDGTGNDYTA----HQGTAVCNRSNAGYEDAYEDVTASVANKPYEETVTDVR 1170
Db 1074 EVYPTDGTGNDYTA----HQGTAVCNRSNAGYEDAYEDVTASVANKPYEETVTDVR 1131
Qy 1171 RDHCEYDRGVNYPPLPAGYMTKELEYFPETDKWIEIGETGKFIYDSVELLMBE 1228
Db 1132 RENPCSNRGYGYTPLPAGYMTKELEYFPETDKWIEIGETGKFIYDSVELLMBE 1189
```

RESULT 15

```
US-10-926-819-9
; Sequence 9, Application US/10926819
; Publication No. US20050049410A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-003, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/281577
; CURRENT APPLICATION NUMBER: US/10/926,819
; CURRENT FILING DATE: 2004-08-26
; PRIOR APPLICATION NUMBER: 60/498,518
; PRIOR FILING DATE: 2003-08-28
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1189
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-926-819-9

Query Match . 54.0%; Score 3495.5; DB 17; Length 1189;
Best Local Similarity 56.9%; Pred. No. 6.9e-259;
Matches 716; Conservative 143; Mismatches 290; Indels 109; Gaps 20;

Qy 7 NENEIT--NALSIIPAVSNHSTOMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGNIAG 64
Db 5 NQNCIPYCNLS-----NPEVLIDGERISTGN-----SSIDISLSVQ 43
Qy 65 RIILGVGVPPAGQIAFYSLVGLMWRGRDQWEIFLEHVEQLINQOITENANTALARL 124
Db 44 FLVSNF-VPGGGPLVGLIDFVWGIVGP---SQWDAFLVQIEQLINERIAEFARNAAIANL 99
Qy 125 QGLGDSFRAYQQSLEQWLENRDDARTSRVLYTOYIALELDFLNAMPLEAIRNOEVPLLMV 184
Db 100 EGGNNFNIVYAEFKWEEDNNPATRTRVDRFRILDGLLERDIPSRISGFVPLLSV 159
Qy 185 YAAANLHLLLRDASLFGSEFGLTSOEIQRYRVEQETRDYSDYCVWYNTGLNSLRG 244
Db 160 YAAANLHLLLRDASLFGSEFGLTSOEIQRYRVEQETRDYSDYCVWYNTGLNSLRG 219
Qy 245 TNAASWRYNQFRDLTLGLVDLVALPSPYDTRYPINTSAQLTREYVYDAIGATGNMA 304
Db 220 STYQDWITYNLRDLTLGLVDLVALPSPYDTRYPINTSAQLTREYVYDAIGATGNMA 275
Qy 305 SMWYNNAPSFAIETAVIRSHLLDFLEQLTIFSTSSRSWATRHMTYWRGHTIQSRPI 364
Db 276 PQLOSVAQLPTFNWMESSAIRNPHLDLNNLTFTD---WFSVGRNFYWGGRHVTSLSI 332
Qy 365 GGLNTSTHGSTNTSINPRLSPFSDRVYWTESYAGVLL---WGIVLEPHIGVPTVRFN 420
Db 333 GGGNITSPYGREANQPPRSTFNGPVFRTLNSPTLRLLQQPWPAPPNLRGVEGEFS 392
Qy 421 FRNPQNTFE---RGTYNSQPYESPGQLKDSFETLPPTTERPNYESSHRLSHLIGLIS 477
Db 393 --TPTNSFTYRGRTV-----DSLTELPPEDNSVPPREGYSHRLCHATFVQ 436
Qy 478 QSRVHV---PVYSWTHRSADRTNTISSDSITQIPLVKSFNLSGTSVWSGPGFTGDI 533
Db 437 RSGTPTFTTGVVFSWTHRSATLNTIDPERINQIPLVKFRVMGGTSVITGPGFTGDI 496
Qy 534 RTNVGSLVSMGLNFNTSILQRYRVRVYAAO-----TWLVRVTGGSTTFDQGFPS 586
Db 497 RRTTFGDFVSLQVNSPITQRYRLFRYASSRDARVIVITGAASTGVGGQSVNMPLOK 556
Qy 587 TMSANESLTSQSFRFAEFP-----VGISASGSQTAGISISNNAAGRTQTFHDKIE 635
Db 557 TMEIGENLTSKTRFYDPSFPSPRANPDIIIGISEQLFCAG-SISGS-----ELYIDKIE 611
```

```

; CURRENT APPLICATION NUMBER: US/10/200,522
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 09/337,280
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 08/980,071
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: 08/757,536
; PRIOR FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 61
; LENGTH: 1189
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant Delta Endotoxin
US-10-200-522-61

Query Match          54.0%; Score 3496.5; DB 14; Length 1189;
Best Local Similarity 56.9%; Pred. No. 5.7e-259;
Matches 716; Conservative 143; Mismatches 290; Indels 109; Gaps 20;

QY 7 NENEII--NALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSAVSTVQTGINIAG 64
DB 5 NQNCIPYCNLS-----NPEVLLDGERISTGN-----SSIDISLSLVQ 43

QY 65 RILGVLPVPGAGIASFYSFLVGLMWRGRDQWEIFLEHVEQLINQOITENARNTALARL 124
DB 44 FLVSNF-VPGGGLVGLIDFWGIVGP---SQWDAFLVQIEQLINERIAEFARNAAIANL 99

QY 125 QGLGDSFRAYQQSLEDWLENRDDARTSVLYTOVIALELDFLAMPFLAIRNQSVPLMW 184
DB 100 EGLGNPNIVYEAFKEWEDPNPATRVIDRFRILDGLLDRDIPSDISGFEVPLLSV 159

QY 185 YAAANLHLLLRDASLFGSEFGLTSEIQIYERQVEQTRDYSDYCVEMYNGLSLRG 244
DB 160 YAAANLHLLLRDASLFGSEFGLTSEIQIYERQVEQTRDYSDYCVEMYNGLSLRG 219

QY 245 TNAASVRYNQFRDLTLGLVDLVALPSPYDTRTPINTSAQLTRVYTDATGATGNMA 304
DB 220 STYQDMITYNLRDLTLVLDIAAPFPYDNRYPPIQPVQGLTRVYTDPL---INFN 275

QY 305 SMWYNNAPSFSAIEFAVIRSHLLDFLBOLTFSTSSRWASATRMHYWRGHTIQSRPI 364
DB 276 POLQSVLAQLPTFNWESSAIRNPHLFDILNNLITFD---WFSYGRNFYWGGRHVSSLI 332

QY 365 GGLNTSTHGSTWTSINPVLSPFSRDVYTESVAGVLL---WGIYLEPIHGVPVTVREN 420
DB 333 GGGNITSPIYGREANQEPFRSFTFNGVFRILSNPTLRLIQQPWAPPPNLRGVGEVFS 392

QY 421 FRNPQTFE---RGTANYSPYESPGLQKDSSETLPPETTERPNYBESYSHRLSHIGLIS 477
DB 393 --TPTNSTYVRGTV-----DSLTELPPEDNSVPPREGYSHRLCHATFVQ 436

QY 478 QSRVHV---PVYSWTHRSADRTNWTSSDITQIPLVKSNNLSGTSVSVSGPFTGDDII 533
DB 437 RSGTPELFTGTVFVSWTHRSATLTNTIDPERINQIPLVGFVWGGTSVITGPGFTGDDIL 496

QY 534 RTVNGSVLSGLNFNTSLQRYVRVRYAASQ-----TWLRLVTVGGSTTFDQGFPS 586
DB 497 RRNTFGDFVLSQVNLNINSPITQRYRLFRYASRRDARVIVITGAASTGVGGVSNVMPLOK 556

QY 587 TMSANESLTSQSPRFABFP-----VGISASGQTAGISISNACRQFPHFKIE 635
DB 557 TMEIGENLTERTFRYTFDFSPFRANPDIIIGISEQLPFGAG-SISGG---ELYIDKIE 611

QY 636 FIPITATFEAYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDPECLDE 695
DB 612 IILADATFEASDLERAQKAVNALFTSNQIGLTKTDVTDYHIDQVSNLVACLSDPECLDE 671

QY 696 KRELLEKVKYAKRLSDERNLLQDNFTSINKQPDFISTNEQSNTSITHEQSEHCWNGSEN 755
DB 672 KRELSEKVKYAKRLSDERNLLQDNFTSINKQPDFISTNEQSNTSITHEQSEHCWNGSEN 713

```

```

QY 756 ITIQEGNDVFKENYVTLPGTFNECYPTIYKQIGSESELKAYTRYQIRGVYEDSQDLEIYL 815
DB 714 ITIQGDDVFKENYVTLPGTVDECYPTIYKQIDESKLKAYTRYELRGVYEDSQDLEIYL 773

QY 816 IRYNAKHETLDVPGTESVWPLSVESPIGRGCPENRCAPHFENWPDLDCCSCRDGKCAHHS 875
DB 774 IRYNAKHEIVNVPGTGSLLMPLSAQSPIGKCGENRCAPHEWNPDLDDCCSCRDGKCAHHS 833

QY 876 HHFSLDIDIGCTDLHENLGVWVVFVKIKTOGHARLGNLFIBKPLILGEALSrvKRAEKK 935
DB 834 HHFTLIDIVGCTDLNEDLGVWVIFIKITODGHARLGNLFLEKPLILGEALSrvKRAEKK 893

QY 936 WRDKREKLOLETRKRVYTEAKEAVDALFVDSQVNRLOADTNIGMIHAADKLVRHIREAYLS 995
DB 894 WRDKREKLOLETRKRVYTEAKEAVDALFVDSQVNRLOADTNIGMIHAADKLVRHIREAYLS 953

QY 996 ELSVIPGVNAEIFEELGRIITAIISLYDARNVVKNGDENNGLACWNVKGVHDV-QQSHHR 1054
DB 954 ELSVIPGVNAEIFEELGRIITAIISLYDARNVVKNGDENNGLACWNVKGVHDV-QQSHHR 1013

QY 1055 SVLVIPEWEAEVSQAVRVCPGRGYILRVYAYKEGYGEGCVTTHIEINNTDELKFKNCEE 1114
DB 1014 SVLVIPEWEAEVSQAVRVCPGRGYILRVYAYKEGYGEGCVTTHIEINNTDELKFKNCEE 1073

QY 1115 EYVPTDTGTCNDYTA----HQGTAVCNRSNAGYEDAYEVDVTTASVNYKPTYBEETDVR 1170
DB 1074 EYVPTDTGTCNDYTA----HQGTAVCNRSNAGYEDAYEVDVTTASVNYKPTYBEETDVR 1131

QY 1171 RDNHCYDRGVNYPPLPAGYMTKELEYEPETDKWIEIGETGKFTVDSVELLMEE 1228
DB 1132 RENPCESNRGYGDTPLPAGYMTKELEYEPETDKWIEIGETGKFTVDSVELLMEE 1189

RESULT 14
US-10-782-020-7
; Sequence 7, Application US/10782020
; Publication No. US20040197916A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargies, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-004, A Delta-Endotoxin Gene and
; FILE REFERENCE: 045600/274139
; CURRENT APPLICATION NUMBER: US/10/782,020
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,810
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1189
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-020-7

```

```

Query Match          54.0%; Score 3495.5; DB 16; Length 1189;
Best Local Similarity 56.9%; Pred. No. 6.9e-259;
Matches 716; Conservative 143; Mismatches 290; Indels 109; Gaps 20;

QY 7 NENEII--NALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSAVSTVQTGINIAG 64
DB 5 NQNCIPYCNLS-----NPEVLLDGERISTGN-----SSIDISLSLVQ 43

QY 65 RILGVLPVPGAGIASFYSFLVGLMWRGRDQWEIFLEHVEQLINQOITENARNTALARL 124
DB 44 FLVSNF-VPGGGLVGLIDFWGIVGP---SQWDAFLVQIEQLINERIAEFARNAAIANL 99

QY 125 QGLGDSFRAYQQSLEDWLENRDDARTSVLYTOVIALELDFLAMPFLAIRNQSVPLMW 184

```



```

Db      774  IRYNAKHEIVNVPCTGSLWPLSAQSPGKCGENRCAPHLEWNPDLDCSCRDGKCAHKS 833
Qy      876  HFFSLDIDICTDLHENLGVVWVFKITQEGHARLGNLEFIEBKPLLGEALSVRKAEKK 935
Db      834  HHFTLIDVCGTDLNEDLGVWVFKITQGHARLGNLEFLEBKPLLGEALAVKAEKK 893
Qy      936  WRDKREKLOLETKRVVTEAKEAVDALFVDSQYNRLQADTNIGMHAADKLVRHREAYLS 995
Db      894  WRDKREKLOLETNIVYKEAKESVDALFVNSQYDLQVDTNMIHAADKVRHREAYLP 953
Qy      996  ELSVIFGVNAEIPFEELEGRITAIISLYDARNVKNVNGDFNNGLLCMWVKGHDV-QQSHR 1054
Db      954  ELSVIFGVNAEIPFEELEGRIFTAYSLYDARNVKNVNGDFNNGLLCMWVKGHDVVEEQNNH 1013
Qy      1055  SVLVIPWEAEVQAVRVCGRGYILRVYAYKEGCGCVTHIEINNTDELKFKNCEE 1114
Db      1014  SVLVIPWEAEVQAVRVCGRGYILRVYAYKEGCGCVTHIEINNTDELKFKNCEE 1073
Qy      1115  EYVPTDGTGNDYTA---HOGTAVCNRNAGYEDAYEDVDTASVNYKPYEBETVTDVR 1170
Db      1074  EYVNNVTVCNNVTGTQEEYEGT--YTSRNOGYDEAYGNNPSVPADYASVYEKSYTDGR 1131
Qy      1171  RDNHCEYDRGVNVPPLPAGYMTKELEYFETDKVWIEIGETGKFTVDSVELLMEE 1228
Db      1132  RENPCSNRGYDGYTLPAGYVTKOLEYFETDKVWIEIGETGFTVDSVELLMEE 1189

RESULT 11
US-10-200-522-2
; Sequence 2, Application US/10200522
; Publication No. US20030195336A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Gilmer, Amy Jelen
; APPLICANT: Mettuss, Anne Marie Light
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE COMPOSITIONS ENCODING LEPIDOPTERAN-T
; FILE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: MECO:213 (11792.0213 DVUS01)
; CURRENT APPLICATION NUMBER: US/10/200,522
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 09/337,280
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 08/980,071
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: 08/757,536
; PRIOR FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1189
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant Delta Endotoxin
US-10-200-522-2

Query Match      54.08; Score 3500.5; DB 14; Length 1189;
Best Local Similarity 57.08; Pred. No. 2.8e-259;
Matches 717; Conservative 143; Mismatches 289; Indels 109; Gaps 20;

Qy      7  NENEIIL--NALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNINPLVSAVQTGNIAG 64
Db      5  NQNCQIPYCNLS-----NPEEVLDDGERISTGN-----SSIDISLSLVQ 43
Qy      65  RILGLVGPVAGQIASYFSLVGLWPRGRDQWEIFLHVQELINQOITENARNALARL 124
Db      44  FLVSNF--VPGGFLVGLIDFWGIVGP---SQMDAFLVQIEQLINERIAEFARMAAIANL 99
Qy      125  QGLGDSFRAVQOSLEDWLENRDDARTSVLYTQVIALELOFLNAMPFLFAINQEVPLMV 184
Db      100  EGLGNFNFIYEAPEKFEEDPNPNPATRVIDRILDGLLERIDPISAFSGFEVPLLSV 159

```

```

Qy      185  YAAQAAHLHLLRLDASLPGSEBGLTSQEIQRYYEROVEQTRDYSDYCVWYNTGLNSLRG 244
Db      160  YAAQAAHLHLLRLDASLPGSEBGLTSQEIQRYYEROVEQTRDYSDYCVWYNTGLNSLRG 219
Qy      245  TNAASVRVYNQPRDRLTLGLVDLVALFPSPVDTRTYPINTSAQLTREVYDTAIGATGVNMA 304
Db      220  STYQDWITNRLRRDRLTLGLVDLVALFPSPVDTRTYPINTSAQLTREVYDTAIGATGVNMA 275
Qy      305  SMNWNNAAPFSAIETAVIRSPHLLDFLEQLTIFSTSSRWSATRMTYWRGHTIISRPI 364
Db      276  POLQSAQALPTFNVMESSAIRNPHLFDILNLLTIFTD--WFSVGRNFYWGGRHVSISSI 332
Qy      365  GGLINTSTHGNTSINPVLRSFFSDRDVWTBSYAGVLL---WGLYLEPIHGVPTVRFN 420
Db      333  GGNNTSPIYGREANOEPFRSFTFNGPVFRTLSNPTLRLLQQPWPAPPFNLRGVGEVFEFS 392
Qy      421  FRNPQTEF--RGTYANSQPYESPCQLKDSSTELPPETTERPNYVESYSHRSHIGLIS 477
Db      393  --TPTNSFYRGRTV-----DSLTELPPEDNSVPPREGYSRHLCHATFVQ 436
Qy      478  QSRVHV---PVYSWTHRSADRNTTSSDSITQIPLVKGFNLNSGTSVVSGPGFTGDI 533
Db      437  RSGTPELTGTVWFSWTHRSATLNTIDPERINQIPLVKGFVWGGTSVITGPGFTGDI 496
Qy      534  RTNVGSLVSMGLNFNNTSLQRYRVRYAASQ-----TWLVRTVVGSTTFDQGFPS 586
Db      497  RRNTFGDFVSLQVNSINSPITQRYRLFRYASSRDAARVILTGAASTGVGGQGVNNMPLQK 556
Qy      587  TMSANESLTSQSPRAEFP-----VGISASGSOTAGISISNNAAGRQFFHPDKIE 635
Db      557  TMEIGENLTSRTFRYTFDFSNPFSFRANPDILIGISEQLFCAG--SISG-----ELYDKIE 611
Qy      636  FIPITAFEAYDLERAQAVNALFTNTNPRRLKTDVTDYHIDQVSNLACLSDSEFCLDE 695
Db      612  IILADATFEASDLERAQAVNALFTSSNQIGLTKTDVTDYHIDQVSNLACLSDSEFCLDE 671
Qy      696  KRELLBKVKAKLSDERNLQDPNTSINKPDPFISTNEQSNFTSIHEGSEHGWGSEN 755
Db      672  KRELSKVKHAKLSDERNLQDPNFRGINRQPD-----RGRWGSTD 713
Qy      756  ITTQEGNDVPKENYVTLPGTFENECYTYLYQKIGESLKAITYQLRGYIEDSQDLIELYL 815
Db      714  ITTQGGDDVFKENYVTLPGTVDECYTYLYQKIDESKLKAYTRYELRGYIEDSQDLIELYL 773
Qy      816  IRYNAKHETLDVPGTESVMPLSVESPIGRGCEPNRCAPHFEMNPDLDCSCRDGKCAHKS 875
Db      774  IRYNAKHEIVNVPCTGSLWPLSAQSPGKCGENRCAPHLEWNPDLDCSCRDGKCAHKS 833
Qy      876  HFFSLDIDICTDLHENLGVVWVFKITQEGHARLGNLEFIEBKPLLGEALSVRKAEKK 935
Db      834  HHFTLIDVCGTDLNEDLGVWVFKITQGHARLGNLEFLEBKPLLGEALAVKAEKK 893
Qy      936  WRDKREKLOLETKRVVTEAKEAVDALFVDSQYNRLQADTNIGMHAADKLVRHREAYLS 995
Db      894  WRDKREKLOLETNIVYKEAKESVDALFVNSQYDLQVDTNMIHAADKVRHREAYLP 953
Qy      996  ELSVIFGVNAEIPFEELEGRITAIISLYDARNVKNVNGDFNNGLLCMWVKGHDV-QQSHR 1054
Db      954  ELSVIFGVNAEIPFEELEGRIFTAYSLYDARNVKNVNGDFNNGLLCMWVKGHDVVEEQNNH 1013
Qy      1055  SVLVIPWEAEVQAVRVCGRGYILRVYAYKEGCGCVTHIEINNTDELKFKNCEE 1114
Db      1014  SVLVIPWEAEVQAVRVCGRGYILRVYAYKEGCGCVTHIEINNTDELKFKNCEE 1073
Qy      1115  EYVPTDGTGNDYTA---HOGTAVCNRNAGYEDAYEDVDTASVNYKPYEBETVTDVR 1170
Db      1074  EYVNNVTVCNNVTGTQEEYEGT--YTSRNOGYDEAYGNNPSVPADYASVYEKSYTDGR 1131
Qy      1171  RDNHCEYDRGVNVPPLPAGYMTKELEYFETDKVWIEIGETGKFTVDSVELLMEE 1228
Db      1132  RENPCSNRGYDGYTLPAGYVTKOLEYFETDKVWIEIGETGFTVDSVELLMEE 1189

```

Db 612 IILADATPEASDRLERAQKAVNALFTSSNQIGLKTVDYDHYDQVSNLVDCLSDFECLDE 671
 Qy 696 KRELLEKVKYAKRLSDERLILQDNPFTSINKQPPDIFSTNEQSNFTSHEQSEHGHWGSEN 755
 Db 672 KRELSEKVKYAKRLSDERLILQDNPFRGINQPD-----RWRGSTD 713
 Qy 756 ITIQGNDVFKENYVTLPGTNECYPTLYQKIGESLKAATRYQLRGYIEDSDLEIYL 815
 Db 714 ITIQGDDVFKENYVTLPGTDECYPTLYQKIDESKLKATRYELRGYIEDSDLEIYL 773
 Qy 816 IRYNAKHETLDVPGTESVWPLSVESPIGRCEPNRCAPHFENWPDLDSCSDRDKGKCAHS 875
 Db 774 IRYNAKHETLDVPGTESVWPLSVESPIGRCEPNRCAPHFENWPDLDSCSDRDKGKCAHS 833
 Qy 876 HFSLDIDIGCTDLHENLGVWVFKITQOEGHARLGNLEFTEERPLLGEALSRVKRAEKK 935
 Db 834 HFTFLDIDVGCTDLNEDLGWVWFKITQDGHARLGNLEFTEERPLLGEALSRVKRAEKK 893
 Qy 936 WRDKREKLQLETKRYVTEAKEAVDALFVDSQYNRLOADYTNIGMHAADKLVRHIREAYLS 995
 Db 894 WRDKREKLQLETKRYVTEAKEAVDALFVDSQYNRLOADYTNIGMHAADKLVRHIREAYLP 953
 Qy 996 ELSVIPGNVABIELEGRIITLALSDYDARVNVKNGDPNNGIACWNVKGVHDV-QQSHHR 1054
 Db 954 ELSVIPGNVABIELEGRIITLALSDYDARVNVKNGDPNNGIACWNVKGVHDV-QQSHHR 1013
 Qy 1055 SVLVIPBEWAEVSOAVRCPGRGVLIRVTAKEGVGSGCVTHIEINNTDELKFNCEEE 1114
 Db 1014 SVLVIPBEWAEVSOAVRCPGRGVLIRVTAKEGVGSGCVTHIEINNTDELKFNCEEE 1073
 Qy 1115 EYVPTDGTGNDYTA----HQGTAVCSNRNAGYEDAYEDVDTASVNYKPYEEETDVR 1170
 Db 1074 EYVPTDGTGNDYTA----HQGTAVCSNRNAGYEDAYEDVDTASVNYKPYEEETDVR 1131
 Qy 1171 RDHCEVDRGVNVPPLPAGWMTKELEYFPETDKWIEIGETGKPIVDSVELLMEE 1228
 Db 1132 RENPCSNRGYDGTPLPAGVYTKDLEYFPETDKWIEIGETGKPIVDSVELLMEE 1189

RESULT 10
 US-09-972-175-2
 ; Sequence 2, Application US/09972175
 ; Publication No. US20030101482A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baum, James A.
 ; Gilmer, Amy Jelen
 ; Mettus, Anne-Marie Light
 ; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
 ; LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS
 ; NUMBER OF SEQUENCES: 76
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Arnold, White & Durkee
 ; STREET: P.O. Box 4433
 ; CITY: Houston
 ; STATE: Texas
 ; COUNTRY: USA
 ; ZIP: 77210
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/972,175
 ; FILING DATE: 05-Oct-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/337,635
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kitchell, Barbara S.
 ; REGISTRATION NUMBER: 33,928
 ; REFERENCE/DOCKET NUMBER: MSCO:206

TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 512/418-3000
 ; TELEFAX: 512/474-7577
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1189 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 ; US-09-972-175-2

Query Match 54.0%; Score 3500.5; DB 10; Length 1189;
 Best Local Similarity 57.0%; Pred. No. 2.8e-259;
 Matches 717; Conservative 143; Mismatches 289; Indels 109; Gaps 20;

Qy 7 NENEII--NALSTPAVSNHSTQMDLSDPARIESLCTAEGNNINPLVSASTVQTGINAG 64
 Db 5 NQNCIPYNCLS-----NPEVLLDGERISTGN-----SSIDISLSLVQ 43
 Qy 65 RILGLVGPAGQIASFYSLVGLMWRGRDQWEIPLHEVLEQLINQOITENARNTALRL 124
 Db 44 FLVSNF--VPGGGLVGLIDFVWGIWGP---SQMDAFLVQIEQLINERIAEFARNAAL 99
 Qy 125 QGLGDSFRAYQQSLEDWLENRDDRARTSVLYTQVIALELDFLAMPFLAIRNOEVPLIMV 184
 Db 100 EGLGNFNFIYVEAFKEWEDPNPATRVIDRFRILDGLLREDIPSAISGFEVPLSV 159
 Qy 185 YQAANLHLLLRDASLFGSEFGLTSQEIORYERYEQVQTRDYSDYCVWYNTGLNSLRG 244
 Db 160 YQAANLHLLLRDASLFGSEFGLTSQEIORYERYEQVQTRDYSDYCVWYNTGLNSLRG 219
 Qy 245 TNAASVRYNQFRDLTLGLVDLVALPSPDYTRTPINTSAQLTRVYTTDAIGATGVNMA 304
 Db 220 STYQDMITNRLRDLTLVLDIAAFPNYDNRYPQIPVQGLTRVYTTDPL-----INFN 275
 Qy 305 SMNWNNAAPSASIAETAVIRSPHLLDFLEQLTIFSTSSRWSATRHMTYWRGHTIOSRPI 364
 Db 276 POLQSVLAQLPTFNVMESSAIRNPHLFDILANLITFTD---WFSVGRNFYWGHRVSSLI 332
 Qy 365 GGLNLTSTHGSTWTSINPVRLSPFRSDVYWTESYAGVLL-----WGIYLEPIHGVPTRFN 420
 Db 333 GGGNITSPIYCREANOEPPRSFTFNGFVFTLNTLRLQLQPPWAPPFPNLRGVEGVEFS 392
 Qy 421 FRNPQTFE---RGTYNSQPYESPGQLKXDSELPETTERPNVYESYSHRISHIGLIS 477
 Db 393 --TPTNSFTYRGRTV-----DSUTELPDSNVPPREGYSHRICHATFVQ 436
 Qy 478 QSRVHV-----PVYSWTHRSADRTNTISSDSITQIPLVKSFNLNSGTSVSGPGFTGGDII 533
 Db 437 RSGTTPFLTGGVFSWTHRSATLNTIDPERINQIPLVKGFVWGGTSVITGPGFTGGDIL 496
 Qy 534 RTVWGSVLGMLNFNNTSLQRYRVRYAASQ-----TMVLRTVVGSTTTFDQGFPS 586
 Db 497 RRNTFGDFVSLQVNSPITQRYRLRFRYASSRDARVILVTGAASTGCGQVSNMPLQK 556
 Qy 587 TMSANESLTSQSFRFAEFP-----VGISASGSQTAGISINNAAGRTFPHDKIE 635
 Db 557 TMEIGENLTRYTRYTDFSNPFSFRANPDIIIGSEQLPFGAG--SISGG-----ELYIDKIE 611
 Qy 636 FIITATFAEYDLERAQAVNALFTNTNPRRLKTDVTDYHIDQVSNLVAACLSDFECLDE 695
 Db 612 IILADATPEASDRLERAQKAVNALFTSSNQIGLKTVDYDHYDQVSNLVDCLSDFECLDE 671
 Qy 696 KRELLEKVKYAKRLSDERLILQDNPFTSINKQPPDIFSTNEQSNFTSHEQSEHGHWGSEN 755
 Db 672 KRELSEKVKYAKRLSDERLILQDNPFRGINQPD-----RWRGSTD 713
 Qy 756 ITIQGNDVFKENYVTLPGTNECYPTLYQKIGESLKAATRYQLRGYIEDSDLEIYL 815
 Db 714 ITIQGDDVFKENYVTLPGTDECYPTLYQKIDESKLKATRYELRGYIEDSDLEIYL 773
 Qy 816 IRYNAKHETLDVPGTESVWPLSVESPIGRCEPNRCAPHFENWPDLDSCSDRDKGKCAHS 875

```

Db 220 STYQDMITNRLRRDLTLVLDIAAFPNYDNRRIQPVQQLTREYVTDPL-----INFN 275
Qy 305 SMWYNNAPSAIETAVIRSPHLLDFLEQLTIFSTSSRSWATRMWYWRGHTIQSRPI 364
Db 276 PQLQSVLAQLPTFNWESSAIRPHLDLNNLITFTD--WFSVGRNFYWGGRHVLSLI 332
Qy 365 GGLINTSTHGSTNTSINPVLSPFSDRVYWTESYAGVLL-----WGIYLEPIHGVTVRFN 420
Db 333 GCGNITSPIYGREANQEPSPFTFNGPVFTLSNPTLRLLQOPWAPPFNLRGVEGVEFS 392
Qy 421 FRNPQTFE---RGTYANSQPYESPGQLKDSSTELPPTETTERPNYESYSHRLSHIGLIS 477
Db 393 --TPTNSFTYRGRTV-----DSLTLPEDNSVPPREGYSHRLCHATFVQ 436
Qy 478 QSRVHV-----PVYSWTHRSADRTNTSSDITQIPLVKFNLNSGTSVVSGPGFTGDI 533
Db 437 RSGTPTLTGTVFSPWTHRSATLNTIDPERINQIPLVKFRVWGTSVIITGPGFTGDI 496
Qy 534 RTNVGSLVSMGLNFNNNTSLQRYRVRVRYAASQ-----TMVLRVTVGGSSTTFDQGFPS 586
Db 497 RNTFGDFVSLQVNSPITQRYRLFRYASSRDARVILVTGAASTGVGGQSVNNPQLOK 556
Qy 587 TMSANESLTSQSFRFAEFP-----VGISASGSQTAGISISNNAGROTFFHDKIE 635
Db 557 TMEIGENLTSRTFRYTDNPFSPFRANPDIIIGISEQLFCAG-SISGG-----ELYDKIE 611
Qy 636 FIPITATFAEYDLERAQAVNALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDFECLDE 695
Db 612 ILLADATFAESDLERAQAVNALFTSSNQIGLTKTDVTDYHIDQVSNLVACLSDFECLDE 671
Qy 696 KRELLEKVKYAKLSDERNLQDPNFTSINKQDPFISTNEQSNFTSIHEQSEHGWSGEN 755
Db 672 KRELSEKVKHAKLSDERNLQDPNFRGINRQPD-----RGRWGSTD 713
Qy 756 ITIOEGNDVPEKENYVTLPGTFNFCYPTLYOKIGESLKAATRYQLRGYIEDSDLEIYL 815
Db 714 ITIOGGDDVPEKENYVTLPGTVDECYPTLYOKIDESKLAATRYELRGYIEDSDLEIYL 773
Qy 816 IRYNAKHETLDVPGTESVWPLSVESPIGRCEPNRCAPHPWPNPDLDSCRCDEKCAHNS 875
Db 774 IRYNAKHEIVNVPGTSLWPLSAQSPGKCGEPNRCAPHPLEWPNPDLDSCRCDEKCAHNS 833
Qy 876 HIFSLDIDICTDLHENLVVWVFKIKTQEGHARLGNLEFIEBKPLLGEALSRVKAEEK 935
Db 834 HHFTLDIDVCTDLNEDLGWVIFKIKTQGHARLGNLEFIEBKPLLGEALSRVKAEEK 893
Qy 936 WRDKREKLOLETKRYVTEAKEADVALFVDSOYNRLQADTNIGMTHAADKLVRHIREAYLS 995
Db 894 WRDKREKLOLETNIVYKEAKESVDALFVNSQYDRLOQVDTNIAHAAKRVHIREAYLP 953
Qy 996 ELSVIPGVNAEIPFEELEGRITITAIISLYDARNVVKNGDFNNGLACWNVKGHDVY-QQSHR 1054
Db 954 ELSVIPGVNAEIPFEELEGRIFTAYSLYDARNVVKNGDFNNGLACWNVKGHDVVEQNNHR 1013
Qy 1055 SVLVIPEWEAEVQAVRVCGRGYILRVATYKSGYEGGCVTIHEINNTDELKFKNCBEE 1114
Db 1014 SVLVIPEWEAEVQAVRVCGRGYILRVATYKSGYEGGCVTIHEINNTDELKFKNCBEE 1073
Qy 1115 EYVPTDGTGNDYTA-----HQTAVCNRSRAGYEDAYEDVDTTASVNYKPYEETVTDYR 1170
Db 1074 EYVNNVTVCNNTYGTQEEYEGT--YTSRNOGYDEAYGNNPSPADYASVYEKSYTDGR 1131
Qy 1171 RDNHCEYDRGVNVPPLPAGMYMKELEYFPETDKVWIEIGETGKFIIVDSVELLMEE 1228
Db 1132 RENPCSNRGYGYTPLPAGVTVYKOLEYFPETDKVWIEIGETGTFIVDSVELLMEE 1189

```

RESULT 9

US-10-200-522-59
; Sequence 59 Application US/10200522
; Publication No. US20030195336A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.

```

; APPLICANT: Gilmer, Amy Jelen
; APPLICANT: Mettuss, Anne Marie Light
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE COMPOSITIONS ENCODING LEPIDOPTERAN-TC
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: MECO:213 (11792.0213 DVUS01)
; CURRENT APPLICATION NUMBER: US/10/200,522
; PRIOR FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 09/337,280
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 08/980,071
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: 08/757,536
; PRIOR FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 1189
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant Delta Endotoxin
; US-10-200-522-59

Query Match 54.1%; Score 3502.5; DB 14; Length 1189;
Best Local Similarity 57.0%; Pred. No. 2e-259;
Matches 717; Conservative 143; Mismatches 289; Indels 109; Gaps 20;

Qy 7 NENEII--NALSIAPVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSVSTVGTGINIAG 64
Db 5 NQNCIIPYNCL-----NPEVLLDGERISTGN-----SSIDISLSLVQ 43
Qy 65 RILGLVGVFPAGQIASFYSLVGLMWRGRDQWEIFLEHVEQLINQOITENARNTALARL 124
Db 44 FLVSNE-VFEGGFLVGLIDFVWGIYGP---SOWDAFLVQLEQLINERIAEFARNAIAANL 99
Qy 125 QGLGDSFRAYQOSLEWLENRRDDARTSVLYTQYIALELDLFLNAMPFLFAIRNOEVPLLMV 184
Db 100 EGLGNFNITYVEAFKEWEEDPNPATRVIDRFRILDGLLERDIPSFSAISGEVFEVLLSV 159
Qy 185 YAAQANLHLLLRDASLFGSEGLTSGEITQRYVEROVEQTRDYSYCVENYNTGLNSLRG 244
Db 160 YAAQANLHLLLRDASLFGSEGLTSGEITQRYVEROVEQTRDYSYCVENYNTGLNSLRG 219
Qy 245 TNAASVRYNQFRRLDITGLVLDLVALPSPYDTRTYPTINTSAQLTREYVTDATGATGNMA 304
Db 220 STYQDMITNRLRRDLTLVLDIAAFPNYDNRRIQPVQQLTREYVTDPL-----INFN 275
Qy 305 SMWYNNAPSAIETAVIRSPHLLDFLEQLTIFSTSSRSWATRMWYWRGHTIQSRPI 364
Db 276 PQLQSVLAQLPTFNWESSAIRPHLDLNNLITFTD--WFSVGRNFYWGGRHVLSLI 332
Qy 365 GGLINTSTHGSTNTSINPVLSPFSDRVYWTESYAGVLL-----WGIYLEPIHGVTVRFN 420
Db 333 GCGNITSPIYGREANQEPSPFTFNGPVFTLSNPTLRLLQOPWAPPFNLRGVEGVEFS 392
Qy 421 FRNPQTFE---RGTYANSQPYESPGQLKDSSTELPPTETTERPNYESYSHRLSHIGLIS 477
Db 393 --TPTNSFTYRGRTV-----DSLTLPEDNSVPPREGYSHRLCHATFVQ 436
Qy 478 QSRVHV-----PVYSWTHRSADRTNTSSDITQIPLVKFNLNSGTSVVSGPGFTGDI 533
Db 437 RSGTPTLTGTVFSPWTHRSATLNTIDPERINQIPLVKFRVWGTSVIITGPGFTGDI 496
Qy 534 RTNVGSLVSMGLNFNNNTSLQRYRVRVRYAASQ-----TMVLRVTVGGSSTTFDQGFPS 586
Db 497 RNTFGDFVSLQVNSPITQRYRLFRYASSRDARVILVTGAASTGVGGQSVNNPQLOK 556
Qy 587 TMSANESLTSQSFRFAEFP-----VGISASGSQTAGISISNNAGROTFFHDKIE 635
Db 557 TMEIGENLTSRTFRYTDNPFSPFRANPDIIIGISEQLFCAG-SISGG-----ELYDKIE 611
Qy 636 FIPITATFAEYDLERAQAVNALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDFECLDE 695
Db 612 ILLADATFAESDLERAQAVNALFTSSNQIGLTKTDVTDYHIDQVSNLVACLSDFECLDE 671
Qy 696 KRELLEKVKYAKLSDERNLQDPNFTSINKQDPFISTNEQSNFTSIHEQSEHGWSGEN 755
Db 672 KRELSEKVKHAKLSDERNLQDPNFRGINRQPD-----RGRWGSTD 713
Qy 756 ITIOEGNDVPEKENYVTLPGTFNFCYPTLYOKIGESLKAATRYQLRGYIEDSDLEIYL 815
Db 714 ITIOGGDDVPEKENYVTLPGTVDECYPTLYOKIDESKLAATRYELRGYIEDSDLEIYL 773
Qy 816 IRYNAKHETLDVPGTESVWPLSVESPIGRCEPNRCAPHPWPNPDLDSCRCDEKCAHNS 875
Db 774 IRYNAKHEIVNVPGTSLWPLSAQSPGKCGEPNRCAPHPLEWPNPDLDSCRCDEKCAHNS 833
Qy 876 HIFSLDIDICTDLHENLVVWVFKIKTQEGHARLGNLEFIEBKPLLGEALSRVKAEEK 935
Db 834 HHFTLDIDVCTDLNEDLGWVIFKIKTQGHARLGNLEFIEBKPLLGEALSRVKAEEK 893
Qy 936 WRDKREKLOLETKRYVTEAKEADVALFVDSOYNRLQADTNIGMTHAADKLVRHIREAYLS 995
Db 894 WRDKREKLOLETNIVYKEAKESVDALFVNSQYDRLOQVDTNIAHAAKRVHIREAYLP 953
Qy 996 ELSVIPGVNAEIPFEELEGRITITAIISLYDARNVVKNGDFNNGLACWNVKGHDVY-QQSHR 1054
Db 954 ELSVIPGVNAEIPFEELEGRIFTAYSLYDARNVVKNGDFNNGLACWNVKGHDVVEQNNHR 1013
Qy 1055 SVLVIPEWEAEVQAVRVCGRGYILRVATYKSGYEGGCVTIHEINNTDELKFKNCBEE 1114
Db 1014 SVLVIPEWEAEVQAVRVCGRGYILRVATYKSGYEGGCVTIHEINNTDELKFKNCBEE 1073
Qy 1115 EYVPTDGTGNDYTA-----HQTAVCNRSRAGYEDAYEDVDTTASVNYKPYEETVTDYR 1170
Db 1074 EYVNNVTVCNNTYGTQEEYEGT--YTSRNOGYDEAYGNNPSPADYASVYEKSYTDGR 1131
Qy 1171 RDNHCEYDRGVNVPPLPAGMYMKELEYFPETDKVWIEIGETGKFIIVDSVELLMEE 1228
Db 1132 RENPCSNRGYGYTPLPAGVTVYKOLEYFPETDKVWIEIGETGTFIVDSVELLMEE 1189

```


APPLICATION NUMBER: US 07/772,027
 FILING DATE: 04-OCT-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Meigs, J. Timothy
 REGISTRATION NUMBER: 38,241
 REFERENCE/DOCKET NUMBER: S-188051
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (919) 541-8577
 TELEFAX: (919) 541-8689
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 US-09-988-462-7

Query Match 87.4%; Score 5659.5; DB 10; Length 1207;
 Best Local Similarity 89.4%; Pred. No. 0;
 Matches 1079; Conservative 34; Mismatches 89; Indels 5; Gaps 2;

QY 27 MDLSPDARIEDSLCIARGNNINPLVASTVQTGINIAGRILGVLGVPPAGQIASFYSLV 86
 DB 1 MDLSPDARIEDSLCIARGNNINPLVASTVQTGINIAGRILGVLGVPPAGQIASFYSLV 60

QY 87 GELWPRGRDQWEIFLEHVEQLINQIITENARNTALRQLGLGDSFRAYQOSLEDWLENRD 146
 DB 61 GELWPRGRDQWEIFLEHVEQLINQIITENARNTALRQLGLGDSFRAYQOSLEDWLENRD 120

QY 147 DARTSRVLYTQYIALELDLFLNAPLFAIRNQEVPLLMVYAQAANLHLLLRDASLFGSEF 206
 DB 121 DARTSRVLYTQYIALELDLFLNAPLFAIRNQEVPLLMVYAQAANLHLLLRDASLFGSEF 180

QY 207 GLTSOETQRYRQVEQTRDYSYCVENWYNTGLNSLGTNAASWVRVYNQFRRDLTLGLVD 266
 DB 181 GLTSOETQRYRQVEQTRDYSYCVENWYNTGLNSLGTNAASWVRVYNQFRRDLTLGLVD 240

QY 267 LVALFSDYDRTYPTINTSAQLTREVTYDAIGATGVNMAWNNNAPSPSAIETAVIRS 326
 DB 241 LVALFSDYDRTYPTINTSAQLTREVTYDAIGATGVNMAWNNNAPSPSAIETAAIRS 300

QY 327 PHLLDFLEQLTIFSTSRWSATHMTYWRGHTTQSRPIGGGLNTSTHGSNTSINPVRLS 386
 DB 301 PHLLDFLEQLTIFSTSRWSATHMTYWRGHTTQSRPIGGGLNTSTHGSNTSINPVRLR 360

QY 387 FFSRDVYWTESYAGVLLWGLYLPPIHGVPTVRNFRNPONTFPGTANYSQPYESGLQL 446
 DB 361 FASRDVYRTESYAGVLLWGLYLPPIHGVPTVRNFRNPONTFPGTANYSQPYESGLQL 420

QY 447 KDSETELPPTETRPNYESYSHRLSHGLISQSRVHVPTVSWTHRSADRNTNTSSDSITQ 506
 DB 421 KDSETELPPTETRPNYESYSHRLSHGLISQSRVHVPTVSWTHRSADRNTNTGPNRITQ 480

QY 507 IPLVKSFLNLSGTSVWSGPGTGGDIIRTNVNGSVLMSGLNFNNTSLQRYRVRVRAASQ 566
 DB 481 IPWVKASELPQGTIVVRGPGTGGDIIRTNVNGSVLMSGLNFNNTSLQRYRVRVRAASQ 540

QY 567 TMVLRTVVGSTFTDQGFPPSTMSANESLTSQSPFAFPFPGVIGSAGSQ-TAGISINNAG 625
 DB 541 DFDFFVSRGTTVNNFRFLTMSNGDELKYNFVRRAFTTPTFTQIQDIIRTSIQGLSG 600

QY 626 RQTFHFQKIEPIPTATFEAYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVA 685
 DB 601 NGEVYIDKIEIIPATATFEAYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVA 660

QY 686 CLSDEFCLDEKRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIHQ 745
 DB 661 CLSDEFCLDEKRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIHQ 720

QY 746 SEHGWSGSEMITQEGNDVFNKENVYVTLPGTFNECYPTLYLQKIGESLKYATRYQLRGI 805
 DB 721 SEHGWSGSEMITQEGNDVFNKENVYVTLPGTFNECYPTLYLQKIGESLKYATRYQLRGI 780

RESULT 7

US-09-826-660-23
 ; Sequence 23, Application US/09826660
 ; Patent No. US20010026940A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cardineau, Guy A.
 ; APPLICANT: Stelman, Steven J.
 ; APPLICANT: Narva, Kenneth E.
 ; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
 ; FILE REFERENCE: MA-714XC2D1
 ; CURRENT APPLICATION NUMBER: US/09/826,660
 ; CURRENT FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 09/178,252
 ; PRIOR FILING DATE: 1998-10-23
 ; PRIOR APPLICATION NUMBER: 60/065,215
 ; PRIOR FILING DATE: 1997-11-12
 ; PRIOR APPLICATION NUMBER: 60/076,445
 ; PRIOR FILING DATE: 1998-03-02
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 23
 ; LENGTH: 1186
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
 US-09-826-660-23

Query Match 78.8%; Score 5108; DB 9; Length 1186;
 Best Local Similarity 80.6%; Pred. No. 0;
 Matches 995; Conservative 76; Mismatches 108; Indels 56; Gaps 8;

QY 1 LTSNRKNEIINALSIPAVSNHSTOMDLSPDARIEDSLCIAEGNNINPLVASTVQTGI 60
 DB 1 MTSNRKNEIINALSIPAVSNHSAQWNLSTDAIEDSLCIAEGNNIDPFVASTVQTGI 60

QY 61 NIAGRILGVLPFAGQIASFYSLVGEAWPRGRDQWEIFLEHVEQLINQIITENARNTA 120
 DB 61 NIAGRILGVLPFAGQIASFYSLVGEAWPRGRDQWEIFLEHVEQLIRQOQVIENTRDTA 120

; CURRENT APPLICATION NUMBER: US/10/809,953
 ; CURRENT FILING DATE: 2004-03-26
 ; PRIOR APPLICATION NUMBER: US/09/661,016
 ; PRIOR FILING DATE: 2000-09-13
 ; PRIOR APPLICATION NUMBER: PCT/EP90/00905
 ; PRIOR FILING DATE: 1990-05-30
 ; PRIOR APPLICATION NUMBER: GB 89401499.2
 ; PRIOR FILING DATE: 1989-05-31
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 10
 ; LENGTH: 1228
 ; TYPE: PRT
 ; ORGANISM: Bacillus thuringiensis
 US-10-809-953-10

Query Match 88.68; Score 5742; DB 16; Length 1228;
 Best Local Similarity 89.18; Pred. No. 0;
 Matches 1098; Conservative 35; Mismatches 90; Indels 10; Gaps 3;

QY	1	LTSNRKNEEINALSIPAVSNHSTOMDLSPDARIEDSLCIAEGNNINPLVASTVOTGI	60
DB	1	LTSNRKNEEIN-----AVSNESAQMDLDPDARIEDSLCIAEGNNIDPFVASTVOTGI	55
QY	61	NIAGRILGLVGPVAGQIASFYSLVGLWPRGRDQWEI FLEHVEQLINQOITENARNTA	120
DB	56	NIAGRILGLVGPVAGQIASFYSLVGLWPRGRDQWEI FLEHVEQLINQOITENARNTA	115
QY	121	LARLQGLGDSFRAYQOQSLWLENRDDRARTSVLYTOYIALELDFLNAPLFAIRNOEVP	180
DB	116	LARLQGLGDSFRAYQOQSLWLENRDDRARTSVLYTOYIALELDFLNAPLFAIRNOEVP	175
QY	181	LLMVYAQAANLHLLLDASLFGSEFGLTSQEIQRVYVEROETRDYSDYCVEMWNTGLN	240
DB	176	LLMVYAQAANLHLLLDASLFGSEFGLTSQEIQRVYVEROETRDYSDYCVEMWNTGLN	235
QY	241	SLRGNTAASWVRYNQPRRDITLGLVDLVALFPSTYDRTYPTINTSAQLTRVYTDAGATG	300
DB	236	SLRGNTAASWVRYNQPRRDITLGLVDLVALFPSTYDRTYPTINTSAQLTRVYTDAGATG	295
QY	301	VNWSMNNYNNAPSFSAIETAVTRSPHLDLLEQLTIFSTSSRSWATRMWYRGHTIQ	360
DB	296	VNWSMNNYNNAPSFSAIETAVTRSPHLDLLEQLTIFSTSSRSWATRMWYRGHTIQ	355
QY	361	SRPIGGGLNTSTHGNTSNINPVLRSFFSRDVTYTESYAGVLLWGLIYLEPIHGVPTVRFN	420
DB	356	SRPIGGGLNTSTHGNTSNINPVLRSFFSRDVTYTESYAGVLLWGLIYLEPIHGVPTVRFN	415
QY	421	FRNPQNTFERGTANYSQPYSPGLQKDSSETLPPTTERPNYESYSHRLSHIGLSQSR	480
DB	416	FTNPQNISDRGTANYSQPYSPGLQKDSSETLPPTTERPNYESYSHRLSHIGLSQSR	475
QY	481	VHVPVYSWTHRSADRTNTISDSITQIPLVKSFNLSGTSVWSPGPGTGDDIIRTNVGS	540
DB	476	VHVPVYSWTHRSADRTNTIGPNRITQIPWKASSELPGQITTVVRGPGTGDDIIRTNVGS	535
QY	541	VLSGMLNFNTSLQRYVRVYRVAASQTMVLRTVVGSTTFDQGPSTMSANESILTSQSPR	600
DB	536	FGIRVTNVGFLQRYRIGRYASTVDFDFVVRGGTTVNFPRLTMSGDELKYGNFV	595
QY	601	FAEFPVGISAGSQ-TAGISINNAGSQTFHFKIEFIPITATFEAYDILERAQEAVAL	659
DB	596	RRAFTPTFTQDIIRTSIQGLSGNGEVYIDKIEIIPVATFEAYDILERAQEAVAL	655
QY	660	FTYTNPRRLKTDVTHIDQVSNLVAELDFECLDEKRELLKVKYAKRLSDERNLLQDP	719
DB	656	FTYTNPRRLKTDVTHIDQVSNLVAELDFECLDEKRELLKVKYAKRLSDERNLLQDP	715
QY	720	NFTSINKQDPFISTNEOSNTSIHQSEHGWGSENITIOEGNDVFKENYVTLPGTFNEC	779
DB	716	NFTSINKQDPFISTNEOSNTSIHQSEHGWGSENITIOEGNDVFKENYVTLPGTFNEC	775
QY	780	YPTYLYQKIGESSELKAYTRYQLRGYIEDSDQLEIYLIRYNNAKHETLDVPGTESLWPLSVE	839

RESULT 6

US-09-988-462-7
 ; Sequence 7, Application US/09988462
 ; Publication No. US20030046726A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kozziel, Michael G.
 ; Desai, Nalini M.
 ; Lewis, Kelly S.
 ; Kramer, Vance C.
 ; Warren, Gregory W.
 ; Evola, Stephen V.
 ; Crossland, Lyle D.
 ; Wright, Martha S.
 ; Merlin, Ellis J.
 ; Launis, Karen L.
 ;
 ; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
 ; INSECTICIDAL ACTIVITY IN MAIZE
 ;
 ; NUMBER OF SEQUENCES: 94
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Syngenta Biotechnology, Inc.
 ; STREET: 3054 Cornwalis Road
 ; CITY: Research Triangle Park
 ; STATE: NC
 ; COUNTRY: USA
 ; ZIP: 27709
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/988,462
 ; FILING DATE: 20-NOV-2003
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 09/547,422
 ; FILING DATE: 11-APR-2000
 ; APPLICATION NUMBER: US 08/459,504
 ; FILING DATE: 02-JUN-1995
 ; APPLICATION NUMBER: US 07/951,715
 ; FILING DATE: 25-SEP-1992

DB	776	YPTYLYQKIGESSELKAYTRYQLRGYIEDSDQLEIYLIRYNNAKHETLDVPGTESLWPLSVE	835
QY	840	SPIGRCCEPNRCAPHFENWPDLCSCRDGKCAHSHHFLSDIDIGCTDLHENLGVWVWF	899
DB	836	SPIGRCCEPNRCAPHFENWPDLCSCRDGKCAHSHHFLSDIDIGCTDLHENLGVWVWF	895
QY	900	KIKTQEGHARLGNLEFIEEKPLLEALSRVKRAEKWRDKREKLQLETKRVYTEAKEAVD	959
DB	896	KIKTQEGHARLGNLEFIEEKPLLEALSRVKRAEKWRDKREKLQLETKRVYTEAKEAVD	955
QY	960	ALFVDSQYNRLQADTNIGMHAADKLVRHIREAYLSLSVPGVNAEIFEELGRITAI	1019
DB	956	ALFVDSQYNRLQADTNIGMHAADKLVRHIREAYLSLSVPGVNAEIFEELGRITAI	1015
QY	1020	SLYDARNVKNVGNPNGLACWNVKGVHDVQOQSHRSVLVPEWEAEVSQAVRVCPRGYI	1079
DB	1016	SLYDARNVKNVGNPNGLACWNVKGVHDVQOQSHRSVLVPEWEAEVSQAVRVCPRGYI	1075
QY	1080	LRVTAYKEGYGEGCVTIHEIENNTDELKPKNCEEEVYPTDGTCDNYTAHQGTAA----	1135
DB	1076	LRVTAYKEGYGEGCVTIHEIENNTDELKPKNCEEEVYPTDGTCDNYTAHQGTAA----	1135
QY	1136	CNSRNGAYEDAYVDTTASVNYKPTVEEETTVTVRRDNHCEYDRGVYVYPPAGYWKTE	1195
DB	1136	CNSRNGAYEDAYVDTTASVNYKPTVEEETTVTVRRDNHCEYDRGVYVYPPAGYWKTE	1195
QY	1196	LEYFPEPTDKWIEIGETEGKFIVDSVELLMEE	1228
DB	1196	LEYFPEPTDKWIEIGETEGKFIVDSVELLMEE	1228

Db 958 DALFVDSQYDLQADTNIGMHAADKLVRHREAYLSLSVPGVNAEIPFEELEGRITTA 1017
Qy 1019 ISLYDARNVKNQDNNGNGLACWNVKGVHDVQOSSHRSVLVPIPEWEAEVSOAVRVCGRGY 1078
Db 1018 ISLYDARNVKNQDNNGNGLACWNVKGVHDVQOSSHRSVLVPIPEWEAEVSOAVRVCGRGY 1077
Qy 1079 ILRVATYKEGYGEGCVTIHEIENNTDELKFNCEEEVYPTDTCNDYTAHQGTAVCNS 1138
Db 1078 ILRVATYKEGYGEGCVTIHEIENNTDELKFNCEEEVYPTDTCNDYTAHQGTAVCNS 1137
Qy 1139 RNAGYDAYEVDVTTASVNYKPTVEEYTTDVRDNHCEYDRGVNYPPLPAGYMTKELEY 1198
Db 1138 RNAGYDAYEVDVTTASVNYKPTVEEYTTDVRDNHCEYDRGVNYPPLPAGYMTKELEY 1197
Qy 1199 FPETDKWIEIGTEGKFI VDSVELLMEE 1228
Db 1198 FPETDKWIEIGTEGKFI VDSVELLMEE 1227

RESULT 4
US-10-926-819-8
; Sequence 8, Application US/10926819
; Publication No. US20050049410A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-003, A Delta-Endotoxin Gene and
; KEYWORDS: Methods for Its Use
; FILE REFERENCE: 045600/281577
; CURRENT APPLICATION NUMBER: US/10/926,819
; PRIOR FILING DATE: 2004-08-26
; PRIOR APPLICATION NUMBER: 60/498,518
; PRIOR FILING DATE: 2003-08-28
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1228
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis serovar entomocidus
US-10-926-819-8

Query Match 88.78; Score 5745; DB 17; Length 1228;
Best Local Similarity 89.14; Pred. No. 0;
Matches 1098; Conservative 35; Mismatches 90; Indels 10; Gaps 3;

Qy 1 LTSNRKNENIINALSIPAVSNHSTOMDLSFDARIEDSLCIAEGNNINPLVSASTVQTGI 60
Db 1 MTSNRKNENIIN-----AVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGI 55
Qy 61 NIAGRILGVLPFPAGQIASFYSLVGLWPRGRDOWEIFLEHVEQLINQOITENARNTA 120
Db 56 NIAGRILGVLPFPAGQIASFYSLVGLWPRGRDOWEIFLEHVEQLINQOITENARNTA 115
Qy 121 LARLOGLDSPRAYQOQSLDLEWNRDARTSVLYTQYIALELDFLNAPLFAIRNOQV 180
Db 116 LARLOGLDSPRAYQOQSLDLEWNRDARTSVLYTQYIALELDFLNAPLFAIRNOQV 175
Qy 181 LLMVYAQAANLHLLLDASLFGSEFGLTQEIQRYYEROVETRDYSDYCVWYNTGLN 240
Db 176 LLMVYAQAANLHLLLDASLFGSEFGLTQEIQRYYEROVETRDYSDYCVWYNTGLN 235
Qy 241 SLRGTAASVVRVYQFRDLTLGVLDLVALFPSSYDTRTPINTSAQLTRVYTDALGATG 300
Db 236 SLRGTAASVVRVYQFRDLTLGVLDLVALFPSSYDTRTPINTSAQLTRVYTDALGATG 295
Qy 301 VNMASWNNYNNAPSFSAIETAVIRSPHLLDFLEBOLTIFPSSRSWATRMVTRWGHITQ 360
Db 296 VNMASWNNYNNAPSFSAIAAIAIRSPHLLDFLEBOLTIFPSSRSWATRMVTRWGHITQ 355

Qy 361 SRPIGGGLTNTSHGSTNTSINPVRSLFFSRDVTWYTESYAGVLLWGIYLEPIHGVPVTRFN 420
Db 356 SRPIGGGLTNTSHGATNTSINPVTLRFSRDRVYRTESYAGVLLWGIYLEPIHGVPVTRFN 415
Qy 421 FRNPQNTFRGTANYSQPYESPGLOIKDSETELPPETTERPNYESSHRLSHLGLISQSR 480
Db 416 FTNPQNISDRGTANYSQPYESPGLOIKDSETELPPETTERPNYESSHRLSHLGLISQSR 475
Qy 481 VHVVPVSWTHRSADRNTTSSDSITQIPLVKSPNLNSGTSVVSGPGFTGGDIIRTNVNGS 540
Db 476 VNVVPVSWTHRSADRNTTGNRITQIPWKASELPQGTIVVRGPGFTGGDIIRTNVNGS 535
Qy 541 VLSMGLNFNNTSLQYRVVRVYAASTWMLRVTVGGSTTFDQGPSPSTMSANESLTSQSR 600
Db 536 FGIPIRVTVANGPLTQYRIGFRYASTVDFDFVSRGGTIVNPRFLRTMNSGDELKYGNFV 595
Qy 601 FAEFPVGISASGSO-TAGISINNAGROTFFHPDKIEFIPITATFEAYDLERAQEAVAL 659
Db 596 RRAFTTPTFTTQIQDIIRTSIQGLSGNGEYVYDIKBIIPVTATFEAYDLERAQEAVAL 655
Qy 660 FTNTNPRRLKTDVTDYHIDQVSNLVACLSDFCDEKRELLEKVKYAKRLSDERNLLQDP 719
Db 656 FTNTNPRRLKTDVTDYHIDQVSNLVACLSDFCDEKRELLEKVKYAKRLSDERNLLQDP 715
Qy 720 NFTSINKQPDFISTNEQSNFTSIHQSEHGWMGSENITIQEGNDVFNKENVYVTLPGTFNEC 779
Db 716 NFTSINKQPDFISTNEQSNFTSIHQSEHGWMGSENITIQEGNDVFNKENVYVTLPGTFNEC 775
Qy 780 YPTLYLQKIGESSELKAYTRYQLRGYIEDSDQLEIYLIRYNKAKHETLDVPGTESVWPLSVE 839
Db 776 YPTLYLQKIGESSELKAYTRYQLRGYIEDSDQLEIYLIRYNKAKHETLDVPGTESVWPLSVE 835
Qy 840 SPIGRCEPNRCAPHEWNPDLDCSCRDGEKCAHSHHSLDIDIGCTDLHENLGVWVWF 899
Db 836 SPIGRCEPNRCAPHEWNPDLDCSCRDGEKCAHSHHSLDIDIGCTDLHENLGVWVWF 895
Qy 900 KIKTOGHARLGNLEFIEEKPLGEALSRVKRAEKKWRDKREKLQLETKRVTYEAKEAVD 959
Db 896 KIKTOGHARLGNLEFIEEKPLGEALSRVKRAEKKWRDKREKLQLETKRVTYEAKEAVD 955
Qy 960 ALFVDSQYDLQADTNIGMHAADKLVRHREAYLSLSVPGVNAEIPFEELEGRITTA 1019
Db 956 ALFVDSQYDLQADTNIGMHAADKLVRHREAYLSLSVPGVNAEIPFEELEGRITTA 1015
Qy 1020 SLVDARNVKNQDNNGNGLACWNVKGVHDVQOSSHRSVLVPIPEWEAEVSOAVRVCGRGY 1079
Db 1016 SLVDARNVKNQDNNGNGLACWNVKGVHDVQOSSHRSVLVPIPEWEAEVSOAVRVCGRGY 1075
Qy 1080 LRVATYKEGYGEGCVTIHEIENNTDELKFNCEEEVYPTDTCNDYTAHQGTAVCNS 1135
Db 1076 LRVATYKEGYGEGCVTIHEIENNTDELKFNCEEEVYPTDTCNDYTAHQGTAVCNS 1135
Qy 1136 CNSRNAGYDAYEVDVTTASVNYKPTVEEYTTDVRDNHCEYDRGVNYPPLPAGYMTKE 1195
Db 1136 CNSRNAGYDAYEVDVTTASVNYKPTVEEYTTDVRDNHCEYDRGVNYPPLPAGYMTKE 1195
Qy 1196 LEYFPETDKWIEIGTEGKFI VDSVELLMEE 1228
Db 1196 LEYFPETDKWIEIGTEGKFI VDSVELLMEE 1228

RESULT 5
US-10-809-953-10
; Sequence 10, Application US/10809953
; Publication No. US20040181825A1
; GENERAL INFORMATION:
; APPLICANT: Van Mellaert, Herman
; APPLICANT: Botterman, Johan
; APPLICANT: Van Rie, Jeroen
; APPLICANT: Joos, Henk
; TITLE OF INVENTION: RECOMBINANT PLANT EXPRESSING NON-COMPETITIVELY BINDING BT INSECTIC
; TITLE OF INVENTION: CRYSTAL PROTEINS
; FILE REFERENCE: 021565-078


```
Qy 541 VLSMGLNPNNTSLQRYRVRVRYAASQTMVLRTVTVGGSTTFDQGFPTMSANESLTSQSF 600
Db 541 VLSMGLNPNNTSLQRYRVRVRYAASQTMVLRTVTVGGSTTFDQGFPTMSANESLTSQSF 600
Qy 601 FAEFPVGISASGSGTAGISINNAAGRTFFDKIEFIPITATFAEYDLERAQAVNALF 660
Db 601 FAEFPVGISASGSGTAGISINNAAGRTFFDKIEFIPITATFAEYDLERAQAVNALF 660
Qy 661 TINTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLKVKYAKRLSDERNLLQDPN 720
Db 661 TINTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLKVKYAKRLSDERNLLQDPN 720
Qy 721 FTSINKQPDFISTNEQSNFTSIHQSEHGWMGSENITIQEGNDVFKENYVTLPGTFNECY 780
Db 721 FTSINKQPDFISTNEQSNFTSIHQSEHGWMGSENITIQEGNDVFKENYVTLPGTFNECY 780
Qy 781 PTLYLYQKIGSELKAYTRYQLRGVIEDSDLEIYLIRYNAKHETLDVPGTESVWPLSVES 840
Db 781 PTLYLYQKIGSELKAYTRYQLRGVIEDSDLEIYLIRYNAKHETLDVPGTESVWPLSVES 840
Qy 841 PIGRCGEPNRCAPHFENWPNLDCSCRDGEKCAHSHHFSLDIDIGCTDLHENLGVWVVK 900
Db 841 PIGRCGEPNRCAPHFENWPNLDCSCRDGEKCAHSHHFSLDIDIGCTDLHENLGVWVVK 900
Qy 901 IKTOEGHARLGNLEFIEBKPLLGALSRVKAEEKWRDKREKLQLETKRVVYTEAKEAVDA 960
Db 901 IKTOEGHARLGNLEFIEBKPLLGALSRVKAEEKWRDKREKLQLETKRVVYTEAKEAVDA 960
Qy *961 LFVDSQYNRLQADTNIQMIHAADKLVRHREAYLSELVPGVNAEIFELEGRITTAIS 1020
Db 961 LFVDSQYNRLQADTNIQMIHAADKLVRHREAYLSELVPGVNAEIFELEGRITTAIS 1020
Qy 1021 LYDARNVVKNGDFNGLACNVKGVHDVQOSHRSVLVPIPEWEAEVSQAVRVCPRGVIL 1080
Db 1021 LYDARNVVKNGDFNGLACNVKGVHDVQOSHRSVLVPIPEWEAEVSQAVRVCPRGVIL 1080
Qy 1081 RVTAYKEGYGEGCVTIHEIENNTDELKFKCEEBEVPTDGTGTCNDYTAHQGTAVCNRN 1140
Db 1081 RVTAYKEGYGEGCVTIHEIENNTDELKFKCEEBEVPTDGTGTCNDYTAHQGTAVCNRN 1140
Qy 1141 AGVEDAYEDVTASVNYKPYEETTYDVRDNCHEYDRGVNYVPPAGYMYKELEBYPP 1200
Db 1141 AGVEDAYEDVTASVNYKPYEETTYDVRDNCHEYDRGVNYVPPAGYMYKELEBYPP 1200
Qy 1201 ETDKVMIEIGETEGKFTVDSVELLMEE 1228
Db 1201 ETDKVMIEIGETEGFTVDSVELLMEE 1228

RESULT 3
US-10-428-961-63
; Sequence 63, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Wei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupar, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
; FILE REFERENCE: MECO201-1
; CURRENT APPLICATION NUMBER: US/10/428,961
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/153,995
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 63
; LENGTH: 1227
```

```
; TYPE: PRF
; ORGANISM: Bacillus thuringiensis
US-10-428-961-63
```

```
Query Match 91.3%; Score 5912.5; DB 15; Length 1227;
Best Local Similarity 91.6%; Pred. No. 0;
Matches 1127; Conservative 36; Mismatches 62; Indels 5; Gaps 3;
```

```
Qy 1 LTSNRKNENIINALSIPAVSNHSTOMDLSPDARIEDSLCIAEGNNINPLVSASTVGTGI 60
Db 1 LTSNRKNENIINALSIPAVSNHSAQNNLSTDAIEDSLCIAEGNNIDPFVSASTVGTGI 60
Qy 61 NIAGRILGVGVPPAGQIASFYSLVAGELWPRGRDQWEIFLEHVEQLINOQITENARNTA 120
Db 61 NIAGRILGVGVPPAGQIASFYSLVAGELWPRGRDQWEIFLEHVEHLIROQVTEENTD 120
Qy 121 LARLOGLDGFRAVQOSLEDWLENRRDARTSVLYTOYIALELDFNAMPLFAIRNOEVP 180
Db 121 LARLOGLDGFRAVQOSLEDWLENRRDARTSVLYTOYIALELDFNAMPLFAIRNOEVP 180
Qy 181 LLMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRVYERQVEOTRDYSDYCVWEYNTGLN 240
Db 181 LLMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRVYERQVEOTRDYSDYCARWYNTGLN 240
Qy 241 SLRGTNASWVRVYNQFRDLTLGVLDLVALPSPYDTRTYPTINTSAQLTRVYVYDAIGATG 300
Db 241 NLRGTNAESWLRVYNQFRDLTLGVLDLVALPSPYDTRTYPTINTSAQLTRVYVYDAIGATG 300
Qy 301 V--NMASMKVNNAPSPSAIETAVRSPLHLDLFLQLTIFSTSSRSWATPHMYWGH 358
Db 301 APGFASTNFWNNAPSPSAIEAAVIRPPLHLDLFLQLTIFSVLSRWSNTQYMYWGH 360
Qy 359 IQSRPFGGGLNTSTHGSTNTSINPRLSPFRSDVYWTESVAGVLLWGIYLEPIHGVPVTR 418
Db 361 LERTTSGSLSTWHTGNTSINPVLQFTSRDVRTTESPAGINI--LLTTPVNGVPPAR 418
Qy 419 FNRPNQNTFERTANYQSPYSGIQLKDSITELPETTERPNYSESYSHRLSHIGLISQ 478
Db 419 FNRPNPLNSL-RGSLLYTIGYTGVTGVTQVLDSETELPETTERPNYSESYSHRLSNIRLISG 477
Qy 479 SRVHVVPVYSWTHRSADORTNTISSDSITQIPLVKSFNLNSGTSVVGPGFTGGDIIRNVN 538
Db 478 NTLRAPVYSWTHRSADORTNTISSDSITQIPLVKSFNLNSGTSVVGPGFTGGDIIRNVN 537
Qy 539 GSVLSMGLNPNNTSLQRYRVRVRYAASQTMVLRTVTVGGSTTFDQGFPTMSANESLTSQS 598
Db 538 GSVLSMGLNPNNTSLQRYRVRVRYAASQTMVLRTVTVGGSTTFDQGFPTMSANESLTSQS 597
Qy 599 FRFAEPVGISASGSGTAGISINNAAGRTFFDKIEFIPITATFAEYDLERAQAVNA 658
Db 598 FRFAEPVGISASGSGTAGISINNAAGRTFFDKIEFIPITATFAEYDLERAQAVNA 657
Qy 659 LFTNTPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLKVKYAKRLSDERNLLQD 718
Db 658 LFTNTPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLKVKYAKRLSDERNLLQD 717
Qy 719 PNFTSINKQPDFISTNEQSNFTSIHQSEHGWMGSENITIQEGNDVFKENYVTLPGTFNE 778
Db 718 PNFTSINKQPDFNSNNEQSNFTSIHQSEHGWMGSENITIQEGNDVFKENYVTLPGTFNE 777
Qy 779 CYPTLYQKIGSELKAYTRYQLRGVIEDSDLEIYLIRYNAKHETLDVPGTESVWPLSV 838
Db 778 CYPTLYQKIGSELKAYTRYQLRGVIEDSDLEIYLIRYNAKHETLDVPGTESVWPLSV 837
Qy 839 ESPIGRCGEPNRCAPHFENWPNLDCSCRDGEKCAHSHHFSLDIDIGCTDLHENLGVWV 898
Db 838 ESPIGRCGEPNRCAPHFENWPNLDCSCRDGEKCAHSHHFSLDIDIGCTDLHENLGVWV 897
Qy 899 FKIKTOEGHARLGNLEFIEBKPLLGALSRVKAEEKWRDKREKLQLETKRVVYTEAKEAV 958
Db 898 FKIKTOEGHARLGNLEFIEBKPLLGALSRVKAEEKWRDKREKLQLETKRVVYTEAKEAV 957
Qy 959 DALFVDSQYNRLQADTNIQMIHAADKLVRHREAYLSELVPGVNAEIFELEGRITTA 1018
```

Db 61 NIAGRILGVLPFAGQASFYSLVGLWPRGRDQWEIFLEHVEQINQOITENARNTA 120
 QY 121 LARLOGLGDSFRAYQOQSLDWNLRDARTSVLYTOYIALELDFNAMPLFAIRNOEVP 180
 Db 121 LARLOGLGDSFRAYQOQSLDWNLRDARTSVLYTOYIALELDFNAMPLFAIRNOEVP 180
 QY 181 LLMVYAAANLHLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSYCVWYNTGLN 240
 Db 181 LLMVYAAANLHLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSYCVWYNTGLN 240
 QY 241 SLRGTNAASWVRYNQFRDLTLGVLDLVALFPSYDTRTPINTSAQITREVVYDAIGATG 300
 Db 241 SLRGTNAASWVRYNQFRDLTLGVLDLVALFPSYDTRTPINTSAQITREVVYDAIGATG 300
 QY 301 VNMAWMNNYNNAPSFSAIETAVIRSPHLLDFLEQLTIFSTSSRWASATRMHTYWRGHTIQ 360
 Db 301 VNMAWMNNYNNAPSFSAIETAVIRSPHLLDFLEQLTIFSTSSRWASATRMHTYWRGHTIQ 360
 QY 361 SRPIGGGLNTSTHGSTNTSINPRLSPFSDRVYWTESYAGVLLWGIYLEPIHGVPTVRFN 420
 Db 361 SRPIGGGLNTSTHGSTNTSINPRLSPFSDRVYWTESYAGVLLWGIYLEPIHGVPTVRFN 420
 QY 421 FRNPQNTFERGTANYSQPYESPGQLKDSSETLPETTERPNYESYSHRSLHGLISQSR 480
 Db 421 FRNPQNTFERGTANYSQPYESPGQLKDSSETLPETTERPNYESYSHRSLHGLISQSR 480
 QY 481 VHPVYVSWTHRSADRNTTSSDSITQIPLVKSFNLSGTSVSGPGTGGDIIRTNVNGS 540
 Db 481 VHPVYVSWTHRSADRNTTSSDSITQIPLVKSFNLSGTSVSGPGTGGDIIRTNVNGS 540
 QY 541 VLSMGLNFNTSLQRYRVRYAASQTMVLRTVVGSTTFDQGPPTMSANESLTSQSPR 600
 Db 541 VLSMGLNFNTSLQRYRVRYAASQTMVLRTVVGSTTFDQGPPTMSANESLTSQSPR 600
 QY 601 FAEPVVCISAGSQTAGISISNNAGROTFFDKIEPIPTATPEAYDLERAQEVNALLP 660
 Db 601 FAEPVVCISAGSQTAGISISNNAGROTFFDKIEPIPTATPEAYDLERAQEVNALLP 660
 QY 661 TTNTPRLKTDVTDYHIDQVSNLVACLSDEFCDKRELEKVKYAKRLSDERNLLQDPN 720
 Db 661 TTNTPRLKTDVTDYHIDQVSNLVACLSDEFCDKRELEKVKYAKRLSDERNLLQDPN 720
 QY 721 FTSINKOPDFISTNEQSNFTSIHQESBGWGWSENITIQECNDVFKENYVTLPGTFNECY 780
 Db 721 FTSINKOPDFISTNEQSNFTSIHQESBGWGWSENITIQECNDVFKENYVTLPGTFNECY 780
 QY 781 PTLYQKIGESSELKAYTRYQLRGYIEDSDLEIYLIRYNKAKHETLDVPGTSEVWPLSVES 840
 Db 781 PTLYQKIGESSELKAYTRYQLRGYIEDSDLEIYLIRYNKAKHETLDVPGTSEVWPLSVES 840
 QY 841 PIGRCGEPNRCAPHFENPDLDCSRRGKCAHSHHFSLDIDIGCTDLHENLGVWVFK 900
 Db 841 PIGRCGEPNRCAPHFENPDLDCSRRGKCAHSHHFSLDIDIGCTDLHENLGVWVFK 900
 QY 901 IKTOEGHARLGNLEFIEBEKPLLGALSRVRAEKWRDKREKLQLETKRVYTAKEAVIDA 960
 Db 901 IKTOEGHARLGNLEFIEBEKPLLGALSRVRAEKWRDKREKLQLETKRVYTAKEAVIDA 960
 QY 961 LFVDSQYRNLQADNTNIGMHAADKLVRIRIYAVLSLSVTPGVNABIFEELEGRITTAIS 1020
 Db 961 LFVDSQYRNLQADNTNIGMHAADKLVRIRIYAVLSLSVTPGVNABIFEELEGRITTAIS 1020
 QY 1021 LYDARNVVKNGDFNGLACNVKGVHDVQOQSHRSVLVIVPEWEAEVSQAVRVCPCRGYIL 1080
 Db 1021 LYDARNVVKNGDFNGLACNVKGVHDVQOQSHRSVLVIVPEWEAEVSQAVRVCPCRGYIL 1080
 QY 1081 RVTAYKEGYEGGCVTIHEIENNTDELKFKNCBEEVYPTDGTGTCNDYTAHQGTAVCNRSN 1140
 Db 1081 RVTAYKEGYEGGCVTIHEIENNTDELKFKNCBEEVYPTDGTGTCNDYTAHQGTAVCNRSN 1140
 QY 1141 AGYEDAYEVDTTASVNYKPYEETTYDVRDHNHCEYDRGVYVPPPLPAGYMTKELEYFP 1200

Db 1141 AGYEDAYEVDTTASVNYKPYEETTYDVRDHNHCEYDRGVYVPPPLPAGYMTKELEYFP 1200
 QY 1201 ETDKWIETGETGKFIQVDSVELLMEE 1228
 Db 1201 ETDKWIETGETGKFIQVDSVELLMEE 1228
 RESULT 2
 US-10-428-961-38
 ; Sequence 38, Application US/10428961
 ; Publication No. US20030237111A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baum, James A.
 ; APPLICANT: Chu, Chih-Rei
 ; APPLICANT: Donovan, William P.
 ; APPLICANT: Gilmer, Amy J.
 ; APPLICANT: Ruper, Mark J.
 ; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
 ; FILE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
 ; CURRENT FILING DATE: 2003-05-02
 ; PRIOR APPLICATION NUMBER: US/10/428,961
 ; PRIOR FILING DATE: 2000-09-13, 322
 ; PRIOR APPLICATION NUMBER: 60/153,995
 ; PRIOR FILING DATE: 1999-09-15
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: Patent in version 3.2
 ; SEQ ID NO 38
 ; LENGTH: 1228
 ; TYPE: PRT
 ; ORGANISM: Bacillus thuringiensis
 US-10-428-961-38
 Query Match 99.8%; Score 6464; DB 15; Length 1228;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1224; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 LTSNRKNEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVASTVQTGI 60
 Db 1 LTSNRKNEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVASTVQTGI 60
 QY 61 NIAGRILGVLPFAGQASFYSLVGLWPRGRDQWEIFLEHVEQINQOITENARNTA 120
 Db 61 NIAGRILGVLPFAGQASFYSLVGLWPRGRDQWEIFLEHVEQINQOITENARNTA 120
 QY 121 LARLOGLGDSFRAYQOQSLDWNLRDARTSVLYTOYIALELDFNAMPLFAIRNOEVP 180
 Db 121 LARLOGLGDSFRAYQOQSLDWNLRDARTSVLYTOYIALELDFNAMPLFAIRNOEVP 180
 QY 181 LLMVYAAANLHLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSYCVWYNTGLN 240
 Db 181 LLMVYAAANLHLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSYCVWYNTGLN 240
 QY 241 SLRGTNAASWVRYNQFRDLTLGVLDLVALFPSYDTRTPINTSAQITREVVYDAIGATG 300
 Db 241 SLRGTNAASWVRYNQFRDLTLGVLDLVALFPSYDTRTPINTSAQITREVVYDAIGATG 300
 QY 301 VNMAWMNNYNNAPSFSAIETAVIRSPHLLDFLEQLTIFSTSSRWASATRMHTYWRGHTIQ 360
 Db 301 VNMAWMNNYNNAPSFSAIETAVIRSPHLLDFLEQLTIFSTSSRWASATRMHTYWRGHTIQ 360
 QY 361 SRPIGGGLNTSTHGSTNTSINPRLSPFSDRVYWTESYAGVLLWGIYLEPIHGVPTVRFN 420
 Db 361 SRPIGGGLNTSTHGSTNTSINPRLSPFSDRVYWTESYAGVLLWGIYLEPIHGVPTVRFN 420
 QY 421 FRNPQNTFERGTANYSQPYESPGQLKDSSETLPETTERPNYESYSHRSLHGLISQSR 480
 Db 421 FRNPQNTFERGTANYSQPYESPGQLKDSSETLPETTERPNYESYSHRSLHGLISQSR 480
 QY 481 VHPVYVSWTHRSADRNTTSSDSITQIPLVKSFNLSGTSVSGPGTGGDIIRTNVNGS 540
 Db 481 VHPVYVSWTHRSADRNTTSSDSITQIPLVKSFNLSGTSVSGPGTGGDIIRTNVNGS 540

seq id no 63 in the provided

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 21, 2005, 04:10:31 ; Search time 1515 Seconds
(without alignments)
269.747 Million cell updates/sec

Title: US-10-614-524-2

Perfect score: 6479

Sequence: 1 LTSNRKNEIINALSIPAV.....IGTEGKFIVDSVELLMEE 1228

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1424015 seqs, 332791073 residues

Total number of hits satisfying chosen parameters: 1424015

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubppa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubppa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubppa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubppa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubppa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubppa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubppa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubppa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubppa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubppa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubppa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubppa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubppa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubppa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubppa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubppa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubppa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubppa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6479	100.0	1228	15	US-10-614-524-2
2	6464	99.8	1228	15	US-10-428-961-38
3	5912.5	91.3	1227	15	US-10-428-961-63
4	5745	88.7	1228	17	US-10-926-819-8
5	5742	88.6	1228	16	US-10-809-953-10
6	5659.5	87.4	1207	10	US-09-988-462-7
7	5108	78.8	1186	9	US-09-826-660-23
8	3502.5	54.1	1189	14	US-09-972-175-59
9	3502.5	54.1	1189	14	US-10-200-522-59
10	3500.5	54.0	1189	14	US-09-972-175-2
11	3500.5	54.0	1189	14	US-10-200-522-2
12	3496.5	54.0	1189	14	US-09-972-175-61
13	3496.5	54.0	1189	14	US-10-200-522-61

14	3495.5	54.0	1189	16	US-10-782-020-7	Sequence 7, Appli
15	3495.5	54.0	1189	17	US-10-926-819-9	Sequence 9, Appli
16	3494.5	53.9	1189	10	US-09-972-175-4	Sequence 4, Appli
17	3494.5	53.9	1189	10	US-09-972-175-6	Sequence 6, Appli
18	3494.5	53.9	1189	14	US-10-200-522-4	Sequence 4, Appli
19	3494.5	53.9	1189	14	US-10-200-522-6	Sequence 6, Appli
20	3493.5	53.9	1189	10	US-09-972-175-12	Sequence 12, Appli
21	3493.5	53.9	1189	14	US-10-200-522-12	Sequence 12, Appli
22	3490.5	53.9	1189	10	US-09-972-175-8	Sequence 8, Appli
23	3490.5	53.9	1189	14	US-10-200-522-8	Sequence 8, Appli
24	3487.5	53.8	1189	10	US-09-972-175-10	Sequence 10, Appli
25	3487.5	53.8	1189	14	US-10-200-522-10	Sequence 10, Appli
26	3482.5	53.8	1189	16	US-10-809-953-8	Sequence 8, Appli
27	3479.5	53.7	1189	14	US-10-102-469-20	Sequence 20, Appli
28	3476.5	53.7	1189	11	US-09-837-961-6	Sequence 6, Appli
29	3476.5	53.7	1189	16	US-10-825-751-6	Sequence 6, Appli
30	3463	53.4	1181	10	US-09-988-462-11	Sequence 11, Appli
31	3463	53.4	1181	10	US-09-988-462-13	Sequence 13, Appli
32	3463	53.4	1181	10	US-09-988-462-17	Sequence 17, Appli
33	3463	53.4	1181	10	US-09-988-462-28	Sequence 28, Appli
34	3463	53.4	1181	15	US-10-136-998A-4	Sequence 4, Appli
35	3463	53.4	1181	15	US-10-136-998A-8	Sequence 8, Appli
36	3463	53.4	1181	15	US-10-136-998A-10	Sequence 10, Appli
37	3463	53.4	1181	15	US-10-136-998A-12	Sequence 12, Appli
38	3460	53.4	1193	9	US-09-873-873-30	Sequence 30, Appli
39	3460	53.4	1193	10	US-09-916-956A-30	Sequence 30, Appli
40	3460	53.4	1193	10	US-09-997-914-30	Sequence 30, Appli
41	3460	53.4	1193	14	US-10-365-645-30	Sequence 30, Appli
42	3460	53.4	1193	15	US-10-672-163-30	Sequence 30, Appli
43	3460	53.4	1193	16	US-10-739-482-30	Sequence 30, Appli
44	3460	53.4	1193	16	US-10-817-182-30	Sequence 30, Appli
45	3459	53.4	1177	9	US-09-873-873-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1

US-10-614-524-2
; Sequence 2, Application US/10614524
; Publication No. US20040016020A1
; GENERAL INFORMATION:
; APPLICANT: Arnaut, Greta
; APPLICANT: Boets, Annemie
; APPLICANT: Damme, Nicole
; APPLICANT: Mathieu, Eva
; APPLICANT: Vanneste, Stijn
; APPLICANT: Van Rie, Jeroen
; TITLE OF INVENTION: Insecticidal proteins from Bacillus thuringiensis.
; FILE REFERENCE: NEWBTSUS2
; CURRENT APPLICATION NUMBER: US/10/614,524
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US/09/739,243
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/173387
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1228
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-614-524-2

Query Match 100.0%; Score 6479; DB 15; Length 1228;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	LTSNRKNEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVASTVQTGI	60
Db	1	LTSNRKNEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVASTVQTGI	60
Qy	61	NIAGRILGLGVPPAGQIAFYFLVGEIWPGRDQWEIFLEHVQLINQOITENARNTA	120